STIC-Biotech/ChemLib

From: Sent:

Chan, Christina

Tuesday, November 05, 2002 9:32 AM

To: Subject: Helmer, Georgia; STIC-Biotech/ChemLib RE: Please Rush Sequence Search-09/782,874-- Point of Contact:

Mona Smith **Technical Information Specialist**

CM1 6A01 Tel: 308-3278

Please rush. Thanks Chris

Chris Chan TC 1600 New Hire Training Coordinator and SPE 1644 308-3973 CM-1, 9B19

----Original Message-----From: Helmer, Georgia

Sent: Monday, November 04, 2002 6:24 PM Chan, Christina

Subject:

Please Rush Sequence Search-09/782,874--

Could you please do a sequence search and an oligo search on SEQ ID No 1 and 2?

On the results for the oligo searches, could you please print out more of the results? Like up to the first 50?

This is for the inhouse and commerce data bases. (no intererence search though)

I need this case for this biweek.

Thanks in advance, Georgia L. Helmer Ph.D. **Patent Examiner** Crystal Mall 1, 9D14 AÚ 1638 703-308-7023 Georgia.Helmer@USPTO.gov

6 contra parties

Searcher: M. Sm 774
Phone:
Location:
Date Picked Up: 11を4/02 Date Completed: 11 do10 2
Date Completed: 11 dol 0 2
Searcher Prep/Review: 10
Clerical:
Online time: 15

TYPE OF S	SEARCH:	
NA Sequences:_		
AA Sequences:_	2	
Structures:		
Bibliographic:		
Litigation:		
Full text:	<u></u> _	
Patent Family:		
Orboniu		

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

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November 5, 2002, 19:16:42; Search time 142 Seconds (without alignments) 8057.824 Million cell updates/sec
                                                                                                                                                                                                 1 GAAATATTCTTTACTTACTT......AGTTTCATCTTCTAAA 3731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                      441362 seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                 OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                    US-09-782-874-1
3731
                                                                                                                                                                  Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                                                                                        Searched:
                                                                                                   Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	નેને	14,		Sequence 2, Appli Sequence 2, Appli	Sequence 14,	194 Sequence 194, App Sequence 1, Appli	342	4	4	Sequence 19,	19	Sequence 17,	17	'n	'n	Sequence 6, Appli	ώ	ť	'n	22	4	'n	Sequence 3, Appli
OI	-08-811-583-	-080	-08-676-967	US-08-676-974-2 US-09-098-487-2	-08-232-463-	US-08-936-165A-1 US-09-415-946-1	-09-134-	8-91	-09-182-	-08-911-445-1	-182-983-1	-08-911-445-1	-09-182-	8-911-4	-09-182-9	-08-911-445-	-09-182-9	-463-4	-09-754-2	S-08-858-207A-	US-09-345-882-4	-08-961-5	US-08-991-677-3
Length DB	3731 4 906 1	7218 1	,	2277 1 2277 2	•	3191 4 17341 4	1248 4	1275 2	1275 4	1458 2	1458 4	1796 2	7	1845 2	1845 4	• •	9	5613	28	1028 4	9	19446 4	88
% Query Match	100.	Н.	ii -	<u> </u>	۲,		6.0	6.0							•								
Score	3731	m	0	36.8	9	o vo	35	35	35	35	35	35	35		35	35	35	35	35	•		34.8	34.6
Result No.	0	ი ო 4	·w	9 2	ω (ი 10	11	12	13	14	15	16	17	18		20			23	24	25	26	27

; NAME_KEY: CDS ; LOCATION: 194..3535 US-08-811-583-1

FEATURE:

Sequence 86, Appl Sequence 62, Appl Sequence 395, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 3, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 3, Appl Sequence 2, Appl Sequence 3, Appl Sequence 2, Appl Sequence 3, Appl Sequence 2, Appl Sequence 2, Appl Sequence 26, Appl Sequence 26, Appl Sequence 26, Appl Sequence 1983, Appl Sequence 1984,	ES ENCODING THE ENZYMATIC ACTIVITY OF AN YMERASE (RGRP) On #1.30
4 US-09-064-838-62 3 4 US-09-004-838-62 4 1 US-09-221-017B-39; 4 1 US-08-465-995A-1 4 2 US-08-465-995A-1 6 1 US-08-145-1 0 1 US-08-145-1 0 1 US-08-145-1 0 4 US-09-345-882-21 9 4 US-09-347-557-3 9 4 US-09-134-010-16; 1 US-08-118-101A-1 3 4 US-08-118-101A-1 3 4 US-08-118-101A-1 3 5 PCT-US95-02708-3 6 3 US-08-70-755-3 6 3 US-08-70-756-3 6 4 US-08-118-101A-1 7 US-08-118-101A-1 8 US-08-118-101A-1 9 5 PCT-US95-02708-3 6 3 US-08-70-758-3 6 4 US-08-70-758-3	ALIGNMENTS 583 ael d ACID MOLECUI IDES HAVING CTED RNA POI S-DOS i #1.0, Versi #1.0, Versi #1.1,583
34.6 0.9 1939 34.4 0.9 738 34.2 0.9 2694 34.2 0.9 2694 34.2 0.9 2694 34.2 0.9 2694 34.2 0.9 2694 33.8 0.9 1867 33.6 0.9 1867 33.6 0.9 1023 33.6 0.9 1939 33.4 0.9 1939 33.4 0.9 1939 33.4 0.9 1939	Application 65,18142 FORMATION: THE WASSENGED THE SANGET. THYOTHION: THYOT
0 0 0 0000 0 0 0 0000 0 0 0 0 0 0 0 0 0	RESULT 1 Sequence 1, Sequence 1, Sequence 1, Septence 1, Septence 1, APPLICAN APPLIC

a a	2101	TGATICITIGAAGGCACAGGGGGCTIIGGAATIGATGTCTCCTGGAGAACACACTAATAI 2160	
QY	216ì 2161	. TCTCAAGGCAATGCTAAACTGTGGTTATAAGCCTGATGCTGAGCCCTTTCTTT	
QY Db	2221	GITGCAAACCITCCGCGCATCCAAGTIGCTCGATITGCGGACTAGATCAAGAAIATTAT 2280 	
Qy Db	2281	TCCAAATGGAAGAACAATGATGGGATGTTTGGATGAATCCAGAACCTTGGAATATGGTCA 2340	
QY Db	2341	GGTGTTTGTTCAGTTTACTGGTGCTGGACATGGAGAGTTTTCTGACGATTTACATCCATT 2400	
QY Db	2401	TAATAACAGCAGATCCACCAACAGTAATTTCATTCTGAAGGGAAATGTGGTTGTTGCAAA 2460 	
Oy Dp	2461	AAATCCATGCTTGCATCCTGGTGATATTCGTGTTTTAAAGGCTGTAAATGTTCGAGGGCT 2520	
QY Dp	2521	GCACCACATGGTAGATTGTGTTGTATTCCCTCAGAAAGGAAAAAAGACCTCATCCGAATGA 2580 	
QY	2581	AIGITCIGGGAGIGATTIGGAIGGGGATAICIACITTGITTGCIGGGAICAAGACAIGAI 2640 	
දුරු පු	2641	CCCGCCAAGGCAAGTCCAGCCGATGGAATATCCTCCAGCACCCAGCATACAGTTGGACCA 2700	
QY Dp	2701	TGATGICACAATTGAGGAAGTTGAAGAGTACTTCACCAACTATTGTGAATGACAGTTT 2760 	
40 0	2761 2761	GGGAATCATAGCAAATGCCCATGTCGTATTTGCAGACAGGAACCTGATATGGCCATGAG 2820 	
QY Db	2821	TGATCCATGCAAAAAACTTGCTGAGCTCTTTTCAATTGCAGTGGACTTTCCAAAGACTGG 2880 	
OY Db	2881	IGTICCGGCTGAAATACCAICTCAGTIGCGCCCTAAAGAATACCCAGACTICATGGATAA 2940 	
Oy Dp	2941	GCCGGACAAGACCAGCTATATCTCAGAAAGAGTTATTGGAAAGCTTTTCAGGAAAGTGAA 3000 	
Q.y D.b	3001	GGACAAAGCACCTCAGGCTAGCTCTATCGCGACCTTCACAAGAGATGTTGCAAGGAGTC 3060 	
0.y Db	3061	ATATGATGCTGATATGGAAGTTGATGGATTTGAAGATTGCATTGACGAAGCTTTTGACTA 3120 	
OY Db	3121	CAAAACTGAATATGACAACTGGGTAATTTAATGGACTACTATGGCATAAAAACAGA 3180 	
Qy Dp	3181	GGCTGAAATACTTAGTGGTGGCATTATGAAGGCATCAAAACTTTTGACCGCAGAAAAG 3240 	

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3421 TCCCTGGTGTGTTTATGACCAGCTAATCCAGATTAAGAAGGACAAAGCACGTAACAGGCC 3480
                                                                                                                                                                                                                                                                                                3481 AGTTCTCAACTTGTCATCTCTCAGGGCTCAACTGAGTCACAGATTAGTGTTGAAATGAGA 3540
                                                                                                                                                                                                                                                                                                                  3541 TTCCAGTCGAGCGTTAAGCTGATATATATATGTAATAGGGTGTGTGATCATAAGAAAAC 3600
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                                                                                          3421 TCCCTGGTGTGTTTATGACCAGCTAATCCAGATTAAGAAGGACAAAGCACGTAACAGGCC 3480
3361 TCATCCTACATATTGGGGTTGCTACAATCAGGGGTTGAAAAGAGCTCATTTCATTAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTTATGCATTGTTGACTACCTTTTGTCTTTAAAACTGCATGAAGCTGCAACATATATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Takesawa, D. APPLICANT: Takesawa, D. APPLICANT: Takesawa, D. APPLICANT: Takesawa, T. J. APPLICANT: Han, T. J. APPLICANT: An, G. H. TITLE OF INVENTION: Control of Growth and Development of TITLE OF INVENTION: Potato Plants
CORRESPONDENCE ADDRESS: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RCT-SS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/10, 874
FILING DATE: UJ/2, 30, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harness, Dickey & Pierce
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US-08-100-874-1/c
'Sequence 1, Application US/08100874
'Patent No. 5498533
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: (800
ATTORNEY/AGENT INFORMATION:
NAME: Smith, DeAnn F.
REFERENCE/DOCKET VUNBER;
TELECOMMUNICATION INFORMATION:
TELEFRAN: (313) 641-1600
TELER: 287637 Harness UR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Harness, Dic
STREET: P.O. Box 828
CITY: Bloomfield Hills
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TOPOLOGY:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEE: Foley & Lardner
: 1800 Diagonal Road, Suite 500
Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #35
APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 304
TELECOMMUNICATION INFORMATION:
                                                                                                                                                            ORGANISM: Solanum tuberosum
INDIVIDUAL ISOLATE: p-PCM-1
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (703)836-9300
(703)683-4109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 899149
INFORMATION FOR SEQ ID NO: 1.
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                              LENGTH: 906 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
IDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 81..530
                                                                                                           CDNA
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                                                                                       TOPOLOGY: li
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-232-463-14/c
                                                                                                                          HYPOTHETICAL:
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                                                                                                                                                                                                                               ; LOCATION:
US-08-100-874-1
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                                                                                                                                                              ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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APPLICANT: Bouguelert, Lydie

TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTONA BINDING PROTEIN (RBP-
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
FILE REFERENCE: GENSET.031A
                                                                                                                                                                                                                                                                                                                                                                                                                                        3207 IGAAGGCATCAAAAACTTTTGACCGCAGAAAAGATGCTGAGGCCCATTAGTGTTGCTGTGA 3266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3267 GGGCCTTGAGGAAGGAGGCAAGAGCCTGGTTCAAGAGGCGTAATGATATAGATGACATGT 3326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3027 TCGCGACCTTCACAAGAGATGTTGCAAGGAGATCATATGATGCTGATATGGAAGTTGATG 3086
                                                                                                                                                                                                                                                                                                                                                         3087 GATTTGAAGATTACATTGACGAAGCTTTTGACTACAAAACTGAATATGACAACAAGCTGG 3146
                                                                                                                                                      0; Gaps
                                                                                                   Ouery Match 1.4%; Score 53.4; DB 1; Length 7218; Best Local Similarity 5.2%; Pred. No. 5.6e-05; Matches 21; Conservative 219; Mismatches 165; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or
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CURRENT FILING DATE: 1999.06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-16-310
PRIOR FILING DATE: 1998-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09345882
Patent No. 6399373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 162450
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; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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LOCATION: 72794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: allele
LOCATION: 88073
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LOCATION: 90842
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US-09-345-882-1
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	GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.	
OM protein - prot	OM protein - protein search, using sw model	
Run on: N	November 6, 2002, 03:33:33 ; Search time 142 Seconds (without alignments) 1616.454 Million cell updates/sec	
Title: Perfect score: 1 Sequence: 1	US-09-782-874-2 1114 1 MGKTIQVFGFPYLLSABVVKRPVLNLSSLRAQLSHRLVLK 1114	
Scoring table: 0	OLIGO Gapop 60.0 , Gapext 60.0	
Searched: 6	671580 seqs, 206047115 residues	
Word size :		
Total number of h	Total number of hits satisfying chosen parameters: 671580	
Minimum DB seq length: 0 Maximum DB seq length: 200000000	gth: 0 igth: 2000000000 .	
Post-processing:	Post-processing: Listing first 50 summaries	

SPTREMBL_21:*

1: Sp_archea:*
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3: Sp_fungi:*
4: Sp_human:*
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8: Sp_organelle:*
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16: Sp_bacteriap:*
17: Sp_archeap:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Q97es6 clostridium Q95zs5 caenorhabdi	Q9cu85 mus musculu	Q9sp43 citrus unsh	Q9dg87 carassius a	Q9iat4 carassius a	Q9y232 homo sapien	Q96yh3 sulfolobus	rabido	096064 mytilus gal	γç	Q96s73 homo sapien	homod	-14	chla	U		Q95zg6 dictyosteli	corynebact		Q9gkj9 sus scrofa	Q9hb48 homo sapien	anabaena	mytilus	mytilus	mytilus	mytilus	mytilus	mytilus	mytil	lovis arie	9 salm	nt43 h	ll rhiz
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ALIGNMENTS

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T 1 992R58 PRELIMINARY; PRT; 1114 AA. 902R58; 01-MAY-1999 (TEMBLrel. 10, Last sequence update) 01-MAY-1999 (TEMBLrel. 10, Last sequence update) 01-MAY-1999 (TEMBLrel. 11, Last annotation update) 01-JUN-2002 (TEMBLrel. 21, Last annotation update) 01-JUN-2002 (TEMBLrel. 21, Last annotation update) 01-JUN-2002 (TEMBLrel. 21, Last annotation update) 02-JUN-2002 (TEMBLrel. 21, Last annotation update) NRA-directed RNA polymerase (BC 2.7.7.48). Lycopersicon esculentum (Tomato). Lycopersicon esculentum (Tomato). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Separatophyta; Magnoliophyta; endicotyledons; core endicots; NSELTAIN-RUTGERS; NNELINE-9055198; Pubmed-9836747; STRAIN-RUTGERS; SCHIEDEL W., Pelissier T., Riedel L., Thalmeir S., Schiebel R., Kempe D., Lottspeich F., Sanger H.L., Wassenegger M.; Finsolation of an RNA-directed RNA polymerase-specific cona clonato. InterPro; IPRO00504; RNA_rec_mot. InterPro; IPRO00504; RNA_rec_mot. InterPro; IPRO0055; RRM_2: InterPro; IPRO0055; RRM_2: InterPro; IPRO0055; RRM_2: INA-GIENCE RNA polymerase; Transferase. SEQUENCE II14 AA; 126807 WW; B6D30ACD41DB37FF CRC64;	DB 10; Length 1114; 0; Indels 0;
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T 1 922258 PRELIMINARY; PRT; 1114 AA. 922258 01-MAY-1999 (TEMBLEel. 10, Created) 01-MAY-1999 (TEMBLEel. 10, Last sequence update) 01-MAY-1999 (TEMBLEel. 11, Last sequence update) 01-UNN-2002 (TEMBLEel. 21, Last sequence update) 01-UNN-2002 (TEMBLEel. 21, Last sequence update) 01-MAY-1999 (TEMBLEel. 21, Last sequence update) 01-MAY-1999 (TEMBLEel. 21, Last sequence update) RNA-directed RNA polymerase (EC 2.7.7.48). EUNOPERSION NA ENGRET (TOMBLE) NOBL TAXID=4081; 11 11 SECUENCE FROM N.A. STRAIN=RUTGERS; SCHIEGE (TOMBLEE) STRAIN=RUTGERS; THAN Adirected RNA POLYMERASE-SPECIFIC CD Plant Cell 10:2087-2102(1998). ENDED: Y10403; CARA/1421.1; TOMBLE (TOMBLEE) INTERPRO 1 PRO00559; RRM_2. INTERPRO 1 PRO00559; RRM_2. INTERPRO 1 PRO00559; RRM_2. SMART; SWO0365; RRM_2. SKART; SWO0365; RRM_2. SKART; SWO0365; RRM_2. SKART; SWO0365; RRM_2. SKART; SWO0365; RRM_2. NUCLEOCIGUILEARSFERSE; RNA-directed RNA POLYMERSE; Tra SKEQUENCE 1114 AA; 12680; MW; B6D30ACD41DB37FF CRC64;	Query Match Best Local Similarity 100. Matches 1114, Conservative
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Nicotiana tabacum (Common tobacco).

Subaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Nicotiana.
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NCBI_TaxID=4102;
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STRAIN-CV. PETIT HAVANA SRI; TISSUB-LEAF;
Schiebel W., Pelissier T., Riedel L., Thalmeir S., Schiebel R.,
Kempe D., Lottspeich F., Saenger H.L., Wassenegger M.;
"Isolation of an RNA-directed RNA polymerase-specific cDNA clone
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ISSUB-LEAF;
Schiebel W., Pelissier T., Riedel L., Thalmeir S., Schiebel Kempe D., Lottspeich F., Saenger H.L., Wassenegger M.;
Isolation of an RNA-directed RNA polymerase-specific cDNA of Tomato.";
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EMBL, AJ011979; CAA09896.1; --
RNA-directed RNA polymerase.
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STRAIN-EV. COLUMBIA: TISSUE-LEAF;
SCHiebel W., Pelissier T., Riedel L., Thalmeir S., Schiebel R.,
Kempe D., Lottspelch F., Saenger H.L., Wassenegger M.;
"Isolation of an RNA-directed RNA polymerase-specific cDNA clone from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress),
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots; Rosidae, eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tomato.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ011977; CAA09894.1;
RNA-directed RNA Polymerase.
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to the EMBL/GenBank/DDBJ databases
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513 AA; 57802 MW; 924FDA2B70EDAE0E CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                            Last sequence update)
Last annotation update)
ALHHMYDCVVFPQKGKRPHPNECSGSDLDGDIYFVCWD
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                                                                                                                                                                                                                                      RNA-directed RNA polymerase (Fragment).
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les 23; Conservative
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Matches
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DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NAR-2002 (TrEMBLrel. 20, Last sequence update)
DF 52P3.11 protein (Putative RN-directed RNA polymerase).
GN F2P3.11 OR T22B4.110 OR AT401130.
OS Arabidopsis thaliana (Mouse-ear cress).
CLEMARYOTA, VIIIdiplantae, Streptophyta; Embryophyta; Tracheophyta;
CC Eukaryota, VIIIdiplantae, Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
CC Spermatophyta; Brassicaceae; Arabidopsis.
CC NCBL_TAXID=3702;
CC STREATED=3702;
CC STREATED
SEQUENCE FROM N.A.

Cheuk R., Shinn P., Berooks S., Buehler E., Chao O., Johnson-Hopson C.,

Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,

Conn L., Conway A., Gorzalez A., Hansen N., Howing B., Koo T., Lam B.,

Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,

Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,

Theologis A., Torium M., Vaysberg M., Yu G., Davis R., Federspiel N.,

Theologis A., Ecker J.,

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AC006917, AAP, 126214 MW, F8FF97691FF82187 CRC64;
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Schiebel W., Palissier T., Riedel L., Thalmeir S., Schiebel R.,
Kempe D., Lottspeich F., Saenger H.L., Wassenegger M.;
"Isolation of an RNA-directed RNA polymerase-specific cDNA clone from
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae, Pooldeae,
Triticeae, Triticum.
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100.0%; Pred. No. 7.2e-11;
tive 0; Mismatches 0; Indels
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EMBL: AJ011978; CAA09895.1; -.
RNA-directed RNA polymerase.
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1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RNA-directed RNA polymerase (Fragment).
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1.9e-15;
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Query Match 1.1
Best Local Similarity 100.
Matches 12; Conservative
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les 12; Conserv
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LD 095WU
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Q9LKP0
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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STRAN=CV. COLOMBIA.
STRAN=CV. COLOMBIA.
Maiti R., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D., Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Fu Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.; "Arabidopsis thaliana chromosome 1 BAC TIG12 genomic sequence."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF080120; AAC35353.1;
EMBL; AL049876; CAB43048.1;
EMBL; AL16531; CAB81214.1;
Nucleotidyltransferase; RNA directed RNA polymerase; Transferase.
SEQUENCE 1133 AA; 129323 MW; 32B72C4E429B20B9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1133;
                                                                                                                                                                                                                                                                                                                                                                                                     Bevan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.W.,
Mayer K.F.X., Schueller C.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                  Sequencing Project.";
the EMBL/GenBank/DDBJ databases.
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                                                                                                                             SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
Strong C., Graves T., Duckels G.;
"The sequence of A. thaliana F2P3.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Waterston R.,
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EU Arabidopsis sequencing project;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Putative RNA-directed RNA polymerase.
TIG12.20 OR T9C3.95.
Arabidopsis thaliana (Mouse-ear cress).
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tive 0;
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                                                                  "The A. thaliana Genome
Submitted (SEP-1998) to
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SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
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SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA,
MULTIAL P., SOLIDA C., CLIDMAYAN T., Feuerbach F., Godon C.,
MULTIAL P., Sanial M., Vo T.-A., Vaucheret H.;
Remoue K., Sanial M., Vo T.-A., Vaucheret H.;
Remoin and Natural Virus Resistance.";
Cell 101:533-542(2000),
REMBI, AC012329; Ad622184.1; -.
REMBI, AL239718; Ad622184.1; -.
REMBI, AL239718; ARF73959.1; -.
REMBI, ARZ39718; ARF73959.1; -.
RWW Adirected RNA Polymerase.
SQUENCE 1196 AA; 136927 MW; 812DEB9CEDC82C8F CRC64;
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Eukaryota, Viridiphantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brasicales; Brassicaceae; Arabidopsis.
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MEDLINE=20306669; PubMed=10850496;
Dalmay T., Hamilton A., Rudd S., Angell S., Baulcombe D.C.;
MAR RNA dependent RNA polymerase gene in Arabidopsis is required for posttranscriptional gene silencing mediated by a transgene but not by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
RNA-dependent RNA-polymerase.
Glardia lamblia (Glardia intestinalis).
Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Glardia.
NCBI_TaxID=5741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Doscue a virus."; cell 101:543-553(2000).
Cell 101:543-553(2000).
RMBL, AF268093; AAF74208.1; -.
RNR-directed RNR polymerase.
""AntenCE 1196 AA; 136747 MW; C1B1961CDC11F708 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RNA-dependent RNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Le
. 0.0028;
ches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.1%; Score 12; DB 100.0%; Pred. No. 0.0 tive 0; Mismatches
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Query Match 0.8
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                     797 CSGSDLDGD 805
                                                                                                                                                                                   274 CSGSDLDGD 282
                                                                                                                                                                                                                                                                                                                                              Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    485 AKYAARLGQ 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     653 AKYAARLGO 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Closterovirus.
NCBI_TaxID=64003;
NCBI_TaxID=44689;
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039857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                           Gaps
                       Lujan H.D.; "Identification of an RNA-dependent RNA-polymerase gene in glardia intestinalis.";
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                                                                                                                                                                                                                                                                                                                                                  Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobactériaceae; Methanothermobacter.
NCBI_TaxID=187420;
                                                                                                                                 0.9%; Score 10; DB 5; Length 1377;
100.0%; Pred. No. 0.51;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 17; Length 583; . 2.9;
                                                      Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF293414; AAK97084.1; ...
InterPro; IPR001865; Ribosomal_S2.
PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
SEQUENCE 1377 AA; 155267 WW; 7453D8646261A0B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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InterPro: IPR01365; A/AMP_deaminase.
PROSITE; PS00485; A_DEAMINASE; UNKNOWN_1.
Hypothetical protein; Complete proteome;
SEQUENCE 583 AA; 66088 WW; A267B146F0EA6B7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium
                                                                                                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
MYPOChetical protein WTH500.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
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                                                                                                                                                                                                                                                                      583 AA
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100.0%; Pred. No. 2.9
ative 0; Mismatches
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                680 SGSDLDGDIY 689
                                                                                                                                                                                 798 SGSDLDGDIY 807
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[1]
SEQUENCE FROM N.A.
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Q9XYP1;
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Q9XYP1
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026600
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 RR RA RA DR DR DR DR DR SS
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SEQUENCE FROM N.A.
Postlethwait P., Steck T.L.;
Postlethwait P., Steck T.L.;
Postlethwait P., Steck T.L.;

Discoideum.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

EMBL, AF117611; AAD129638.1;
EMBL, AF117611; AAD129638.1;
SEQUENCE 1069 AA; 122832 MW; BE6815D3869AICIC CRC64;
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grapevine leafroll-associated virus 2.
Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
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SEQUENCE FROM N.A.

Abou-Ghanem N.;

"The nucleotide sequence of the 3'terminal region of grapevine

leafroll associated closterovirus 2.";

Submitted (JAN-1998) to the EMBL/GenBank/DDBU databases.

EMBL; Y14131; CAA74566.1;

EMBL; Y14131; CAA74566.1;

EMBL; P1131; CAA74566.1;

EMBL; P1185; Closter_coat.

SEQUENCE 198 AA; 21630 MW; 15D631E408BD3F01 CRC64;
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Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                  Length 1069;
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SEQUENCE FROM N.A.
Shiu P.K.T., Raju N.B., Metzenberg R.L.;
Shiu P.K.T., Raju N.B., Metzenberg R.L.;
Majotic Silencing of Unpaired DNA.',
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY029284; AAK11733.1;
InterPro: IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 184233 MW; 7BC58EA66373D9BE CRC64;
SEQUENCE 1638 AA; 184233 MW; 7BC58EA66373D9BE CRC64;
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01-JUN-2001 (TIEMBLIEL: 17, Created)
01-JUN-2001 (TIEMBLIEL: 17, Last sequence update)
01-JUN-2002 (TIEMBLIEL: 17, Last sequence update)
01-JUN-2002 (TIEMBLIEL: 21, Last annotation update)
SUPPLESSOR of ascus dominance.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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100.0%; Pred. No. 7.6;
ative 0; Mismatches
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100.0%; Pred. No. 5.1;
tive 0; Mismatches
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REC STEALN—ATCC 824 DSM 792 / VKM B-1787;

REC STEALN—ATCC 824 DSM 792 / VKM B-1787;

RED MEDLING—21359325; PubMed-11466286;

RA Glbson R. J. Breton G., Omelchenko M.V. Makarova K.S., 2eng Q.,

RA Glbson R. J. Sabathe F., Doucettee Stamm L., Soucaille P., Daly M.J.,

RA Tatusov R. L., Sabathe F., Doucettee Stamm L., Soucaille P., Daly M.J.,

RA Bennett G.N., Koonin E.V., Smith D.R.;

Benome sequence and comparative analysis of the solvent-producing

RT Genome sequence and comparative analysis of the solvent-producing

RT Decterion 183:4823-4838(2001).

BRI. AE007800; AAK80971.1;

CHECPIO: IPRO0185; Aminotransf1/2.

RICHEPRO: IPRO0185; Aminotransf1/2.

RTGREAMS; TICSR01141; hisc: 1.

PROSITE; PS00399; AA_TRANSFER_CLASS_2; UNKNOWN_1.

PROSITE; PS00399; AA_TRANSFER_CLASS_2; UNKNOWN_1.

PROSITE; PS00399; AA_TRANSFER_CLASS_2; COMPLEDECGECE CRC64;

SEQUENCE 352 AA; 40220 MW; 3375021EBECGECE CRC64;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Clostridiales; Clostridiaceae; Clostridium.
NCBI_TaxID=1488;
Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
"Nucleotide sequence and predicted functions of the entire
Sinchizoblum mellioti pSymA megaplasmid.";
Binchizoblum mellioti pSymA megaplasmid.";
EMBL: AE007292; AAK65723.1; -.
InterPro; IPR000620; DUF6.
Flam; PF00892; DUF6; 1.-
Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 286 AA; 30992 MM; 4D8CC747B026FDA4 CRC64;
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0.7%; Score 8; DB 16; Length 352;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels
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0.7%; Score 8; DB 16; Length 286;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels
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01-0cT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2002 (TrEMBLrel. 21, Last annotation update)
Histidinol-phosphate aminotransferase.
CAC3031.
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Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
F56A8.3a protein.
Caenorhabditis elegans.
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SEQUENCE FROM N.A.
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251 SKLLDLRT 258
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Q952S5;
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Q97ES6
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Q952S5
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Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,

Barloy-Hubler F., Bowser L., Capela D., Gallbert F., Gouzy J.,

Barloy-Hublar R., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,

Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
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YORZUZOW.
YORZUZOW.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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                                  Query Match 0.7%; Score 8; DB 12; Length 198; Best Local Similarity 100.0%; Pred. No. 14; Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

BOYET J., Fairhead C., Gaillon L., Galisson F., Michaux Thierry A., Dujon B., To the EMBL/GenBank/DDBJ databases. Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-FY1679;
Galisson F., Dujon B.;
Galisson F., Dujon B.;
Submitted (OCT. Dujon B.;
ENBL, Z75128; CAA9943 I.;
ENBL, X92441; CAA63183.1; -.
SGD; S0005746; YOR220W.
SEQUENCE 265 AA; 29255 WW; 4A184C5C1218A617 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIPS;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Chromosome XV reading frame ORF YOR220W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 PPKSPSIT 259
                                                                                                                                                                                                       13 LLSAEVVK 20
                                                                                                                                                                                                                                                      Q12044
Q12044;
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                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
012044
1D 012044
1D 012044
AC 012044
DT 01-NO
D
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Gaps

Gaps

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Length 490;

DB 11; 5. 32;

us-09-782-874-2.oli.rspt

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1
53417 MW; 01DDC00B35C5BDA6 CRC64;
                                                                                                                                0.7%; Score 8; DB 1
100.0%; Pred. No. 32;
tive 0; Mismatches
                                                                                                    Ouery Match
Best Local Similarity 100...
8, Conservative
ATP-binding.
NON_TER 1
SEQUENCE 490 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  445 LAFSSSOL 452
                                                                                                                                                                                                                                                                                                                   334 RLYFGSSY 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 LAFSSSQL 41
                                                                                                                                                                                                                                                                        68 RLYFGSSY 75
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Best Local S:
Matches 8;
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Q9SP43;
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Q9SP43
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Q9DG87
       SOFE
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SILDBAR A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Arawa K., Izawa M., Nishi K., Kiyoswa H., Kondo S., Yamanaka I.,

Asaito T., Okazaki Y., Golobori T., Bono H., Rasukawa T., Salto R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washlo T.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washlo T.,

Brownstein M.J., Boifelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchlonni L., Mashima J., Mazzareli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Suzuki H., Toyo-oka K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nyanaki S., Wang K., Hasegawa Y., Kawaji H., Kohtsuki S.,

M. Wynshaw-Borlis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_raxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Match 0.7%; Score 8; DB 5; Length 444; Local Similarity 100.0%; Pred. No. 29; ess 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                        WCMurray A.A.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                  investigating biology.";
Science 282:2012-2018(1998).
EMBL, 282230; CAC42204.1; -.
InterPro: Int
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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EMBL; AK017309; BAB30684.1; -.
MGD; MG1.19163.2; Pex.1.
InterPro; IPR003593; AAA_AIPase.
InterPro; IPR003959; AAA_AIPase_centr.
InterPro; IPR003959; AAA_Sub.
Pfam; PF00004; AAA; 1.
SWART; SM00382; AAA; 1.
PROSITE; PS00674; AAA; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5430414H02Rik protein (Fragment).
PEX1 OR 5430414H02RIK.
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     637 DSLKAQEA 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 DSLKAQEA 163
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                                                                                                                                                                           McMurray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches
                                                                                                                                                                                                                                                                                                                                                none;
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Citrus unshiu (Satsuma orange).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Sapindales; Rutaceae; Citrus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carassius auratus (Goldfish).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) (ADP-glucose synthase) (ADP-glucose pyrophosphorylase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ő
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-!- CATALYTIC ACTIVITY: ATP + ALPHA-D-GLUCOSE 1-PHOSPHATE = DIPHOSPHATE + ADP-GLUCOSE.
-!- STMILARITY: BELONGS TO THE BACTERIAL AND PLANTS GLUCOSE-1-PHOSPHATE ADENYLITIANSFERASE FAMILY.
EMBL; AF184597; AD556041.1; -...
InterPro; IPRO/0125; NUP_transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Arion Arion B25; Nurland Brase; 1. Brootest NTP transferase; 1. Brootest NTP transferase; 1. Brootest Bro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Glutamic acid decarboxylase isoform 65 (EC 4.1.1.15)
GAD65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 0.7%; Score 8; DB 10;
Local Similarity 100.0%; Pred. No. 33;
Nes 8; Conservative 0; Mismatches
515 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       583 AA.
PRT;
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PRELIMINARY;
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NCBI_TaxID=7957;
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SEQUENCE FROM N.A.
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Testis-specific CHROMODOMAIN Y-like protein.
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Q96YH3
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Bosma P.T., Blazquez M., Docherty K., Trudeau V.L.;
"Cloning and expression of multiple forms of glutamate decarboxylasse
from goldfish.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: PYRIDOXAL PROSPHATE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
TYRDC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                               Carassius auratus (Goldfish).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
NCBI_TaxID-7957;
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                      ö
                                                                                                                                                                 0.7%; Score 8; DB 13; Length 583; 100.0%; Pred. No. 37; 7; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13; Length 583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                            EMBL, AF045594, AAG33931.1; ...
InterPro; IPR002129; Pyridoxal_dec.
Pfam: PF00282; pyridoxal_dec; 1.
PR031FE; PS00392; DDC_GAD_HDC_YDC; 1.
Decarboxylase: Lyase; Pyridoxal_phosphate.
SEQUENCE 583 AA; 65375 MW; 8C43E1A264D95001 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AF149832; AAF73186.1; -.
InterPro; IPR002129; Pyridoxal_dec.
Pfam; PF00282; pyridoxal_dec; 1.
PR0SITE; PS00392; DDC_GAD_HDC_YDC; 1.
Decarboxylase; Lyase; Pyridoxal phosphate.
SEQUENCE 583 AA; 65361 MW; 9C4326BFD2023DB6 CRC64;
                                                                                                                                                                                                                                                                                             01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 19, Last annotation update)
Glutamic acid decarboxylase isoform 65 (EC 4.1.1.15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                            583 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
0.7%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09Y232 PRELIMINARY, PRT, 09Y232; 01-NOV-1999 (TrEMBLrel. 12, Last seq; 01-NOV-1999 (TrEMBLrel. 12, Last seq; 01-MAR-2002 (TrEMBLrel. 20, Last ann
                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                         Query Match
Best Local Similarity 100.
Local 8; Conservative
                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         404 LYSTDLLP 411
                                                                                                                                                                                                        404 LYSTDLLP 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 LYSTDLLP 97
                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                       Q9IAT4;
                                                                                                                                                                                                                                                                           Q9IAT4
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09Y232
ID 09Y23
AC 09Y23
DT 01-NO
DT 01-NO
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Q91AT4
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PubMed=11572479;
Rawarabayasa Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Rawarabayasa Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oquchi A.,
Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
Ogshima T., Kikuchi H.;
                                                                                                                                                                                                      Lahn B.T., Page D.C.;
"Retroposition of autosomal mRNA yielded testis-specific gene family on human Y chromosome.";
"Nat. denet. 21:429-433(1999).
"STORCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
"SIMILARITY: COURTINS 1' CHROMO' DOMAIN.
EMBL, AF081259; AAD22734.1; -..
EMBL, AF081259; AAD22734.1; -..
INTERPRO; IPRO00953; Chromo.
InterPro; IPRO00953; Chromo.
InterPro; IPRO01753; BGCOA_hydrtse.
Pfam: PF00185; Chromo; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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DANA Res. 8:123-140(2001).

EMBL, AP000989: BAB65304.1; -.

InterPro; IPR003309; FRN_enzyme.

InterPro; IPR00332; Glu_synthase.

InterPro; IPR055 Glu_synthase.

Hypothetical protein: Complete proteome.

SEQUENCE 635 AA; 68139 MW; BD6BEE204F66812F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 598;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative glutamate synthase large subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.7%; Score 8; DB 4;
100.0%; Pred. No. 38;
ative 0; Mismatches
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                                                                                                                                                      TISSUE-TESTIS;
MEDLINE-99206615; PubMed=10192397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00504; CHROMODOMAIN.
SMART; SM00298; CHROMO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00598; CHROMO_1; 1. PROSITE; PS50013; CHROMO_2; 1.
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Best Local Similarity 100.(
Matches 8; Conservative
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NCBI_TaxID=111955;
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                                                                                                                         SEQUENCE FROM N.A.
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                                                         NCBI_TaxID=9606;
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SEQUENCE 598 A
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Length 635;

DB 17;

Score 8;

0.78;

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162 LITLLSTL 169
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                                                                                                                                                                                                                                                                                          Paramyosin.
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                                                                                                  RESULT 26
096064
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053347
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Bevan M., Massenet O., Clabault G., Quigley F., Mache R., Bancroft I., Mewes H.W., Mayer K., Schueller C., Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Massenet O., Clabault G., Quigley F., Mache R., Mewes H.W., Lemcke K., Mayer K.E.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                   protein).
F2188.200 OR F16G20.10 OR AT4G23310.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudlootyledons; core eudloots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                              Gaps
                                                                                                                                                                                                                                                                                                           01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Serine/threonine kinase - like protein (Serine/threonine kinase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00269; PENTAXIN; UNKNOWN_1.
PROSITE; PS00107; PROTEIN_KINASE_ATF; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATF-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 830 AA; 92315 MW; C1785EEC50E482EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EU Arabidopsis sequencing project;
Submitted (MRR-2000) to the EMBL/GenBank/DDBJ databases.
--- SINITARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL; AL022347; CAA18478.1; --
EMBL; AL031326; CAA20452.1; --
EMBL; AL031326; CAA20452.1; --
EMBL; AL031326; CAB79286.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 617-830 FROM N.A.
Watson M.D., Gibbons T., Bartley J., Mewes H.W., Lemcke K.,
Mayer K.F.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10; Length 830; . 52;
                              Indels
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ilarity 100.0%; Pred. No. 52;
Conservative 0; Mismatches
     Pred. No. 40;
                              Mismatches
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INTERPRO: IRRO02902; DIF26.
INTERPRO: IRRO02902; DLK_pkinase.
INTERPRO: IRRO01719; Bentaxin.
INTERPRO: IRR001759; Pentaxin.
INTERPRO: IRR002909; Ser_thr_pkinase.
InterPro: IRR004040; STY_pkinase.
Pfam; PF01657; DUF26; 3.
Ffam; PF00669; pkinase; 1.
ProDom; PF00069; UNA.pkinase; 1.
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0
100.0%;
Best Local Similarity 100.
Matches 8; Conservative
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8; Conserv
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                                                                            498 SRETLSVL 505
                                                                                                                           319 SRETLSVL 326
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065482
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Harris D.,
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                                                                                                                                                                                                                                                                                                                     "Compilete amino acid sequence of Mytilus anterior byssus retractor paramyosin and its putative phosphorylation site.";
J. Exp. Zool. 286:24-35(200).

EMBL; ABO16070; BaA24-15(-1);
InterPro; IPR004827; IF.bzIP.
Fign. PF01576; Myosin_tail.

SEQUENCE 8000338; BRLZ; I.
SEQUENCE 804 AA; 99572 MW; EF7C8ED73A5742B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=9829587; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Shornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Seeger K., Skelton S., Squares S., Squares R., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
                                                                                                                                      Būkaryota; metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
SEQUENCE FROM N.A.
STRAIN-CDC 1551 / OSHKOSH;
Fleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative ATP-dependent DNA helicase (Helicase, UvrD/Rep family).
RV3201C OR MTV014.45C OR MT3295.
Mycobacterium tuberculosis.
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0
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
ISSUB-ANTERIOR BYSSUS RETRACTOR MUSCLE;
MEDLINE-2007-51: Pubmed-10607366;
Watabe S., Iwasaki K., Funabara D., Hirayama Y., Nakaya M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 864;
                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                    Mytilus galloprovincialis (Mediterranean mussel)
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864 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.7%; Score 8; DB 5
ilarity 100.0%; Pred. No. 54;
Conservative 0; Mismatches
PRT;
                                    01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAR-2002 (TrEMBLrel. 20,
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PRELIMINARY;
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es 8; Conserv
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Matches

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PexlpG843D.
PEXIG843D.
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Q96S71
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Q8S921
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Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Phenotype-Genotype Relationships in Peroxisome Biogenesis Disorders of PEXI-Defective Complementation Group 1 Are Defined by PexIp-Pex6p Interaction.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                 "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    096573;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
PEXID-634de1690.
PEXII-634DEE1690.
Homo sapiens (Human).
Bukaryota; Metazoa; Ohordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Kondo N., Fujiki Y.;
                                                                                                                                                                                                                                                                                                                                                           h Similarity 100.0%; Score 8; DB 16; Length 1101; Similarity 100.0%; Pred. No. 67; 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1226;
                                                                                                   laboratory strains...;
Submitted (APR-2001) to the EKBL/GenBank/DDBJ databases.
EMBL, ALCO142; AAR47638.1;
HSSP; P56255; 1PJR.
HTGR; M73295; ...
InterPro; IPR00212; UvrD-helicase.
Pfam; PF0589; UvrD-helicase.
Filol AA, 116687 WW; 269C6AAD3657412B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AB052090; BAB59061.1; -.
InterPro; IPR003969; AAA_ATPase_centr.
InterPro; IPR003960; AAA_Sub.
Pfam; PF00004; AAA_Sub.
PROSTITE; PS00064; AAA_SUB.
PROSTITE; PS00664; AAA, UNKNOWN_1.
SEQUENCE 1226 AA, 136584 MW; 28125C8B785DA8E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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Last annotation update)
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100.0%; Pred. No. 74;
tive 0; Mismatches
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Q96S72;
01-DEC-2001 (TEMBLEEL 19,
01-DEC-2001 (TEMBLEEL 19,
01-MAR-2002 (TEMBLEEL 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100...
8; Conservative
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                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   1021 SVAVRALR 1028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            374 SVAVRALR 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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PEX1L664P.
                                                                 Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    096873
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Q96S73
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Q96S72
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SEQUENCE FROM N.A.

Tamura S., Matsumoto N., Imamura A., Shimozawa N., Suzuki Y.,
Kondo N., Fujiki Y.,
"Phenotype-Genotype Relationships in Peroxisome Biogenesis Disorders
of PEX1-Defective Complementation Group 1 Are Defined by Pex1p-Pex6p
                                                                                                SEQUENCE FROM N.A.

Tamura S., Matsumoto N., Imamura A., Shimozawa N., Suzuki Y.,
Kondo N., Fujiki Y.,
"Phenotype-Genotype Relationships in Peroxisome Biogenesis Disorders
Phenotype-Genotype Relationships in Peroxisome Biogenesis Disorders
Interaction.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                 Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. BMBL; AB052091; BAB59062.1; -
InterPro; IPR003959; AAA_HPase_centr.
InterPro; IPR003960; AAA_sub.
Pfam; PF00004; AAA, 2ub.
PROSTIE; PS006044; AAA; UNKNOWN_1.
SEQUENCE 1283 AA; UAKNOWN, C33AD8A68893D77A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
BMBL; AB052092; Bab59063.1;
InterPro; IPR003959; AAA_ATPase_centr.
InterPro; IPR003960; AAA_ATPase_centr.
Pfam; PF00004; AAA; 2
PROSITE; PF000674; AAA; UNKNOWN.1.
SEQUENCE 1283 AA; 142924 MW; 9CF230C26F02AFD9 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Chloroplast-resident DNA methyltransferase.
CRMET1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.7%; Score 8; DB 4
100.0%; Pred. No. 77;
iive 0; Mismatches
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100.0%; Pred. No. 77;
iive 0; Mismatches
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Best Local Similarity luv...
8; Conservative
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nes 8; Conservative
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Nellen W.;

"RNA! in Dictyostellum: developmental regulation and the role of RdRPs and dsRNase.";

Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, A314919.0 CAC41975.1;

InterPro; IPR00140; DEAD.

InterPro; IPR00150; Helicase_C.

InterPro; IPR001201; PAP_25A_core.

Pfam; PF00271; helicase_C; 1.
                                                                                                                                                                                                                                           Nellon W.; "RNAi in Dictyostellum: developmental regulation and the role of RdRPs and dsRNase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Martens H., Novotny J., Oberstrass J., Steck T.L., Postlethwait P.,
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Martens H., Novotny J., Oberstrass J., Steck T.L., Postlethwait P.,
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                                                                                                                                                                                                                                                                                                     Submitted (JUN 2001) to the EMBL/GenBank/DDBJ databases.

REMBL; AJ314909; CAC41974.1; -

R InterPro; IPR001410; DEAD.

R InterPro; IPR00150; Helicase_C.

R InterPro; IPR00150; PAP_25A_core.

R InterPro; IPR00150; PAP_25A_core.

R InterPro; IPR00150; PAP_25A_core.

R Pfam; PF00270; DEAD; I'

R Pfam; PF00271; PABLO3Se_C; I.

R RPOSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.

R ATP-binding; Helicase.

I 1883 As; 217454 MW; IBID9B9738B15094 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 0.7%; Score 8; DB 5; Length 1883; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1964;
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                                                                        Dictyostelium discoideum (Slime mold).
Eukaryota: Mycetozoa; Dictyostellida; Dictyostellum.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative RNA dependent RNA polymerase (Fragment).
01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Putative RNA dependent RNA polymerase (Fragment).
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0952G6;
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Matches
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
    Chlamydomonas reinhardtii.
Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
NCBL_TaxID=3055;
                                                                                                                                                                            Nishiyama R., Itoh M., Yamaguchi Y., Koizumi N., Sano H.; "A chloroplast-resident DNA methyltransferase is responsible for hypermethylation of chloroplast genes in Chlamydomonas maternal
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0.7%; Score 8; DB 10; Length 1344;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 0; Indels
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EMBL; AL033556. CAA22142.1; -
InterPro; IPR003439; ABC_transportr.

InterPro; IPR00163; DnaJ_N.

ProDom; PR00005, ABC_transportr; 2.

ProDom; PR00211; ABC_transportr; 2.

PROSITE; PS00211; ABC_TRANSPORTE; UNKNOWN_2.

PROSITE; PS00231; ABC_TRANSPORTE; UNKNOWN_1.

SEQUENCE 1564 AA; 176701 MM; DC66A3E7ED8DC50F CRC64;
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EMBL, AB073989; BAB31073.1, -
Transferase; Methyltransferase.
SEQUENCE 1344 AA, 142361 MW; 96D3876E7EEB477F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
11-NOV-1999 (TrEMBLrel. 20, Last annotation update)
153010A.9 protein.
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01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                       STRAIN-CC683;
MEDLINE-21980658; PubMed-11983892;
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MEDLINE=99069613; PubMed=9851916;
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hes 8; Conserv
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| 150 LSSLRAQL 157
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Q9XW49;
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Q952G7
ID Q952G
AC Q952G
DT 01-DE
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Matches
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09XW49

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Query Match
Best Local Similarity luv...
7; Conservative
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Best Local Similarity 100.0
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Q9HB48;
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Q9GKJ9
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MEDINE-21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takai S., Hines S.A., Sekizaki T., Nicholson V.M., Alperin D.A., Osaki M.; Takamatsu D., Nakamura M., Suzuki K., Ogino N., Kakuda T., Dan H., Prescott U.F.;
Dan H., Prescott U.F.;
Dan H., Prescott U.F.;
DNA sequence and comparison of virulence plasmids from Rhodococcus equi ArCC 33701 and 103.";
Infect. Immun. 68:6840-6847(2000).
EMBL; APOLIO104; BAB16635.1;
InterPro; IPR001669; Halicase_C.
InterPro; IPR001669; Halicase_C.
From: Pro0271; halicase_C:
SMART; SM00487; DEXDC: 1.
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STRAIN-ATCC33701, AND 103; PLASMID-PREAT701 (P33701), AND VIRULENCE;
PubMed=11083803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. TARAMID=PREAT701 (F33701);
TATAIN=ARCG3701, FLASMID=PREAT701 (F33701);
TATAI S., SEKIZAKI T., KAKUGA T., NAKAMURA M., SUZUKI K., Ogino N.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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0
                                                                                                                                                                                                                                                                                              Corynebacterium equii (Rhodococcus equi).
Plasmid pREAT701 (p33701), and Plasmid virulence.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
NCBI_TaxID=43767;
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100.0%; Pred. No. 1.8e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP-binding, Helicase, Methyltransferase, Plasmid.
SEQUENCE 3229 AA, 351003 MW; C1E03A6005424F1A CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein STY1874a.
                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                          PRT; 3229 AA
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nes 8; Conservative
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                                                                                          PRELIMINARY;
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NCBI_TaxID=601;
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Q826B7;
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Q9ETKO;
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Q8Z6B7
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
41-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Hypothetical 5.4 Kba protein.
Hypothetical 5.4 kba protein.
Hypothetical 5.4 kba protein.
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Whitehead S., Barrell B.G.; Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CTLB."; Nature 413:848-852(2001).

Nature 413:848-852(2001).

Hypothetical protein Complete proteome. SEQUENCE 29 AA: 3223 MW; 2A834B159BD06DB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
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Van Poucke M., Yerle M., Tuggle C., Chardon P., Van Zeveren A.,
Van Poucke M., Yerle M., Tuggle C., Chardon P., Van Zeveren A.,
Peelman L.J.;
"Integration of porcine chromosome 13 maps.";
Submitted (JAN-2200) to the EMBL/GenBank/DDBJ databases.
EMBL; AF222911; AAG41124.1;
HSSP; P15309; 2HPA.
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Othan L., Chenhong D., Hongling Z.;
Othan L., Chenhong D., Hongling Z.;
"Putative human lung cell protein.";
Submitted (2701-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF281279; AAG13933.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 AA; 3943 MW; 50C57B8C770EA10C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Prostatic acid phosphatase (Fragment).
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100.0%; Pred. No. 36;
Live 0; Mismatches
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Pfam; PF00328; acid_phosphat; 1.
NON_TER 1 1 1
NON_TER 36 36
SEQUENCE 36 AA; 3943 MW; 50C57BRC
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Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
NCBI_TaxID=6550;
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Eukaloidas; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
NCBI_TaxID=6550;
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Warner S.C., Waite J.H.;
"Expression of multiple forms of an adhesive plaque protein in individual mussel, Witilus edulis.";
Mar. Biol. 134:729-734(1999).
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF286147; AAR982891 j. -.
SEQUENCE 72 AA; 8214 MW; 7600241DB84D6BF4 CRC64;
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF286136; AAF89278.1; -.

SEQUENCE 72 AA; 8295 MW; 7D42746A91010D99 CRC64;
                                                                                                                               Length 70;
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Eur. J. Biochem. 239:172-176(1996).
EMBL; AB049579; BAB16314.1; -.
SEQUENCE 70 AA; 8003 MW; A902E3E300F5B9EA CRC64;
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01-00T-2000 (TrEMBLrel. 15, Last sequence update)
01-00T-2000 (TrEMBLrel. 15, Last annotation update)
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Last annotation update)
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100.0%; Pred. No. 68;
tive 0; Mismatches
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                                                                                                                DB : 66;
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Local Similarity 100.0%; Pred. No. 66;
nes 7; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last seq
01-0cT-2000 (TrEMBLrel. 15, Last ann
Foot protein-3 precursor variantl.
MEFP3.
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Best Local Similarity 100.
Matches 7; Conservative
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SEQUENCE FROM N.A.
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MEDLINE-21595285; PubMed=11759840;

ARDAROR T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

Ardanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,

Makazaki N., Shimpo S., Sugimoto M., Matsuno A., Muraki A.,

Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

A Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

A Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

A Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

A Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

A Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

A Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

A Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

A Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

A Nakazaki N., Shimpo S., Sugimoto M., Nakazawa M., Yamada M.,

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A Nakazaki N., Shimpo S., Sugimoto M., Nakazawa M., Yamada M.,

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A Nakazaki N., Shimpo S., Sugimoto M., Nakazawa M., Yamada M.,

A Nakazaki N., Shimpo S., Sugimoto M., Nakazawa M., Yamada M.,

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A Nakazaki N., Shimpo S., Sugimoto M., Nakazawa M., 
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Eukayota, Metazoa; Mollusca, Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
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MEDLINE-96305382; Miki D., Odo S., Harayama S., Waite H.;
Inoue K., Takeuchi Y., Miki D., Odo S., Harayama S., Waite H.;
"Cloning, sequencing and sites of expression of genes for the
hydroxyarginine-containing adhesive-plaque protein of the mussel
Mytilus galloprovincialis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBL_TaxID=103690;
                                                                                                                               0; Indels
                                                                      Length 43;
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   5388 MW; OFB612B8E31EBA71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
10-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MGFP-3A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Asr4522.
                                                                   DB 4;
                                                               Score 7; DB 4;
; Pred. No. 42;
0; Mismatches
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Best Local Similarity 100.0%; Pr
Matches 7; Conservative 0;
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Best Local Similarity luv...
7; Conservative
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   43 AA;
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                                                                                                                                                                                              127 LKKFFFF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 VQPPEGI 266
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21 LKKFFFF 27
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   SEQUENCE
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Q9GUX8
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Q8YNP2
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7; Conservative
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                                   555 RYGGYKG 561
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Q9NAU2
  Matches
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Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
NCBI_TaxID=6550;
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Bukaryota, Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
NCBI_TaxID=6550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Warner S.C., Waite J.H.;
"Expression of multiple forms of an adhesive plaque protein in individual mussel, Myttilus edulis.";
Mar. Biol. 134:729-734(1999).
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Warner S.C., Walte J.H.;
"Expression of multiple forms of an adhesive plaque protein in individual mussel, Wytilus edulis.";
Mar. Biol. 134:729-734(1999).
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Warner S.C., Walte J.H.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF286148; AAF892290.1; -.
SEQUENCE 72 AA; 8249 MW; 3198746A89796D81 CRC64;
                Length 72;
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Warner S.C., Waite J.H.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF28611480291.1; -.
SEQUENCE 72 AA, 8299 WW; 7602746A8D6D6BF4 CRC64;
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7602746A8D6D6BF4 CRC64;
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
10-007-2000 (TrEMBLrel. 15, Last annotation update)
Foot protein-3 precursor variantll.
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100.0%; Pred. No. 68;
iive 0; Mismatches
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Pred. No. 68;
        DB 5
68;
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              0.6%; Score 7; DB 5
100.0%; Pred. No. 68;
iive 0; Mismatches
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              Query Match 0.6
Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity
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52 RYGGYKG 58
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Q9NAU4;
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Matches
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Q9NAU3
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Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
NCBI_TaxID=6550;
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Eukaryota: Metazoa: Mollusca: Bivalvia: Pteriomorphia: Mytiloida;
Mytiloidea: Mytilidae: Mytilus.
NCBI_TaxID=6550;
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Warner S.C., Waite J.H.;
"Expression of multiple forms of an adhesive plaque protein in individual mussel, Mytilus edulis.";
Mar. Biol. 134:729-734(1999).
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Warner S.C., Watte J.H.;
"Expression of multiple forms of an adhesive plaque protein in individual mussel, whitilus edulis.";
Mar. Biol. 134:729-734(1999).
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Warner S.C., Waite J.H.;
submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF2661550; AAF892922.1;
SEQUENCE 72 AA; 8261 MW; B2B1746A98989D90 CRC64;
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WATHER S.C., Walter J.H.;
Submitted (ULL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF2861156; AAF89298.1; -.
SEQUENCE 72 AA; 8327 MW; 6CB3DF69ED6DFF4 CRC64;
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                                            Olocy-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2001 (TrEMBLrel. 17, Last annotation update)
Foot protein-3 precursor variant13.
MEFP3.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
Foot protein-3 precursor variantly
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72 AA
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SEQUENCE FROM N.A.
STATIS-MARTEN-20099;
MASTIN-MARTEN-20099;
MACTAIN-MARTEN-20099;
MACTAIN-MARTEN-20099;
MACTAIN-MARTEN-20099;
MACTAIN-MARTEN-2009;
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Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL137543; CAB70801.1;
InterPro; IPR004934; Tropomodulin.
Pfam; PR03250; Tropomodulin; 1.
Hypothetical protein.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
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Bacteria: Proteobacteria: alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
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                    Length 79;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 10.1 kba protein (Fragment).
DKF2P434P2119.
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01-007-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein mil2618.
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             DB 16;
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          0.6%; Score 7; DB 1
100.0%; Pred. No. 74;
iive 0; Mismatches
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Pred. No.
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                                                                             Conservative
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          Query Match
Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                         456 SVWMFAS 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           652 ENTNILK 658
                                                                                                                                                                                 73 SVWMFAS 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 ENTNILK 54
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                                                                                                                                                                                                                                                                                                                                                            Q9NT43;
Q9NT43;
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MEDLINE=21534947; PubMed=11677608;

MEDLINE=21534947; PubMed=11677608;

MEDLINE=21534947; PubMed=11677608;

MEDLINE=21534947; PubMed=11677608;

A Churcher C., Mungall K.L., BentLey S.D., Holden M.T.G., Sebalina M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Rornin A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Antheread S., Barrin B.G., Antheread S., Barrin B.G., Mintened S., Moule S., O'Gaora P., Parry C., Antheread S., Barrin B.G., Mintened S., Barrin B.G., Barri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Breast basic conserved protein 1 (Fragment).
Ovis aries (Sheep).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; NCBL_TAXID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
TISSUB-PULMONARY VEIN;
Sander F.C., Raj J.U.;
"Breast Basic Conserved Gene (BBC1) In Fetal Pulmonary Vascular
Development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF192977; AAF03752.1; -
Interpro; IPR001380; Ribosomal_L13E.
Pfam; PF01294; Ribosomal_L13E; 1.
ProDOM; PD004443; Ribosomal_L13E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 AA; 8924 MW; 54EBA54962C35E2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6;
                                                                                                                                                                                                  78 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.6%; Score 7; DB (100.0%; Pred. No. 73; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative membrane protein.
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Best Local Similarity 100.،
ابات 7; Conservative
                                                                                                                                                                                               PRELIMINARY;
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52 RYGGYKG 58
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SEQUENCE
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Q821J9;
                                                                                                                           RESULT 47
09TTV1
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Q8Z1J9
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δλ qq DDT TO DD

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Gaps

Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps Qy 347 SITLDDG 353
Db 60 SITLDDG 66

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Search completed: November 6, 2002, 03:37:49 Job time: 163 secs

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November 6, 2002, 03:39:18 ; Search time 45 Seconds (without alignments) 3298.693 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseqy-embl/AA1981.DAT:*
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| SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1988.DAT:*
                                                                                                                                                                                                                                                                                                                                                    1 MGKTIQVFGFPYLLSAEVVK.....RPVLNLSSLRAQLSHRLVLK 1114
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                 OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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5864
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
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                                                                                                                                                                                                                                                                                                                                                          Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | SIDS2/goddata/geneseq/geneseqp-embl/AA1990.bdr; |
| SIDS2/goddata/geneseq/geneseqp-embl/AA1991.bdr; |
| SIDS2/goddata/geneseq/geneseqp-embl/AA1992.bdr; |
| SIDS2/goddata/geneseq/geneseqp-embl/AA1993.bdr; |
| SIDS2/goddata/geneseq/geneseqp-embl/AA1994.bdr; |
| SIDS2/goddata/geneseq/geneseqp-embl/AA1995.bdr; |
| SIDS2/goddata/geneseq/geneseqp-embl/AA1995.bdr; |
| SIDS2/goddata/geneseq/geneseqp-embl/AA1995.bdr; |
| SIDS2/goddata/geneseq/geneseqp-embl/AA1999.bdr; |
| SIDS2/goddata/geneseq/geneseqp-embl/AA1999.bdr; |
| SIDS2/goddata/geneseq/geneseqp-embl/AA1999.bdr; |
| SIDS2/goddata/geneseq/geneseqp-embl/AA1000.bdr; |
| SIDS2/goddata/geneseq/geneseqp-embl/AA2001.bdr; |
| SIDS2/goddata/geneseq/geneseqp-embl/AA2002.bdf; |

	Description	***************************************	Tomato RNA-directe	Tomato C-protein h	Soybean RNA-direct	Maize RNA-directed	Amino acid sequenc	Maize RNA-directed	Rice RNA-directed	Tomato RNA-directe	Maize partial RNA-	Maize RNA-directed
SUMMARIES	q		~	AAE00897	AAB28533	AAB28530	AAG67235	AAB28531	AAB28532	AAE00898	AAB28529	AAB28534
	B O	;	22	22	21	21	22	21	21	22	21	21
	Length		1114	1114	1125	1108	1196	1164	836	218	417	230
	% Query e Match Length DB I		100.0	100.0	62.1	53.6	27.6	27.1	24.4	20.5	17.3	11.9
	Score		5864	5864	3643	3140.5	1621	1591	1430.5	1182	1013.5	697.5
	Result No.		п	(7)	m	4	S)	9	7	89	σ	10

WPI; 2001-595798/67. N-PSDB; AAS17837.

Neurospora crassa	Æ	RNA	Rice RNA-directed	Staphylococcus lug	Drosophila melanog	Herbicidally activ	Maize partial RNA-	Macaca mulatta rha	L human	human	_	Novel human diagno	human	Beetle luciferase	a)	coccus pol	Arabidopsis thalia	Protein involved i	AMEPV MRNA capping	~	Mutant luciferase	Listeria monocytog	H. pylori transmem	Carboxydothermus h		Arabidopsis thalia		ᆈ	Novel human diagno	Staphylococcus aur	io Ø	snood	Beetle luciferase	lucif
4AB13956	AAB28537	AAB28536	AAB28535	AAE20967	ABB68683	ABB91193	4AB28528	AAB53193	ABG05469	ABG30156	ABG12986	4BG13923	ABG10172	AD01219	4AY06850	ABP26865	AAG14283	4AY37454	ABB77619	AAU01222	AAY06853	ABB49921	84	37	340	AAG14284	ABG22122	AAW56107	ABG20134	AAU33733	AAU36532	ABB55148	AAU01225	85
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11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	9 2	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Tomato, RGRP, RNA-directed RNA polymerase; in vitro transcription; cytostatic; virucide; RNA synthesis inhibitor; antibody; immunogen; transgenic plant; transgenic animal; cancer; viral infection; immunoprecipitation; immunolocalisation; EC 2.7.7.48; gene therapy. Tomato RNA-directed RNA polymerase (RdRP) protein. Sanger HL; Schiebel W, AAU10006 standard; Protein; 1114 AA 97US-0811583. 08-FEB-2001; 2001US-0782874. (first entry) Wassenegger M, Riedel L, Lycopersicon esculentum. (WASS/) WASSENEGGER M. (RIED/) RIEDEL L. US2001023067-A1. 05-MAR-1997; 38-MAY-2002 20-SEP-2001 AAU10006; RESULT 1 AAU10006

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601

661 199 721

YLNROLITLLSTLGVKDEVLEQKQKEAVDQLDAILHDSLKAQEALELMSPGENTNILKAM 601 YLNRQLITLLSTLGVKDEVLEQKQKEAVDQLDAILHDSLKAQEALELMSPGENTNILKAM LNCGYKPDAEPFLSMMLQTFRASKLLDLRTRSRIFIPNGRTMMGCLDESRTLEYGOVFVO

SKCGLQYTPSAFQIRYGGYKGVVGVDPDSSMKLSLRKSMSKYESDNIKLDVLGWSKYQPC

720 780

LNCGYKPDAEPFLSMMLQTFRASKLLDLRTRSRIFIPNGRTMMGCLDESRTLEYGGVFVQ

FIGAGHGEFSDDLHPFNNSRSTNSNFILKGNVVVAKNPCLHPGDIRVLKAVNVRALHHMV FTGAGHGEFSDDLHPFNNSRSTNSNFILKGNVVVAKNPCLHPGDIRVLKAVNVRALHHMV

721

781 781 841

720

840

780

900 900

DCVVFPQKGKRPHPNECSGSDLDGDIYFVCWDQDMIPPRQVQPMEYPPAPSIQLDHDVTI **EEVEEYFINYIVNDSLGIIANAHVVFADREPDMAMSDPCKKLAELFSIAVDFPKTGVPAE** IPSQLRPKEYPDFMDKPDKTSYISERVIGKLFRKVKDKAPQASSIATFTRDVARRSYDAD MEVDGFEDY IDEAFDYKTEYDNKLGNLMDYYGIKTEAEILSGGIMKASKTFDRRKDAEAI

841

901

961

DCVVFPQKGKRPHPNECSGSDLDGDIYFVCWDQDMIPPRQVQPMEYPPAPSIQLDHDVTI

YDQLIQIKKDKARNRPVLNLSSLRAQLSHRLVLK 1114

1081

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SVAVRALRKEARAWFKRRNDIDDMLPKASAWYHVTYHPTYWGCYNQGLKRAHFISFPWCV

1021

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us-09-782-874-2.rag

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This sequence represents the tomato RNA-directed RNA polymerase (RdRP)

protein of the invention. The invention comprises the nucleic acid and

protein sequences of RARP. The protein of the invention can catalyse in

vitro transcription of short single stranded RNAs into DNA molecules,

this transcription can be either primed by RNA or DNA oligonucleotides

cor be unprimed. The protein may have cytostatic or virucide activities.

The sequences of the invention may be used in gene therapy or as an RNA

directed RNA synthesis inhibitor. The RdRP cDNA sequence and a template

cor molected and equile derived from a nucleic acid molecule which causes

disease are useful for treating a disease caused by the undesired

expression or overexpression of a nucleic acid molecule which causes

a disease are useful for treating the molecules. This system can be used in the

preparation of any desired gene by transferring the RdRP system to

corganisms that either lack a comparable mechanism or do not sufficiently

expression of any desired gene by transferring the RdRP system to

corganisms that either lack a comparable mechanism or do not sufficiently

express their own RdRP. An antibody or an antagonist or inhibitor to the

protein are useful for inhibiting RNA directed RNA synthesis and for

corganisms that either lacks a comparable mechanism or do not sufficiently

expression, as primers for amplification of the control of gene

as tools for the detection of expression in transgenic organisms.

The sequence is useful for probes and/or for the control of gene

as tools for the detection of expression in humans and animals. The RdRP

systems as therapeutic agent for the control of cancer and virus

systems as a therapeutic agent for the control of cancer and virus

infection in humans and animals and the antibody is useful for

inmunoprecipitation or immunologialisation of the protein, identification

cof polypeptides interacting with it and screening expression libraries.
New nucleic acid molecule encoding a polypeptide having the enzymatic activity of RNA-directed RNA polymerase, for modulating gene expression and treating cancer and virus infection in human and animals
                                                                                                                                      Claim 1; Page 19-22; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
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240 360 120 180 240 300 360 LVTPCKVYFCGPEVNVSNRVLRNYSEDIDNFLRVSFVDEEWEKLYSTDLLPKASTGSGVR 420 9 9 1 MGKTIQVFGFPYLLSAEVVKSFLEKYTGYGTVCALEVKQSKGGSRAFAKVQFADNISADK 1 MGKTIQVFGFPYLLSAEVVKSFLEKYTGYGTVCALEVKQSKGSRAFAKVQFADNISADK 61 IITLANNRLYFGSSYLKAWEMKTDIVQLRAYVDQMDGITLNFGCQISDDKFAVLGSTEVS 121 IQFGIGLKKFFFFLSSGSADYKLQLSYENIWQVVLHRPYGQNAQFLLIQLFGAPRIYKRL ENSCYSFFKETPDDQWVRTTDFPPSWIGLSSSLCLQFRRGVRLPNFEESFFHYAERENNI TLQTGFTFFVSQKSALVPNVQPPEGISIPYKILFKISSLVQHGCIPGPALNVYFFRLVDP RRRNVACIEHALEKLYYIKECCYDPVRWLTEQYDGYLKGRQPPKSPSITLDDGLVYVRRV Length 1114; Indels DB 22; ô 100.0%; Score 5864; 100.0%; Pred. No. 0; iive 0; Mismatches Conservative Similarity Matches 1114; Query Match 121 181 181 241 301 301 361 셤 ŏ ద δy g ò q δŽ g δ g Qγ

Tomato; gene therapy; RNA-directed RNA polymerase; RdRP; gene expression; transgenic plant; tissue culture; plant breeding; therapy; C-protein. Tomato C-protein having RNA-directed RNA polymerase (RdRP) activity. forfor for331..346 /label= P432 /note= "C-protein-specific antibody immunisation of rabbits" /note= "C-protein-specific antibody immunisation of rabbits" 1007..1020 antibody 377..390
/label= P430
/note= "C-protein-specific animunisation of rabbits"
784..797 1081 YDQLIQIKKDKARNRPVLNLSSLRAQLSHRLVLK 1114 Ş AAE00897 standard; Protein; 1114 /label= P433 (first entry) Lycopersicon esculentum, 04-JUL-2001 AAE00897; Key Region Region Region RESULT 2 d

Region

TNIXERILSTLRKGEVIGDKKFEFLAFSSSQLRDNSVWMFASRPGLTANDIRAWMGDFSQ 480 TNIYERILSTLRKGFVIGDKKFEFLAFSSSQLRDNSVWMFASRPGLTANDIRAWMGDFSQ 480 IKNVAKYAARLGQSFGSSRETLSVLRHEIEVIPDVKVHGTSYVFSDGIGKISGDFAHRVA 540

421 481

421

g οy

Wed Nov

480

600 660 9 720 720 780 780 840 900

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Soybean; plant; RNA-directed RNA polymerase; gene mapping; gene marker; plant virus resistance; plant breeding.
      THISTILSTERGEVIGDKKFEFLAFSSSOLRDNSVWMFASRPGLFANDIRAWMGDFSQ
                                                                       601 YLNRQLITLLSTLGVKDEVLEQKQKEAVDQLDAILHDSLKAQEALELMSPGENTNILKAM
                                                                                                                                                                                                                                                                  LNCGYKPDAEPFLSMMLQTFRASKLLDLRTRSRIFIPNGRTMMGCLDESRTLEYGQVFVQ
                                                                                                                                                                                                                                                                                                                              EEVEEYFTNY IVNDSLGI IANAHVVFADREPDMAMSDPCKKLAELFSIAVDFPKTGVPAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          901 IPSQLRPKEYPDFMDKPDKTSYISERVIGKLFRKVKDKAPQASSIATFTRDVARRSYDAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481 IKNVAKYAARLGQSFGSSRETLSVLRHEIEVIPDVKVHGTSYVFSDGIGKISGDFAHRVA
                                                                                                                  SKCGLQYTPSAFQIRYGGYKGVVGVDPDSSMKLSLRKSMSKYESDNIKLDVLGWSKYQPC
                                                                                                                                                                                YLNRQLITLLSTLGVKDEVLEQKQKEAVDQLDAILHDSLKAQEALELMSPGENTNILKAM
                                                                                                                                                                                                                                               INCGYKPDAEPFLSMMLQTFRASKLLDLRTRSRIFIPNGRTMMGCLDESRTLEYGQVFVQ
                                                                                                                                                                                                                                                                                                            FIGAGHGEFSDDLHPFNNSRSTNSNFILKGNVVVAKNPCLHPGDIRVLKAVNVRALHHMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPSQLRPKEYPDFMDKPDKTSYISERVIGKLFRKVKDKAPQASSIATFTRDVARRSYDAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVAVRALRKEARAWFKRRNDIDDMLPKASAWYHVTYHPTYWGCYNQGLKRAHFISFPWCV
                                                                                                                                                                                                                                                                                                                                                                          DCVVFPQKGKRPHPNECSGSDLDGDIYFVCWDQDMIPPRQVQPMEYPPAPSIQLDHDVTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEVDGFEDY IDEAFDYKTEYDNKLGNLMDYYGIKTEAEILSGGIMKASKTFDRRKDAEAI
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                                                                                                                                                                                                                                                                                                                       New nucleic acid molecules encoding polypeptides with RNA-directed RNA polymerase enzymatic activity, useful in modulating gene expression in plants, humans and animals, as well as in plant cell/tissue cultures or
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                    for
/label= P431
/note= "C-protein-specific antibody
immunisation of rabbits"
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RIEDEL L.
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plant breeding
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Matches 1114;
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Best Local
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                  Zhong
                  'n
                  Wang
                  Cahoon RE,
                 Sakai H,
                                                                                                                                                           Claim 10; Page 50-54; 62pp; English
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                  Weng
                                                                                            New nucleic acid fragments
                                                                                                                            plant virus resistance
                 EW,
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                 Orozco
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1125 AA; Sequence

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                                                                                                                  SMMSRANNILRTLRYGTSYLKAREMERDIVPRPRYFLHSLDDVKLSFGCQISKGRFSVLW 120
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                                                                                                                                                     GSTEVSIQFGIGLKKFFFFLSSGSADYKLQLSYENIWQVVLHRPYGQNAQFILIQLFGAP 174
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                           Gaps
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                                                 MGKTIQVFGFPYLLSAEVVKSFLEKYTGYGTVCALEVKQSKGG-SRAFAKVQFADNISAD 59
                                                                 PGPALNVYFFRLVDPRRRNVACIEHALEKLYYIKECCYDPVRWLTEQYDGYLKGRQPPKS
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  Length 1125;
                         Indels
 62.1%; Score 3643; DB 21; 62.8%; Pred. No. 1.5e-317;
                         226;
                        Mismatches
          Similarity 62.8%; Pre-
2; Conservative 154;
                        712;
Query Match
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                                                                                                                                                                       Maize; plant; RNA-directed RNA polymerase; gene mapping; gene marker; plant virus resistance; plant breeding.
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                  PGDVRVLQAVDVPDLYHMYDCVVFPQKGPRPHPNECSGSDLDGDIYFVCWDHELIPSRPI
                                                                                                                     LAELFSIAVDFPKTGVPAEIPSQLRPKEYPDFMDKPDKTSYISERVIGKLFRKVKDKAPQ
                                                                                                                                                                                                          ASSIATFTRDVARRSYDADMEVDGFEDYIDEAFDYKTEYDNKLGNLMDYYGIKTEAEILS
  MMGCLDESRTLEYGQVFVQFTGAGHGEFSDDLHPFNNSRSTNSNFILKGNVVVAKNPCLH
                                                 PGDIRVLKAVNVRALHHMVDCVVFPQKGKRPHPNBCSGSDLDGDIYFVCWDQDMIPPRQV
                                                                                                      QPMEYPPAPSIQLDHDVTIEEVEEYFTNYIVNDSLGIIANAHVVFADREPDMAMSDPCKK
                                                                                                                                                                                                                                                             GGIMKASKTFDRRKDAEAISVAVRALRKEARAWFKRRN--DID----DMLPKASAWYHVT
                                                                                                                                                                                                                                                                           YHPTYWGCYNQGLKRAHFISFPWCVYDQLIQIKKDKARNRPVLNLSSLRAQLSH 1109
                                                                                                                                                                                                                                                                                                                              1072 YHPSYWGCYNEGMNRDHYLSFSWCVYPLLVQIKKEK-----LSIRRSSLEY 1117
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for controlling gene expression and
plant virus resistance
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expression and provide mechanisms to engineer plant virus resistance. They are also useful for plant breeding to develop lines with desired phenotypes.
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                                                                                              ADKIITLANNR-LYFGSSYLKAWEMKTDIV-QLRAYVDQMDGITLNFGCQISDDKF-AVL
                                                                                                                                                    GSTEVSIQFGIGLKKFFFFLSSGSADYKLQLSYENIWQVVLHRP--YGQNAQFLLIQLFG
                                                                                                                                                                                   173 APRIYKRL-----ENSCYSFFKETPDDQWVRTTDFPPS-WIGLSSSLCLQFRRGVRL
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                                                   DB 21;
                                                   tch 53.6%; Score 3140.5; DB 21 al Similarity 57.1%; Pred. No. 2.1e-272; 637; Conservative 163; Mismatches 270;
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                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEPHAFVHFAVFESÅGRAMDAAGQCNLILDGQPLKVSLGPKNPYSLNQRRRTTVPYKLAG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a plant SGS2 polypeptide. SGS2 is an RNA-dependent RNA polymerase and is involved in transgene silencing. Inactivation of SGS2 is used to increase transgene stability and expression in plants, particularly crop plants, especially maize, conbarley, sorghum, soya, sugar cane, beet, tobacco or cotton plants. Overexpression of SGS2 can be used to increase resistance to viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
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QASSIATFTRDVARRSYDADMEVDGFEDYIDEAFDYKTEYDNKLGNLMDYYGIKTEAEIL
                                SGGIMKASKTFDRRKDAEAISVAVRALRKEARAWFKRRNDIDD----MLPKASAWYHVTY
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llarity 34.6%; Pred. No. 9.9e-136;
Conservative 191; Mismatches 414;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of a plant SGS2 polypeptide.
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N-PSDB; AAH77704.
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Best Local Similarity
Matches 431; Conservi
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ITLNFGCQISDDKFAVLGSTEVSIQFGIGLKKFFFFLSSGSADY	RNBPCFGEPVSDHFFCIHHKEGISIPYKILFKISSLVQHGCIPGPAL	PPKSPSITLDDGLVYVRRVLYPCKVYFCGPEVNVSNRVLRNYSEDIDNELRVSFYDEEW	GLTANDIRA: :	DIERNGYVFSDGIGTITPDLADEVMEKLKLDVHYSPCAYQIRYAGWKLSLRKSMSKYESDNIKLDVLGWSKYQPCYLNRQLITLLSTLGVK	YKLNRILDDTDVAFEVL-TASCAEGGNTAAIMLSAGFKEKTEFHLRGMILSSYRIAQLWGL RTRSRIFIPNGRTWMGCLDESRTLEYGQVFVQFTGAGHGEFSDDLHPFN : :: : : : REKSRIFVTSGRWLMGCLDEAGILEHGQCFIQVSKPSIENCFSKHGSRFKETKTDLE NSRSTNSNFILKGNVVAKNPCLHPGDIRVLKAVNVRALHHWVDCVVFPQKGKRPHPNBC :: : :: :	SGSDLDGDIYEVCWDQDMIPP-RQVQP-MEYPPAPSIQLDHDVTIEEVEEYFTNYIVNDS	FRKUKDKAPQASSIATETRDVARRSYDADMEVDGFEDYID	ARAWEKRRDD DDMLPRASAWYHTYHPYWGZYNGLK FRKVEETIPDHENLSBEBKNILYBKRASAWYHYYHPE-WYKKSLELQDPDES -RAHFISFPWCVYDQLIQIKKDKARNRPVLNLSSLRAQ 1106
98 135 142 194 195 249	251 293 293	4 0 0 E	5 7 7	7 7 8 7 7	693 689 752 738 809	798 860 856 920	3 7 8 1	1031 1098 1070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 VRDEPEFGERWQDLFFCVQHAEGLKFP--VLFLVNALVHKGVISQHHLTPEFFGLLQRKE 332
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                                                                                                                                                                                                  Maize; plant; RNA-directed RNA polymerase; gene mapping; gene marker; plant virus resistance; plant breeding.
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Cahoon RE,
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Best Local Similarity 39.0%; Pred. No. 4.7e-133;
Matches 397; Conservative 168; Mismatches 346;
                                                                                                                                                                        Maize RNA-directed RNA polymerase, SEQ ID NO: 8.
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                                                                                     AAB28531 standard; Protein; 1164
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LPKASTGSGVRTNIYERILSTLRKGFVIGDKKFEFLAFSSSQLRDNSVWMFASRPGLTAN
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|DLLEKARIFVPKGRWLMGCLDELGVLEQGQCFIRATVPSLNSYFVKHGSRFS------
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                                                                'n
                                                                 Wang
                                                                Cahoon RE,
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40.9%; Pred. No. 7.2e-119;
Live 140; Mismatches 267;
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                                                                 Sakai
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                                                                                                                             New nucleic acid fragments encoding
for controlling gene expression and
plant virus resistance
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                        (DIOPO ) DU PONT DE NEMOURS & CO (PION-) PIONEER HI-BRED INT INC.
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                                                                                                      N-PSDB; AAC63741
37-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Tomato; gene therapy; RNA-directed RNA polymerase; RdRP; gene expression;
transgenic plant; tissue culture; plant breeding; therapy; C-protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid molecules encoding polypeptides with RNA-directed RNA polymerase enzymatic activity, useful in modulating gene expression in plants, humans and animals, as well as in plant cell/tissue cultures or plant breading -
                                                                                                            1031 ARAWFK------KRADIDDMLPKASAWYHVTYHPTYWGCYNQGL-----KRAH 1072
                                         AFDYKTEYDNKLGNLMDYYGIKTEAEILSGGIMKASKTFDRRKD--AEAISVAVRALRKE 1030
                                                                          678 AWQCKCSYDAQLSALLSQYRVRTEAELVTGHITFLVKNSSKKQGDIKDRLKTAYSALRKE 737
                                                                                                                                            738 FKSTFESIASDQCEIGDDEKNLLYEM--KASAWYQVTYHPK-WVEKSRGILGPDGEEIPA 794
       KEDGQSYKSEKILGRLYRSIQ----EASNGDVVSQEVCTPNDLPYDIDLEVPGASDFLAS 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                              Tomato RNA-directed RNA polymerase 800 (RdRP800) protein.
                                                                                                                                                                                 1073 FISFPWCVYDQLIQIK---KDKARNRPVLNLSSLRAQLSHRL 1111
                                                                                                                                                                                                                   SLSFAWIPVDYLARIKLRCHGKVRVEGQKPVERLAAYISERI 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ħ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1182; DB 22;
Pred. No. 1.6e-97;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sanger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schiebel W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Column 39-42; 31pp; English.
                                                                                                                                                                                                                                                                                                           Ā
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Best Local Similarity 100.0%; Pi
Matches 218; Conservative 0;
                                                                                                                                                                                                                                                                                                           AAE00898 standard; Protein; 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0811583.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lycopersicon esculentum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WASSENEGGER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-289830/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIEDEL L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wassenegger M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6218142-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                              04-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                           AAE00898;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIED/)
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         622
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Zhong G;
                                                                                                                                                                                                                New nucleic acid fragments encoding RNA-directed RNA polymerase useful for controlling gene expression and providing mechanisms to engineer plant virus resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is part of a plant RNA-directed RNA polymerase protein. Polynucleotides encoding RNA-directed RNA polymerases were isolated from plant cDNA libraries. They are useful as probes for genetically and physically mapping genes, and as markers for traits linked to those genes. They are useful for controlling gene expression and provide mechanisms to engineer plant virus resistance. They are also useful for plant breeding to develop lines with desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IRYGGYKGVVGVDPDSSMKLSLRKSMSKYESDNIKLDVLGWSKYQPCYLNRQLITLLSTL 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              498 SRETLSVLRHEIEVIPDVKV--HGTSYVFSDGIGKISGDFAHRVASKCGLQ--YTPSAFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 417;
                                                                                                         Þ,
                                                                                                         Wang
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                                                                                                           Cahoon RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 6.9e-82;
; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
17.3%; Score 1013.5;
Best Local Similarity 48.3%; Pred. No. 6.9e
Matches 200; Conservative 80; Mismatches
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                                                                                                           Sakai
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                                        (DUPO ) DU PONT DE NEMOURS & CO (PION-) PIONEER HI-BRED INT INC.
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99US-0128094.
                                                                                                              Weng
                                                                                                              Odell JT, Orozco EM,
                                                                                                                                                    WPI; 2000-679376/66.
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                                                                                                                                                                            N-PSDB; AAC63738
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TSYISERVIGKLFRKVKDKAPQASSIATFTRDVARRSYDADMEVDGFEDYIDEAFDYKTE
                     1 ANAHVVFADQERMKAESPPCVQLAKLFSIAVDFPKTGVPALIPHELHVKEYPDFMEKLDK
ANAHVVFADREPDMAMSDPCKKLAELFSIAVDFPKTGVPAEIPSQLRPKEYPDFMDKPDK
                                                                                                                                                                                                                                                                                                                                                                                                                                    Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAA65171
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200050581-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid fragments encoding RNA-directed RNA polymerase useful for controlling gene expression and providing mechanisms to engineer plant virus resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is part of a plant RNA-directed RNA polymerase protein. Polymucleotides encoding RNA-directed RNA polymerases were isolated from plant cDNA libraries. They are useful as probes for genetically and physically mapping genes, and as markers for traits linked to those genes. They are useful for controlling gene expression and provide mechanisms to engineer plant virus resistance. They are also useful for plant breeding to develop lines with desired
                                                                                                                                          -QPFFCNDDGKT---AVIVGKVAITKNPCLHPGDVRVLEAVIDPGLDARGLIDCVVFPQR 300
                                                                                                                                                                                                 LHPF--NNSRSTNSNFILKGNVVVAKNPCLHPGDIRVLKAVNVRAL--HHMVDCVVFPQK 788
    GVKDEVLEQKQKEAVDQLDAILHDSLKAQEALELMSPGENTNILKAMLNCGYKPDAEPFL 673
                                                             SMMLQTFRASKLLDLRTRSRIFIPNGRTMMGCLDESRTLEYGQVFVQFT-GAGHGEFSDD 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polymerase; gene mapping; gene marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhong
                                                                                GKRPHPNECSGSDLDGDIYFVCWDQDMIPPRQVQPMEYPPAPSIQLDHDVTIEEVEEYFT
                                                                                                                                                                                                                                         NYIVNDSLGIIANAHVVFADREPDMAMSDPCKKLAELFSIAVDFPKTGVPAEIP 902
                                                                                                                                                                                                                                                            11.9%; Score 697.5; DB 21; Length 230; ilarity 60.1%; Pred. No. 6.5e-54; Conservative 30; Mismatches 56; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cahoon RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Maize RNA-directed RNA polymerase, SEQ ID NO: 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sakai H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plant virus resistance; plant breeding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23; Page 55-56; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                 AAB28534 standard; Protein; 230 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plant; RNA-directed RNA
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N-PSDB; AAC63743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 140; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Orozco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200060097-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                        733
                                                                                           186
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32;
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                                                                        980 YDNKLGNLMDYYGIKTEAEILSGGIMKASKTFDRRKDAEAISVAVRALRKEARAWFKRRN 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    386 EDIDNFLRV---SEVDEEWEKLYSTDL------LPK-------ASTGSG 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               419 VRINIYERILSTLRKGFVIGDKKFE-FLAFSSSQL-----RDNSVWMFASRPGLTANDI 471
                                                                                                        Gaps
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Novel polynucleotide encoding a polypeptide which has a silencing activity and comprising a RNA-dependent RNA polymerase domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.1%; Score 297; DB 21; Length 1402;
llarity 20.4%; Pred. No. 1.4e-16;
Conservative 133; Mismatches 323; Indels 228;
                                                                                                                                                                                      1040 DIDD----MLPKASAWYHVTYHPTYWGCYNQGLKRAHFISFPWCVYDQLIQIK 1088
                                                                                                                                                                                                                   3ene silencing; quelling deficient; qde-1; al-1.
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                                                                                                                                                                                                                                                                                                                                                                                   AAB13956 standard; Protein; 1402
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nes 175; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRALR-----KEARAWFKRRNDIDDMLPKASAWYHVTYHPTYWGCYNQGLKRAHFISFP 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----PKFV 1321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAWMGDFSQIKNVAKYAARLGQSFGSSRETL---SVLRHEIEVIPDVKVHGTSYVFSDGI
                                                                                            -----SRI-----SPGTGEVMILEPHQIRHKTDLL---SPSGTGEVMNDGV
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Soybean; plant, RNA-directed RNA polymerase; gene mapping; gene marker; plant virus resistance; plant breeding.
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Gaps

Sequence

Query Match

Local

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The present invention relates to von Willebrand factor binding protein o polypeptide (vWb) from Staphylococci. The vWb and immunogens of vwb are useful in vaccines to combat infections caused by Staphylococci. The invention is also useful for detection of staphylococcal infection and purifying von Willebrand factor from a complex solution. The present sequence is Staphylococcus lugdunensis vWbl protein.
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                                                                                589 LDVLGWSKYQPCYLNRQLITLLSTLGVKDEVLEQKQKEAVDQLDAILHDSLKAQEALELM 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 YLLSAEVVK-----SFLEKYTGYGTV----CALEV-KQSKGGSRAFAKVQFADNISAD 59
                                                                                                                                                                                                                                                                                                                                                                                                                            factor binding protein; vWb; immunogen; antibacterial;
                                                                                                         New von Willebrand factor binding protein from Staphylococci, useful for determining and treating staphylococcal infection
                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus lugdunensis von Willebrand factor binding protein.
                                               5
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                                                                                                                                                         669
                                                                                                                                                                                         111
             Length 111;
                                                                                                                                                                          649 SPGENTNILKAMINCGYKPDAEPFLSMMLQTFRA-SKLLDLRTRSRIFIPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.5%; Score 146; DB 23;
19.9%; Pred. No. 0.01;
ive 94; Mismatches 243;
                                                 49;
             ; Score 167; DB 21;
; Pred. No. 9.3e-07;
18; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ahlen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..4/
/label= Signal_peptide
48..2060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                   AAE20967 standard; Protein; 2060 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         claim 3; Page 35-41; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jacobsson K,
               2.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-APR-2001; 2001WO-SE00766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-OCT-2000; 2000SE-0003573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus lugdunensis.
                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BIOS-) BIOSTAPRO AB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-304928/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2060 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 147; Conserv
                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAD3337;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Willebrand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200228892-A1
                                                                                                                                                                                                                                                                                                                                                        01-JUL-2002
                                                   43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
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                                The present sequence is part of a plant RNA-directed RNA polymerase protein. Polymerases enceding RNA-directed RNA polymerases were isolated from plant cDNA libraries. They are useful as probes for genetically and physically mapping genes, and as markers for traite linked to those genes. They are useful for controlling gene expression and provide mechanisms to engineer plant virus resistance. They are also useful for plant breeding to develop lines with desired
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                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                         1 MGKTIQVFGFPYLLSAEVVKSFLEKYTGYGTVCALEVKQSKGG-SRAFAKVQFADNISAD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rice; plant; RNA-directed RNA polymerase; gene mapping; gene marker;
plant virus resistance; plant breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang J,
                                                                                                                                                                                                                                                                      23; Indels
                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                  Score 197; DB 21;
Pred. No. 1.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rice RNA-directed RNA polymerase, SEQ ID NO: 16.
                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                     SMMSRANNILRTLRYGTSYLKAREMERDIV 90
                                                                                                                                                                                                                                                                                                                                                                               60 KIITLANN---RLYFGSSYLKAWEMKTDIV 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid fragments encoding
for controlling gene expression and
plant virus resistance
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                                                                                                                                                                                                                  3.4%; Scor.
48.9%; Pred
Page 59; 62pp; English.
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                                                                                                                                                                                                 90 AA;
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N-PSDB; AAC63744
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or

Db 263 Qy 114 Db 311 Qy 170 Db 481 Qy 297 Db 530 Qy 351 Db 573 Qy 411 Db 619 Qy 471 Db 670 Qy 557 Db 730 Qy 557 Db 730 Qy 617 Db 785 Db 785

Search completed: November 6, 2002, 03:44:43 Job time: 51 secs

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Sequence 3, Appli
Sequence 8, Appli
Sequence 69, Appl
Sequence 112, App
Sequence 69, Appl
Sequence 69, Appl
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Sequence 5438, Ap
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5864
1 MGKTIQVEGFPYLLSAEVVK......RPVLNLSSLRAQLSHRLVLK 1114
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1: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/PacKfiles1.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-269-861A-8
US-08-974-549A-112
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US-09-430-323-69
US-09-430-323-69
US-09-430-123-69
US-08-488-940-1
US-08-56-737-11
US-08-754-490-10
US-08-754-490-10
US-09-253-31A-10
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US-09-253-341-10
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US-09-134-001C-5438
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                                                                                                                                                                                                                                                                                                                                            Title:
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Sequence 52, Appl Sequence 28, Appl Sequence 28, Appl	Sequence 2, Appli Sequence 4, Appli Sequence 3, Appli Sequence 1, Appli	Sequence 18, Appl Sequence 26, Appl Sequence 26, Appl	Sequence 26, Appl Sequence 26, Appl Sequence 26, Appl	Sequence 26, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 25, Appli
US-09-315-793-52 US-09-224-024-28 PCT-US94-07902-28	US-09-232-446B-2 US-08-48B-940-4 US-08-48B-940-3 US-08-75-527-1	US-08-488-940-18 US-08-754-490-26 US-08-922-505A-26	US-09-260-952A-26 US-09-253-341-26 US-09-253-331A-26	US-09-261-040-26 US-08-882-083-2 US-08-558-107-2 US-09-243-539-2 US-09-453-7028-257
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ALIGNMENTS

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RESULT 1

US-08-415-581-2

US-08-6115-581-2

Sequence 2, Application US/08811583

Patent No. 6218142

GENERAL No. 6218142

GENERAL INFORMATION:

APPLICANT: Riedel, Monitied

APPLICANT: Schiedel, Winfited

APPLICANT: USA

CORRESPONDENCE ADDRESS:

ADDRESSEE: FISH New York

COMPUTER: READABLE FORM:

WEDIUM TYPE: Floppy disk

COMPUTER: READABLE FORM:

WEDIUM TYPE: Patentin Release #1.0, Version #1.30

COMPUTER: READABLE FORM:

WEDIUM TYPE: Retain Number: US/08/911,583

FILLING DATE: APPLICANTION DATA:

APPLICANTION NUMBER: WPO-1

FELEPAN: APPLICANTION NUMBER: WPO-1

TELEPAN: 212-59-9000

INFORMATION TYPE: PROTEIN

MOLECULE TYPE: Amino acids

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1 MGKTIQVFGFPYLLSAEVVKSFLEKYIQYGTVCALEVKQSKGGSRAFAKVQFADNISADK 60

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                                                          IQFGIGLKKFFFFLSSGSADYKLQLSYENIWQVVLHRPYGQNAQFLLIQLFGAPRIYKRL 180
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                                                                                                            ENSCYSFEKETPDDOWVRTTDFPPSWIGLSSSLCLOFRRGVRLPNFEESFFFYAERENI
                                                                                                                                                                                                                                  LVTPCKVYFCGPEVNVSNRVLRNYSEDIDNFLRVSFVDEEWEKLXSTDLLFKASTGSGVR
                                                                                                                                        TLQTGFTFFVSQKSALVPNVQPPEGISIPYKILFKISSLVQHGCIPGPALNVYFFRLVDP
                    IITLANNRLYFGSSYLKAWEMKTDIVQLRAYVDQMDGITLNFGCQISDDKFAVLGSTEVS
 MGKTIQVFGFPYLLSAEVVKSFLEKYTGYGTVCALEVKQSKGGSRAFAKVQFADNISADK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         700 RIMMGCLDESRILEYGQVFVQFTGAGHGEFSDDLHPFNNSRSINSNFILKGNVVVAKNPC
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                                                                          APPLICANT: Wassenegger, Michael
APPLICANT: Riedel, Leonhard
APPLICANT: Schiebel, Winfried
APPLICANT: Schiebel, Winfried
APPLICANT: Sanger, Heinz
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: POLYPEPTIDES HAVING THE ENZYMATIC
TITLE OF INVENTION: RNA-DIRECTED RNA POLYMERASE (RGRP)
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 20.2%; Score 1182; DB 4; I Best Local Similarity 100.0%; Pred. No. 2.3e-112; Matches 218; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        880 KKLAELFSIAVDFPKTGVPAEIPSQLRPKEYPDFMDKP 917
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STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,583
FILING DATE: 05-MAR-1997
CLASSIFFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-09-269-861A-8
US-09-269-861A-8
; Sequence 8, Application US/09269861A
; Patent No. 6468775
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MPG-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
                Sequence 3, Application US/08811583 Patent No. 6218142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-811-583-3
                                                              GENERAL INFORMATION:
US-08-811-583-3
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1012 DRRKDAEAISVAVRALRKEARAWFKRRN-----DIDDM-----LPKASAWYHVTYHPT 1059
952 VARRSYDADMEVDGFEDYIDEAFDYKTEYDNKLGNLMDYYGIKTEAEILSGGIMKASKTF 1011
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                                         587 LGRKLRKMFIPSPGY-DYIVSA----DYSQIELRLLAHF--SEEPKLIEA--YQKGEDI
                                                                                                                           637 HRKTASEVFGVSLEEVTPEMRAHAKSVNFGIVYGISDFGLGRDLKIPREVAGKYI----
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                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.9%; Score 112.5; DB 3;
ilarity 18.2%; Pred. No. 0.12;
Conservative 109; Mismatches 258;
                                                                                                                                                                                                                                                    Sequence 69, Application US/08851843A

Sequence 69, Application US/08851843A

Patent No. 6093809

GENERAL INFORMATION

APPLICANT: Cech, Thomas R.

APPLICANT: Lingner, Joachim

APPLICANT: Chapman, Karen B.

APPLICANT: Maxamura, Toru

APPLICANT: Marenews, William H.

TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

APPLICANT: Andrews, William H.

TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOWNSend and Townsend and Crew L.
CITY: San Francisco
STATE: California
COUNTRY: United States ~ [ ]
ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
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Matches 128; Conserva
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APPLICANT: Ankenbauer, Waltraud
APPLICANT: Markau, Ursula
APPLICANT: Markau, Ursula
APPLICANT: Warkau, Ursula
APPLICANT: Warkau, Ursula
APPLICANT: Schmitz-Agheguian, Gudrun
APPLICANT: Reiser, Astrid
APPLICANT: Reiser, Astrid
APPLICANT: Benbichler, Christine
APPLICANT: Benchard
APPLICANT: Bonch-Osmolovskaya, Elizaveta
APPLICANT: Bonch-Osmolovskaya, Elizaveta
APPLICANT: Bonch-Osmolovskaya, Elizaveta
APPLICANT: Bonch-Osmolovskaya, Elizaveta
TITLE OF INVENTION: THERMOSTĀBLE DNA POLYMERASE FROM CARBOXYDOTHERMUS HYDROGENOFORMAN
TITLE REFERENCE: 4494
CURRENT FILING DATE: 1999-11-22
PRIOR FILING DATE: 1997-10-01
PRIOR FILING DATE: 1997-10-01
PRIOR FILING DATE: 1997-10-03
PRIOR FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    410 LPKASTGSGVRTNIYERILSTLRKGFVIGDKKFEFLAFSSSOLRDNSVWMFASRPGLTAN 469
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1.9%; Score 113.5; DB 4; Length 831;
Best Local Similarity 19.0%; Pred. No. 0.068;
Matches 158; Conservative 119; Mismatches 298; Indels 257
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; ORGANISM: Carboxydothermus hydrogenoformans
US-09-269-861A-8
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LENGIH: 831
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LSSGSADYKLQLSYENIWQVVLHRPYGQNAQFLLIQLFGAPRIYKRLENSCYSFFKETPD 193
                                                                 LVSTFPNYLISILESKNWQ-------LLLEIIGSDAMHYLLSKG--SIFEALPN 174
                                                                                                                                                                                                                DNYLQISGIPLFKNNVFEETVSKKRKRTIETSITQNKSARKEVSWNSISISRFSIFYRSS 234
                                                                                                                                                                                                                                                                                     RLPNFEESFFHYAERENNITLQTGFTFFVSQKSALVPNVQPPEGISIPYKILFKISSLV-
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                                                                                                                                              DOWVRITDFP------PSWIGLSSSLCLQFRRGV
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APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               590 TRSRIFIPNGRT-----MMGCLDE--SRTLEYGQVFVQ 720
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2.08-974-549A-112
; Sequence 112, Application US/08974549A
; Patent No. 6166178
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APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: California
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281 QHGCIPGPALNVYFFRLVDPRRRNVACIEHALEKLYYIKECCYDPVRWLTEQYDGYLKGR 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           341 QPPKSPSITLDDGLV--YVRRVLVTPCKVYFCGPEVNVSN-RVLRNYSEDIDNFLRVSFV 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 LVSTPPNYLISILESKNWQ------LLLEIIGSDAMHYLLSKG--SIFEALPN 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 DQWVRITDFP------PSWIGLSSSLCLQFRRGV 221
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COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn BATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 10-OCT-1996
PRIOR APPLICATION NUMBER: US 08/44,419
FILING DATE: US 08/844,419
FILING DATE: US 08/846,017
FILING DATE: US 08/851,843
FILING DATE: US 08/851,843
FILING DATE: US 08/851,843
FILING DATE: US 08/851,951
FILING DATE: US 08/851,550
FILING DATE: US 08/851,550
FILING DATE: US 08/811,312
FRICK APPLICATION NUMBER: US 08/911,312
FRICK APPLICATION NUMBER: US 08/912,951
FILING DATE: US 08/911,312
FRICK APPLICATION NUMBER: US 08/915,503
FILING DATE: US 08/915,503
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1.9%; Score 112.5; DB 4;
Best Local Similarity 18.2%; Pred. No. 0.12;
Matches 128; Conservative 109; Mismatches 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPA: (415) 576-0200
TELEPA: (415) 576-0300
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 988 amino acids
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TOPOLOGY: linear
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| | : | : | : | : | | : | 329 DDEKILSYSLKPUVVPAFLRSILV---RVF---PKLIWGNQRIFEIILKDLETFLKLSRY 382
                                                                                                       ESFSLHYIMSNIKISEIEWLVLGKRSNAKMCLSDFEKRKQIFAEFIYWLYNSFIIPILQS 442
                                                                                                                                                                                -----MGDFSQIKNVAK-YAARLGQS---FGSSRETL----SVLRH----EIEVIP-DVK 516
                                                                                                                                                                                                                                                                                                                            VHGTSYVFSDGIGKISGDFAHRVASKCGLQYTPSAFQIRYGGYKGVVGVDPDSSMKLSLR 576
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COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFCATION: 536
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         690 TRSRIFIPNGRT------MMGCLDE--SRTLEYGQVFVQ 720
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APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Greeg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE O' INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                  EFLAFSSSQLRDNSV-----WMFASRPGLTANDIRAW----
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APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
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APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
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Patent No. 6261836
GENERAL INFORMATION:
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CLASSIFICATION: 536
PRIOR APPLICATION DATE: 08/724,643
PILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATCORNEY AGENT INCOMATION: 08/724,643
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
RECISTRATION NUMBER: 36,429
REEFERNENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INPORMATION:
TELETEAX: (415) 576-0200
TELETEAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 69:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 988 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-854-050-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222
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516

632 644

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GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENITION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC

TITLE OF INVENITION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT PAPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

NUMBER OF EXQ ID NOS: 5674

LENGTH: 1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             539 VASKCG--LQYTPSAFQ--IRYGGYKGVVGVDPDSSMKLSLRKSMSKYESDNIKLDVLGW 594
QHGCIPGPALNVYFFRLVDPRRRNVACIEHALEKLYYIKECCYDPVRWLTEQYDGYLKGR 340
                                           ----NHYCPYIDTH 328
                                                                                                                                                                                                                                                                                                 443 FFYITESSDLRNRTVYFRKDIWKLLCRPFITSMKMEAFEKINENNVRMDTQKTTLPPAVI 502
                                                                                                                                                                                                                                                                                                                                                                                                                                               517 VHGTSYVFSDGIGKISGDFAHRVASKCGLQYTPSAFQIRYGGYKGVVGVDPDSSMKLSLR 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    645 MV-----PFEKVVQLLSMKTSDTLFVDFVDYWTKSSSEIF--KMLKEHLSGHIVKIGNSQ 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  595 SKYQPCYLNRQLITLLSTLGVKD---EV-LEGKQKEAVDQLDAILHDSL-KAQEALBLMS
                                                                                                                                                                                                                                                                                                                                                         475 -----MGDFSQIKNVAK-YAARLGQS---FGSSRETL----SVLRH----EIEVIP-DVK
                                                                                                                DE-------EWEKLYSTDLLPKASTGSGVRTNIYERILSTLRKGFVIGDKKF
                                                                                                                                                                                                                     383 ESFSLHYLMSNIKISEIEWLVLGKRSNAKMCLSDFEKRKQIFAEFIYWLYNSFIIPILQS
                                                                                                                                                                                                                                                                                                                                                                                   577 KSMSKYESDNIKLD----VLGWSKYQPCYLNRQLITLLSTLGVKDEVLEQKQKEAVDQLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           633 AILHDSLKAQEALELMSPGENTNILKAMLNCGYKPDAEPFLSMMLQTFRASKLLDL---R
                                                                                                                                                                                                                                                                  443 EFLAFSSSQLRDNSV-----WMFASRPGLTANDIRAW-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               563 VYMKLLTFKKDLLK-----HRM-------FGRKKYFVRLDIKSCY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         690 TRSRIFIPNGRT------MMGCLDE--SRTLEYGQVFVQ 720
                                           287 OSTVVPKRLLKVY--PLIEQTAKRLHRI--SLSKVY------
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1.9%; Score 109; DB 4; Labet Local Similarity 19.1%; Pred. No. 0.4;
Matches 117; Conservative 85; Mismatches 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
US-09-134-001C-5319
Sequence 5319, Application US/09134001C
; Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Staphylococcus epidermidis US-09-134-001C-5319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVSTFPNYLISILESKNWQ-------LLEIIGSDAMHYLLSKG--SIFBALPN 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLPNFEESFFHYAERENNITLQTGFTFFVSQKSALVPNVQPPEGISIPYKILFKISSLV- 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 LSSGSADYKLQLSYENIWQVVLHRPYGQNAQFLLIQLFGAPRIYKRLENSCYSFFKETPD 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----PSWIGLSSSLCLOFRRGV 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNYLQISGIPLEKNNVFEETVSKKRKRTIETSITQNKSARKEVSWNSISISRFSIFYRSS 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDITUR TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                               LLP
                                                                                                                                                                                                  Morin, Gregg B.

Morin, Gregg B.

Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE:
Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.9%; Score 112.5; DB 4; Best Local Similarity 18.2%; Pred. No. 0.12; Matches 128; Conservative 109; Mismatches 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAPLICATION DATE:

FILING DATE: 29-Oct-1999
CLASSIFICATION: (UNKNOWN)
CLASSIFICATION: (UNKNOWN)
CRASSIFICATION NUMBER: US 08/854,050
FILING DATE: 09-MX-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MX-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-09-430-323-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
                                               Sequence 69, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
                                                                                                              cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                     APPLICANT: Cech,
                            US-09-430-323-69
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       RESULT 7
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---RDVARRSYDADMEVDG-----FEDYIDEAFDYKTEYDNKLGNLMDY
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; MOLECULE TYPE: protein
US-08-488-940-1
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Best Local Similarity
Matches 176; Conserva
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US-08-488-940-1
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                                                            339
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   SFRNSGNNPSWMILDVLPIIPPEIRPMVQLDGGRFATSDLNDLYRRVINRNNRLKRLLDL 282
                                                                                                                                                                       | | : : : : | | | : : | | 400 RMDDEVWDVLEDVITEHPVLLNRAPTLHRLGIQAFEPTLVEGRAIRLHPLVTTAYNADFD
                                                                                                                                                                                                                                   --SRIFIPNGRTMMGCLDES--RTLEYGQVFVQFTGAGHGEFSDDLHPFNNSRSTNSNFI
                                                           283 GAPGIIVONEKRM---LOEAVDALIDNGKRGRPVTGPGNRPLKSLSHMLKGKOGRFRONL
                                                                                           L-----KGNVVVAKNP------CLHPGDIR------VLK------AVNVR-----
                                                                                                                                                   775 ------NECSGSDLD
                                                                                                                                                                                                               ---CWDQDMIPPRQVQPMEYPPAPSIQLDHDVTIEEVEEYF
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APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REPRENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
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20.5%; Pred. No. 0.29;
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Matches 67; Conservative
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US-09-562-737-11
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                                                                                        218 RRGVRLPNFEE-SFFHYAERENNITLQTGFTFF-----VSQKSALVPNVQPPEG-ISIP 269
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GEEHEQTHRAIFRFVPRHEDELELEVDDPLLVELQAEDYWXEAYNMRT---GARGVFPAY
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STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER: ELOPPY disk

COMPUTER: IBM PC compatible

COMPUTER: PATEM: PC-DOS/MS-DOS

SOFTWARE: PATEMIT Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,940

FILING DATE: 09-JUN-1995

CLASSIFICATION: 514

ATTORNEY/AGBNT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Reed, GUY L.
TILLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 105.5; DB 2; ilarity 19.9%; Pred. No. 0.89; Conservative 114; Mismatches 360;
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REGISTRATION NUMBER: 34,819
REFREENCE/POCKET NUMBER: 0543:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1194 amino acids
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                       511
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408 DLLPKASTGSGVRTNIYERILSTLRKGFVIGDKKFEFLAFSSSQLRDNSVWMFASRPGLT 467
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                                                                  -NDIRAWMGDFSQ----IKNVAKYAARLGQSFGSSRETLSVLRHEIEV
                                                                                                596 IYERDSSIVTHDNDIFRTILPMDQEFTYRVKN-REQAYRINKKSGLNEE-----
                                                                                                                                  IPDVKVHGTSYVFSDGIGKISGDFAHRVASKCGLQYTP----SAFQIRYGGYKGVVGV
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TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
COUNTRY: USA
COMPUTER READBLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,940
FILING DATE: 09-JUN-1995
CLASSIFTCATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street CITY: Boston STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08488940
Patent No. 5854049
GENERAL INFORMATION:
APPLICANT: Reed, Guy L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fraser, Janis K. REGISTRATION NUMBER: 34,819
                                                                                                                                                                    ----INNIDITSE---
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                                                                                                                                                                                                                                                 ; DB 2; Length 1181; 0.98;
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                                                                                                                                                                                                                                                   Query Match 1.8%; Score 105; DB 2; LA
Best Local Similarity 19.9%; Pred. No. 0.98;
Matches 174; Conservative 114; Mismatches 359;
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   05433/009001
                                                                                                                                                                                                                                                                                                                                                                                                 276 ISSLVQH--GCIPG--PALNVYFFRL--
REFERENCE/DOCKET NUMBER: 0543
TELECOMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1181 amino acids
                                                                                                                                                               not relevant
                                                                                                                                                                                                 MOLECULE TYPE: protein US-08-488-940-2
                                                                                                                                              amino acid
                                                                                                                                                                                linear
                                                                                                                                              TYPE: amino a STRANDEDNESS:
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VLEQKQKEAVDQLDAI --- LHDSLKAQEALELMSPGENTNILKAMLNCGYKPDAEPFLSM 675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367 VYFCGPEVNVSNRVLRNYSEDIDNFLRVSFVDEEWEKLYST--DLLPK----ASTGSGVR 420
                                                                                                                                                                                                                                                 ---YRTLSSTLYRRPFNIG-----INNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTV 407
728 EFSDDLHPFNNSRSTNSNFILKGNVVVAKNPCLHPGDIRVLKAVNVRALHHMVDCVVFPQ
                                                                                                                                                                                                                                                                                                                                                                            408 DSLDEIPPQNNNVPPRQGFSHRLSHVSMFRS-----GFSNSSVSIIRAPMFSWTHRSAT
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                                                                                                                                              ----PLYGTMGNAAPQQRIVAQLGQGV-
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                                                                                                                                                                                                              121 TNIYERILSTL-RKGFVIGDKKFEFLAFSSSQLR--DNSVWMFASRPGLTA-----
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 03-SEP-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/08922505A
Sequence 10, Application US/08922505A
Patent No. 6110464
GENERAL INFORMATION
ARIVAR: MAIVAR: Thomas
APPLICANT: Gilmer, Amy Jelen
TITLE OF INVENTION: BROAD-SPECTRUM (-ENDOTOXINS NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
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NAME: KITCHEL!, BALDAIRS S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:163
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P.O. Box 4433
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STREET: P.O. Bo
CITY: Houston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 FGCQISDDKFAVLGSTEVS----IQFGIGLKKFFFFLSSGSADYKLQLSYENIWQVVLH 156
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                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Malvar, Thomas
APPLICANT: Malvar, Any Johan
APPLICANT: Gilner, Any Johan
TITLE OF INVENTION: BELIA-ENDOTOXINS WITH NOVEL BROAD SPECTRUM
TITLE OF INVENTION: INSECTICIDAL ACTIVITY
NUMBER OF SEQUENCES: 30
CORRESPONDENCES: 30
CORRESPONDENCES: ADDRESSE: ADDRE
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Best Local Similarity 18.2%; Pred. No. 1.2;
Matches 168; Conservative 112; Mismatches 301; Indels 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----EGISIPYKILFKISSLVQHGCIPGPALN-----
                                                                                           1018 AYRINKKSGLNEEINNTDLISEKYYVLKKGEKPYD 1052
                                      LGNLMDYYGIKTE---AEILSGG---IMKASKTFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 474-757
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/754,490
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Arnold, White & Durkee P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
                                                                                                                                                                                                              US-08-754-490-10
; Sequence 10, Application US/08754490
; Patent No. 6017534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1177 amino acids
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TOPOLOGY: linea.
N.ECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Sequence 10, Application US/09260952A

Patent No. 6224649

GENERAL INFORMATION:
APPLICANT: Malvar, Thomas
APPLICANT: Glimer, Amy Jelen
TITLE OF INVENTION: NOVEL BROAD SPECTRUM INSECTICIDAL ACTIVITY
FILE REFERENCE: MGO-217

CURRENT APPLICATION NUMBER: US/09/260,952A

CURRENT PILIC DATE: 1999-03-02

SOFTWARE: PATENTIN VOY: 2.1

SEQ ID NO S: 30

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 1.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PV---LENFDGSFRGSAQGIERSIRSPHLMDILNSITIYTDAHRGYYYWSGHQIMASP-- 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 FGCQISDDKFAVLGSTEVS----IQFGIGLKKFFFFLSSGSADYKLQLSYENIWQVVLH 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 RPYG--QNAQFLL-----IQLFGAPRIYKRLE--NSCYSFFKETPDDQWVRTTDFP 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------VYFFRLVDPRRRNVACIEHALEKLYYIKECCYD 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 DSLDEIPPQNNNVPPRQGFSHRLSHVSMFRS-----GFSNSSVSIIRAPMFSWTHRSAT 461
 --ETVNVPGTGSLWPLSAQSP 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      462 PINTIDPERIIQIPLVKAHTLQSGITVVRGPGFTGGDILRRTSGGPFAVTIVNINGQLPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 YNC-LSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL-VDIIWGI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 PSWIGLSSSLCLQFRRGVRLPNFEESFFHYAERENNITLQTGFTFFVSQKSALVPNVQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 RVWGPDSRDWVRYNQFRRELTLTVLDIVALFPNYDSRRYPIRTVSQLTREIY----TN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367 VYFCGPEVNVSNRVLRNYSEDIDNFLRVSFVDEEWEKLYST--DLLPK----ASTGSGVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 INIYERILSTL-RKGFVIGDKKFEFLAFSSSQLR--DNSVWMFASRPGLTA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------NDIRAWMGDFSQIKNVAKYAARLGQSFGSSRETLSVLR-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: coding US-09-260-952A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.8%; Score 104; DB 4; L. Best Local Similarity 18.2%; Pred. No. 1.2; Matches 168; Conservative 112; Mismatches 301;
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     ---EIYLIRYN---AKH-
                                                                     812
                                      788 KGKRPHPNECS----GSDLD 803
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                                                                     792 IGKCGEPNRCAPHLEWNPDLD
       756 EDSQDL-----7
                                                                                                                         RESULT 14
US-09-260-952A-10
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                                                                                                                                                                                             1.8%; Score 104; DB 3; Length 1177;
ilarity 18.2%; Pred. No. 1.2;
Conservative 112; Mismatches 301; Indels 340;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (512)418-3000
TELEFAX: (512)474-7577
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERIZIES:
LENGTH: 1177 amino acids
                                                                                                      TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-922-505A-10
                                                                                                                                                                                                             Best Local Similarity
Matches 168; Conserva
                                                                                                                                                                                              Query Match
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102 FGCQISDDKFAVLGSTEVS----IQFGIGLKKFFFFLSSGSADYKLQLSYENIWQVVLH 156
                          13 YNC-LSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL-VDIIWGI---
                                                                                                                                                                           -----EGISIPYKILFKISSLVQHGCIPGPALN------
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Job time : 28 secs
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                                                                                                                                            PINPALREEMRIQF-------
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                                  522 RYRARIRYASTTNLRIYVTVAGERIFAGQFNKTMDTGDPLTFQSFSYATINTAFTFFPMSQ 581
                                                                                                                     519 VLEQKQKEAVDQLDAI --- LHDSLKAQEALEIMSPGENTNILKAMINCGYKPDAEPFLSM 675
                                                                                                                                                 640 VTDYH----IDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQ 695
                                                                                                                                                                              MLQTFRASKLLDLRTRSRIFIPNGRTMMGCLDES-RTLEYGQV-----FVQFTGAGHG 727
                                                                                                                                                                                                                                      EFSDDLHPFNNSRSTNSNFILKGNVVVAKNPCLHPGDIRVLKAVNVRALHHMVDCVVFPQ 787
                                                                                                                                                                                                                                                                EDSQDL-----EIYLIRYN---AKH-----EIVNVPGTGSLWPLSAQSP 791
      ----DPDSSMKLSLRKSMSKY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/09/253,341
FILING DATE: 19-Feb-1999
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: BROAD-SPECTRUM (-ENDOTOXINS NUMBER OF SEQUENCES: 35 CORRESPONDANCE ADDRESS: 35 ADDRESS: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston STATE: Texas COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
1.8%; Score 104; DB 4; L
Best Local Similarity 18.2%; Pred. No. 1.2;
Matches 168; Conservative 112; Mismatches 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERRNCE/DOCKET NUMBER: MECO:163
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-253-341-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/922,505
FILING DATE: 03-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (512)418-3000
TELEPAX: (512)474-7577
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1177 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/09253341 Patent No. 6242241 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Malvar, Thomas
Gilmer, Amy Jelen
                                                                                                                                                                                                                                                                                                                          IGKCGEPNRCAPHLEWNPDLD 812
       PSAFQIRYGG ----YKGVVGV --
                                                                                                                                                                                                                                                                                               788 KGKRPHPNECS----GSDLD 803
                                                               ESDNIKLDVLGWSKYQPCYLNR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 77210
COMPUTER READABLE FORM:
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                                                                                                                                            --FGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAES----FREWEAD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----NDMNSALTTAIPLFA-----VQNYQVP 156
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                                                                                                                                                                                                                                                                                                          PSWIGLSSSLCLQFRRGVRLPNFEESFFHYAERENNITLQTGFTFFVSQKSALVPNVQPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---VYFFRLVDPRRRNVACIEHALEKLYYIKECCYD
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IQLFGAPRIYKRLE - - NSCYSFFKETPDDQWVRTTDFP
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Sequence 2, Appli
Sequence 52,9, Ap
Sequence 12125, Ap
Sequence 12125, Ap
Sequence 368, Appl
Sequence 4, Appl
Sequence 2, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 28, Appl
Sequence 370, Appl
Sequence 370, Appl
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1188.490 Million cell updates/sec
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1 MGKTIQVFGFPXLLSAEVVK......RPVLNLSSLRAQLSHRLVLK 1114
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Sequence 1066, Appli Sequence 1, Appli Sequence 17, Appli Sequence 18, Appli Sequence 23, Appl Sequence 5640, Ap Sequence 1204, Appl Sequence 140, Appl Sequence 123, Appl Sequence 612, Appl Sequence 5610, Appl Sequence 1313, Appl Sequence 10623, Appl Sequence 10623, Appl Sequence 10623, Appl Sequence 10623, Appl Sequence 10623, Appl Sequence 1349, Appl Sequence 1349, Appl Sequence 1349, Appli Sequence 1349, Appli	
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ALIGNMENTS

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Schiebel, Winfried
Schiebel, Winfried
Sanger, Heinz
Intle Of Invention: NUCLEIC ACID MOLECULES ENCODING
POLYPEPTIBES HAVING THE ENCYMATIC ACTIVITY OF AN RNA-DIRECTED RNA POLYMERASE (RGRP)
                                                                                                                                                                                                                                                                                                                                                                                   CONDUTER READABLE FORM:

AMBUIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,874
FILING DATE: 08-F6D-2001
CLASSIFICATION: CURROWN>
                                                                                                                                                                                                                                                                                              ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITK: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/811,583
FILING DATE: 05-MAR-1997
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MPG-1
                   Sequence 2, Application US/09782874
Patent No. US20010023067A1
GENERAL INFORMATION:
APPLICANT: Wassenedger, Michael
Riedel, Leonhard
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TELEPHONE: 212-596-9000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1114 amino acids
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                                                                                                                                                                                                                                                       SEQUENCES:
                                                                                                                                                                                                                                                       NUMBER OF
US-09-782-874-2
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Sequence 1066, Ap

Sequence Seguence

101.5

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QF.
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                                                              ; Score 5864; I; Pred. No. 0; 0; Mismatches
                                 ID NO:
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ
                                                              100.0%;
100.0%;
                                                                        Best Local Similarity 100.
Matches 1114; Conservative
                                          US-09-782-874-2
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Sanger, Heinz.
INVENTION: NUCLEIC ACID MOLECULES ENCODING
POLYPEPTIDES HAVING THE ENZYMATIC ACTIVITY .
RNA-DIRECTED RNA POLYMERASE (RGRP)
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MEVDGFEDYIDEAFDYKTEYDNKLGNLMDYYGIKTEAEILSGGIMKASKTFDRRKDAEAI
                         1021 SVAVRALRKEARANFKRRNDIDDMLPKASAWYHVTYHPTYWGCYNQGLKRAHFISFPWCV
                                                                                  SVAVRALRKEARAWFKRRNDIDDMLPKASAWYHVTYHPTYWGCYNQGLKRAHFISFPWCV
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5.1e-100;
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COMPUTER: READABLE FORM:

COMPUTER: IBM PC COMPATIBLE

COMPATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ver

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/782,874

FILING DATE: 08-Feb-2001

CLASSIFICATION: <UNKNOWN>

PRIOR APPLICATION NUMBER: US 08/811,583

FILING DATE: 05-MAR-1997
                                                                                                                                                                                                                 1114
                                                                                                                                                                       1081 YDQLIQIKKDKARNRPVLNLSSLRAQLSHRLVLK 1114
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                                                                                                                                                                                                1081 YDQLIQIKKDKARNRPVLNLSSLRAQLSHRLVLK
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: MPG-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Haley, James F. REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wassenegger, Michael
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TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                             Riedel, Leonhard
Schiebel, Winfried
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ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of t
                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09782874 Patent No. US20010023067A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
STATE: New York
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Best Local Similarity
Matches 218; Conserv
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Db 214 -EYKTLSHQMKHSDIVVTV	OY 698 NGRTMAGGLDESKTLEYGOVEVOETGAGHGEFSDDLHPFNNSRSTNSNFILKGNVVVAKN 757 Db 361RELE-BOLVYSDEAHDEKLEEIKNEYTLAGSEOSDVNN 397 OY 758 PCLHPGIRVLKAVNVRLHHHWVDCVPPQ	APPLICANT: Ohlsen, Kari L. APPLICANT: Oplsen, Kari L. APPLICANT: Zyskind, Judith W. APPLICANT: Travick, John D. APPLICANT: Travick, John D. APPLICANT: Travick, John D. APPLICANT: Carr, Grant J. APPLICANT: Carr, Grant T. APPLICANT: Vanamoto, Robert T. APPLICANT: Vanamoto, Robert T. APPLICANT: Vanamoto, Robert T. APPLICANT: Vanamoto, Robert T. APPLICANT: Van, H. HOWARD TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A TITLE OF INVENTION: DATE: 2001-03-21 PRIOR FILING DATE: 2000-03-21 PRIOR PRILING DATE: 2000-05-23 PRIOR FILING DATE: 2000-05-23 PRIOR FILING DATE: 2000-10-23 PRIOR PLICATION NUMBER: 60/242,578 PRIOR PLICATION NUMBER: 60/242,578 PRIOR PLIING DATE: 2000-110-23 PRIOR FILING DATE: 2000-110-23 PRIOR FILING DATE: 2000-110-23 PRIOR FILING DATE: 2000-11-27 PRIOR FILING DATE: 2000-11-27 PRIOR FILING DATE: 2000-11-27 PRIOR FILING DATE: 2000-11-27
Db 61 LHPGDIRVLKAVNVRALHHMVDCVVFPQKGKRPHPNECSGSDLDGDIYFVCWDQDMIPPR 120 Qy 820 QVQPMEYPPAPSIQLDHDVTIEEVEEYTNYIVNDSLGIIANAHVVFADREPDMAMSDPC 879	Sequence 5229, Application Us/09815242 sequence 5229, Application Us/09815242 sequence 5229, Application Us/09815242 sequence 5229, Application Us/09815242 patent No. Us202020051565A1 APPLICANT: Howard Rari L. APPLICANT: Systind, Judith W. APPLICANT: Trawick, John D. APPLICANT: Wall, Boward TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes TITLE REPERENCE: ELITRA, 011-07 TITLE REPERENCE: ELITRA, 011-07 PRIOR PRILING DATE: 2001-03-21 PRIOR PELLING DATE: 2001-03-21 PRIOR PELLING DATE: 2000-10-23 PRIOR PELLING DATE: 2000-11-27 PRIOR PELLING DATE: 2000-11-27 PRIOR PELLING DATE: 2000-11-27 PRIOR APPLICATION NUMBER: 60/257, 931 PRIOR PELLING DATE: 2000-11-27 PRIOR APPLICATION NUMBER: 60/257, 931 PRIOR APPLICATION NUM	Ouery Match Best Local Similarity 18.2%; Pred. No. 0.28; Query Match Best Local Similarity 18.2%; Pred. No. 0.28; Matches 162; Conservative 124; Mismatches 299; Indels 305; Gaps 40; Qy 324 DPVRW-ITEQYDGYLKGROPPKSPITLDDGLVYVRYULYPCKVYFCGPEVNVSNRVLR 382; ::

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APPLICANT:
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                                                                                                                                                                                            DPVRW-LTEQYDGYLKGRQPPKSPSITLDDGLVYVRRVLVTPCKVYFCGPEVNVSNRVLR 382
                                                                                                                                                                                                                                                  NYSE---DIDNFLRVSFVDEEWEKLYSTDLLPKASTGSGVRTNIYERILSTLRKGFVIGD 439
                                                                                                                                                                                                                                                                            -----NEVIVT-RRLYRSGE 110
                                                                                                                                                                                                                                                                                                       LKYKKRKAESLNKLDQTEDNLTRVEDILYDLE------GRVEPLKEEAAIAK-- 214
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                                                                                                                                        Length 1188;
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                                                                                                                                      tch 1.9%; Score 112.5; DB 10; Length al Similarity 18.2%; Pred. No. 0.28; 162; Conservative 124; Mismatches 299; Indels
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12125
LENTH: 1188
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12125
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                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Sec
TITLE REFRENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03.07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
LENGTH: 1579
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No. US20020128250Alman, Thea
Sequence 368, Application US/09801368 Patent No. US20020128250A1 GENERAL INFORMATION:
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                                                                            APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
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Sherman, Amir
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Milne, Todd
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CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21 PRIOR FILING DATE: 2000-05-23 PRIOR APPLICATION NUMBER: 60/207,727 PRIOR APPLICATION NUMBER: 60/207,727 PRIOR PILING DATE: 2000-05-26 PRIOR PILING DATE: 2000-05-36 PRIOR PILING DATE: 2000-10-33 PRIOR PILING DATE: 2000-11-27 PRIOR PILING DATE: 2000-11-27 PRIOR PILING DATE: 2000-11-27 PRIOR PILING DATE: 2000-12-22 PRIOR APPLICATION NUMBER: 60/259,308 PRIOR PILING DATE: 2001-02-16 NUMBER OF SEQ ID NOS: 14410 SEQ ID NO 11997 LENGTH: 1357 TYPE: PRI CORGANISM: Pseudomonas aeruginosa US-09-815-242-11997	Query Match Best Local Similarity 18.9%; Pred. No. 1.1; Best Local Similarity 18.9%; Pred. No. 1.1; Matches 156; Conservative 107; Mismatches 268; Indels 296; Gaps 40 Qy 331 EQYDGYLKGRQPPRSPITLDDGLVYVRRULVTPCKVFCGPEVNVSNRVL 381	LSQFMDQNNPLSEITHKRRVSALGPGGLTRERAG FQIRYGGYKGVVGVDPDSSMKLSLRKSMKKESDNIKLDVLGWSKYQPCYLNRO ::	Qy 689 RTRSRIFIPNGR-TMMGCLDESRTLEYGQVFVQFTGAGHGEFSDLHPFNNSRSTNSN 745
	0.1	14041KYVDF1A29 960 DMEVDGFEDYIDEAFDYKTEYDNKLGNLMDYYGIKTEAEILSGGIMKASKTFDRRKDA 1017	WESULT 6 US-09-815-242-11997 Sequence 11997, Application US/09815242 Patent No. US2002006156931 APPLICANT: Haselbeck, Robert APPLICANT: Oblese, Kari L. APPLICANT: Zyskind, Judith W. APPLICANT: Wall, Daniel APPLICANT: Taraick, John D. APPLICANT: Mamonto, Robert T. APPLICANT: Wention: Identification of Essential Genes in TITLE OF INVENTION: Identification Prokaryotes FILE REFERENCE: ELITRA.011A CURRENT APPLICATION NUMBER: US/09/815,242

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Db 686	RESULT 8 US-09-737-149-35 US-09-737-149-35 Sequence 35, Application US/09737149 Patent No. US2002007466A1 Patent No. US2002007466A1 Sequence 35, Application US/09737149 Sequence 36, Seven K APPLICANT: Spaderna, Steven K APPLICANT: Spaderna, Patent A. PAPLICANT: Spaderna, Padigaru APPLICANT: Spaderna, Padigaru APPLICANT: Spates, Richard A. PAPLICANT: Spates, Rimber14 PRICK: Spytek, Kimber14 PRICK: 1506-620 CIP CURRENT PERFERENCE: 1509-620 CIP CURRENT PILING DATE: 2001-06-15 PRICK: PAPLICATION NUMBER: 60/170,564 PRICK: PAPLICATION NUMBER: 60/173,165 PRICK: PAPLICATION NUMBER: 60/173,362 PRICK: PAPLICATION NUMBER: 60/173,544 PRICK: PAPLICATION NUMBER: 60/173,544 PRICK: PAPLICATION NUMBER: 60/173,544 PRICK: PAPLICATION NUMBER: 60/173,544 PRICK: PAPLICATION NUMBER: 60/174,404 PRICK: PAPLICATION NUMBER: 60/174,404 PRICK: PAPLICATION NUMBER: 60/174,902 PRICK: PILING DATE: 2000-01-07 PRICK: PILING DATE: 2000-01-07 PRICK: PILING DATE: 2000-08-09 NUMBER: OF SEQ ID NOS: 49 SEQ ID NO 35	; LENTH: 1135; ; CRGANISM: Rattus norvegicus ; ORGANISM: Rattus norvegicus ; ORGANISM: Rattus norvegicus US-09-737-149-35 Ouery Match 1.8%; Score 105.5; DB 10; Length 1135; Best Local Similarity 18.5%; Pred. No. 1.1; Dest Local Similarity 18.5%; Pred. No. 1.1; Db 275 NIT-DFLLITANNEKFHLESVINITANLSSTKDLLSFLOVQMDNIRNSTPINVMFGC 330 OY 108 DDKFAVLGSTEVSIQFGIGIKKFFFFLSSGSADXKLQLSYENIWQVVLHRPY 159 Db 331 -DMDSIRQIFEMSTQFGLSPPELHWVLGDSQNVEELRTEGLPLGLIAHGKTTQSVFEY-Y 388 OY 160 GQNAQFLLIQLFG APRIKKRLENSCYSFFKETPDDQWVRTTDFP
Db 905KLLRAIFGEKASDVKDTSLRVPTGTKGTVIDVQVFTRDGVERDSRALSIEKM 956 Oy 962 EVDGFEDYIDEAFDYKTEYDNKLGNIAMDYYGIKTEAEILSGGIMKASKTFDRRKDAEA 1019 ::	TITLE OF INVENTION: NUCLEIC MICHAEL SENCODING HUMAN TRANSPORTER PROTEINS, TITLE OF INVENTION: NUCLEIC MICHAEL SENCODING HUMAN TRANSPORTER PROTEINS, TITLE OF INVENTION: NUCLEIC MICHAEL SENCODING HUMAN TRANSPORTER PROTEINS, CURRENT APPLICATION NUMBER: US/09/781,558 CURRENT APPLICATION NUMBER: US/09/781,558 CURRENT APPLICATION NUMBER: US/09/781,558 PRIOR FILING DATE: 2000-04-26 60/199,811 PRIOR FILING DATE: 2000-09-18 PRIOR FILING DATE: 2000-09-18 NUMBER OF SEQ ID NOS: 48 NUMBER OF SEQ ID NOS: 48 SEQ ID NO 4 LENGTH: 1080 TYPE: PRT ORGANISH: Rattus norvegicus SEQ 1D NO 4 LENGTH: 1080 TOPE: NAT ORGANISH: Rattus norvegicus SSO -09-781-558-4 QUETY MATCh Best Local Similarity 18-54; Pred: NO. 1; Matches 135; Conservative 102; Mismatches 249; Indels 245; Gaps 37; Matches 135; Conservative 102; Mismatches 249; Indels 245; Gaps 37; ATPE: PRT ORGANISH: RATTLANNERINGSSYLKAWEMMTDIVOLRAYDOMNENSTPHWWFGC 304 ON 55 NISADATILANNERINGSSYLKAWEMMTDIVOLRAYDOMNENSTPHWWFGC 304 ON 55 NISADATILANNERINGSSYLKAWEMMTDIVOLRAYDOWNENTPRY 159 11:	OY 208 GLSSSLCLOFRRGVRLPNFEESFFHYABERINITLOTGFTFFVSQKSALVPNVQPPEG 265

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444 GLSGSIKVKGSTIISSENNFFIWNLQHDPMGKPWWTRLGSWQGGRIVMDSGIWPEQA 500 266ISIPYKILFKISSLVQH	09 385 SEDIDNEL	US-09-966-561-2 Patent No. US200200969651 Patent No. US200200969641 GENERAL INFORMATION: APPLICANT: University of Southern California APPLICANT: University of Southern California APPLICANT: Dang, Zhao Hui APPLICANT: Dang, Zhao Hui APPLICANT: Dang, Zhao Hui APPLICANT: Dang, Yan TITLE OF INVENTION: APOPTOSIS INHIBITION FILE REPERBREMCE: 13761-724 CURRENT APPLICATION NUMBER: US/09/966,561 CURRENT APPLICATION NUMBER: EARLIER PAPLICATION NUMBER: 09/419,694 PRIOR FILING DATE: BALLIER FILING DATE: 1999-10-14 NUMBER OF SEQ ID NOS: 3 SOFTWARE: PASTSEQ for Windows Version 3.0 LENGTH: 711 FYPE: PRI TYPE: PRI T	Ouery Match 1.8%; Score 104.5; DB 10; Length 711; Best Local Similarity 20.2%; Pred. No. 0.62; Matches 53; Conservative 40; Mismatches 99; Indels 71; Gaps 13; 781 DCVVFPQKGKRPHPNECSGSDLDGDIYFVCWDQDMIPPRQVQPMEVPPAPS 831 1
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APPLICANT: Malvar, Thomas
APPLICANT: Malvar, Thomas
APPLICANT: Glimer, Amy Jelen
TITLE OF INVENTION: Polyuculeotide Compositions Encoding Broad-Spectrum S-Endotoxi
TITLE OF INVENTION: Polyuculeotide Compositions Encoding Broad-Spectrum S-Endotoxi
CURRENT PELICATION NUMBER: US/09/873,873
CURRENT PELICATION NUMBER: US/09/253,341
PRIOR FILING DATE: 1999-02-19
PRIOR FILING DATE: 1997-09-03
PRIOR RELING DATE: 1997-09-03
PRIOR RELING DATE: 1997-09-03
PRIOR RELING DATE: 1996-11-20
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Version 3.0
LENGTH: 1177
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                               884 ELFSIAV-----DFPKTGVPAEIPSQLRPKEYPDFMDKPDKTSYISERVIGKLFRKVKDK 938
                                                                                                      ---RDVARRSYDADMEVDG-----FEDYIDEAFD 975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Hybrid Delta-Endotoxin 09-873-873-10
                                                                                                                                                                                                                                                                                                                                              ULT 10
09-873-873-10
equence 10, Application US/09873873
attent No. US20020064865A1
ENERAL INFORMATION:
                                                                                                                                                                                                             976 YKTEYDNKLGNLMDYYGIKTEAE 998
                                                                                                                                                                                                                                                   531 MRT---GARGVFPAYAIEVTKE 550
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                                                                                                      939 APQASSIATET-----
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QY 421 TNIYERILSTL-RKGFVIGDXKFEFLAFSSSQLRDNSVAMFASRPGLTA 468	: : : : : : : : : : :
469NDIRAWAGDESQIKNVAKYAARLGQSEGSRETLSVLR	QY 204 PSWIGLSSSLCLQFRRGVRLPNFEBSFFHYAERENNITLQTGFTFFVSQKSALVPNVQPP 263
507HEIEVIPDVKVHGTSVVFSDGIGKISGDFAHRVASKCGLQYT	QY 264EGISIPYKILEKISSLVQHGCIPGPALN
40Z FINILDPEKLITQIPLVKAHILQSGITVVKGFGFTGGDILKKISGGFFATTIVNINGQLPQ 549 PSAFQIRYGGYKGVVGVDPDSSMKLSLRKSMSKY :	QY 292
522 RYRAKIRYASTINLRIYVIVAGERIFAGGFNKTMDIGDPLIFGSFSYATINTAFIFPMSQ 583 ESDNIKLDVLGWSKYQPCXLNR	Qy 325 PVRMLIEQYDGYLKGRQPPKSPSITLDDGLVYVRRVLVTPCK 366
582 SSFTVGADTFSSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTD 619 VLEQKQKEAVDQLDAILHDSLKAQEALELMSPGENTNILKAMLNCGYKPDAEPFLSM [Qy 367 VYFCGPEVNVSNRVLRNYSEDIDNFLRVSFVDEEWEKLYSTDLLPKASTGSGVR 420 1 1 1 1 1 1 1 1 1
640 VTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQ 676 MLQTFRASKLLDLRTRSRIFIPNGRTMMGCLDES-RTLEYGQVFVQFTGAGHG ::::	QY 421 INIYERILSTL-RKGFVIGDKKFEFLAFSSSQLRDNSVWMFASRPGLTA 468
696 LDRGWRGSTDITIQRGDDVFKENYVTLFGTFDECYPTYLYQKIDESKLKAFTRYQLRGYI 728 EFSDDLHPFNNSRSTNSNFILKGNVVVAKNPCLHPGDIRVLKAVNVRALHHMVDCVVFPQ	Qy 469 NDIRAWMGDFSQIKNVAKYAARLGQSFGSSRETLSVLR 506
Db 756 EDSQDLEIYLIRYNAKHETVNVPGTGSLWPLSAQSP 791 Qy 788 KGKRPHPNECSGSDLD 803	Qy 507HEIEVIPDVKVHGTSYVFSDGIGKISGDFAHRVASKCGLQYT 548
Db 792 IGKCGEPNRCAPHLEWNPDLD 812 RESULT 11	QY 549 PSAFQIRYGGYKGVVGVDPDSSMKLSLRKSMSKY 582
US-09-873-873-12 ; Sequence 12, Application US/09873873 ; Patent No. US20020064865A1 ; GENERAL INFORMATION:	QY 583 ESDNIKLDVLGWSKYQPCYLNRQLITLLSTLGVKDE 618
APPLICANT: Malvar, Thomas APPLICANT: Gilmer, Amy Jelen TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxins FILE REFERENCE: MECO:2102	QY 619 VLEQKQKEAVDQLDAILHDSLKAQEALELMSPGENTNILKAMLNCGYKPDAEPFLSM 675
; CURRENT APPLICATION NUMBER: US/09/873,873 ; CURRENT FILING DATE: 2001-08-20 ; PRIOR APPLICATION NUMBER: US 09/253,341 ; PRIOR FILING DATE: 1999-02-19	QY 676 MLQTFRASKLLDLRTRSRIFIPNGRTMMGCLDES-RTLEYGQVFVQFTGAGHG 727 ::
; PRIOR APPLICATION NUMBER: US 08/922,505 ; PRIOR FILING DATE: 1997-09-03 ; PRIOR PILING DATE: 1996-11-20	QY 728 EFSDDLHPFNNSRSTNSNFILKGNVVVAKNPCLHPGDIRVLKAVNVRALHHMVDCVVFPQ 787
NUMBER OF SEQ ID NOS: 35 ; SOFTWARE: Patentin version 3.0 ; SEQ ID NO 12 ; LENGTH: 1177	QY 788 KGKRPHPNECSGSDLD 803
; TYPE: PRT ; ORGANISM: Artificial Sequence ; FEATURE: ; OTHER INFORMATION: Hybrid Delta-Endotoxin US-09-873-873-12	RESULT 12 US-09-873-14 Sequence 14, Physication US/09873873
Query Match 1.8%; Score 104; DB 10; Length 1177; Best Local Similarity 18.2%; Pred. No. 1.6; Matches 168; Conservative 112; Mismatches 301; Indels 340; Gaps 45;	; FATERIA NO: OSZOVZOOGOGOSZA; ; GENERAL NO: TROCKMATION: ; APPLICANT: Malvar, Thomas ; APPLICANT: Glimer, Amy Jelen ; APPLICANT: Climer, Amy Jelen ; APPLICANT: Climer, Any Jelen
QY 102 FGCQISDDKFAVLGSTEVSIQFGIGLKKFFFFLSSGSADYKLQLSYENIWQVVLH 156 13 : : : : :	FILE OF INVENTOR: FIJENCE OF TAXABLE MEGO. 210 - 2 CURRENT APPLICATION NUMBER: US/09/873,873 CURRENT FILING DATE: 2011-08-20 PRIOR APPLICATION NUMBER: US/09/853,341
QY 157 RPYGQNAQFLLIQLFGAPRIYKRLENSCYSFFKETPDDQWVRTTDFP 203	; PRIOR FILING DATE: 1999-02-19

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                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLE 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MLQTFRASKLLDLRTRSRIFIPNGRIMMGCLDES-RTLEYGQV-----FVQFTGAGHG 727
                                                                                                                                                                                                                                                      FGCQISDDKFAVLGSTEVS----IQFGIGLKKFFFFLSSGSADYKLQLSYENIWQVVLH 156
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PRIOR APPLICATION NUMBER: US 08/922,505
PRIOR FILING DATE: 1997-09-03
PRIOR APPLICATION NUMBER: US 08/754,490
PRIOR FILING DATE: 1996-11-20
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 14
LENGTH: 1177
                                                                                                                                                    OTHER INFORMATION: Hybrid Delta-Endotoxin US-09-873-873-14
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                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                TYPE: PRT
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US-09-873-28
Sequence 28, Application US/09873873
Sequence 28, Application US/09873873
Sequence 28, Application US/09873873
Sequence 28, Application US/09873873
Sequence 28, Application Thomas
APPLICANT: Malvar. Thomas
TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxi
FILE REFERENCE: MC0.210--2
CURRENT APPLICATION NUMBER: US 09/253,341
PRIOR RPILING DATE: 1999-02-19
PRIOR RPILING DATE: 1999-02-19
PRIOR PLILING DATE: 1999-02-19
PRIOR FILING DATE: 1996-11-20
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 28
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EFSDDLHPFNNSRSTNSNFILKGNVVVAKNPCLHPGDIRVLKAVNVRALHHMVDCVVFPQ 787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Hybrid Delta-Endotoxin US-09-873-873-28
                                                                                                        ---EIYLIRYN---AKH-
                                                                                                                                                                                                                                                                                                                                                                      792 IGKCGEPNRCAPHLEWNPDLD 812
                                                                                                                                                                                                                                                 788 KGKRPHPNECS----GSDLD 803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDRGWRGSTDITIQRGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLKAFTRYQLRGYI 755
  905 ----
                                 DSLDEIPPQNNNVPPRQGFSHRLSHVSMFRS-----GFSNSSVSIIRAPMFSWIHRSAE 461
                                                                                                                FINIIASDSITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYIIVNINGQLPQ 521
                                                                                                                                                                                                                                                                ESDNIKLDVLGWSKYQPCYLNR--------QLITLLSTLGVKDE 618
                                                                                                                                                                                                                                                                                                                                                       VLEQKQKEAVDQLDAI---LHDSLKAQEALELMSPGENTNILKAMLNCGYKPDAEPFLSM 675
                                                                                                                                                                                                                                                                                                                                                                                                  VTDYH----IDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQ 695
                                                                                                                                                                                                                                                                                                                                                                                                                                               MLQIFRASKLLDLRTRSRIFIPNGRTMMGCLDES-RTLEYGQV-----FVQFTGAGHG 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFSDDLHPFNNSRSTNSNFILKGNVVVAKNPCLHPGDIRVLKAVNVRALHHMVDCVVFPQ 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----ETVNVPGTGSLWPLSAQSP 791
                                                                                      -----BIEVIPDVKVH----GTSYVFSDGI--GKI----SGDFAHRVASKCGLQYT
                                                                                                                                                                            PSAFQIRYGG-----YKGVVGV-------DPDSSMKLSLRKSMSKY----
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APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: DENGRAYOUES
FILE REFERENCE: ELITAR.011A
CURRENT FILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-25
PRIOR FILING DATE: 2000-03-26
PRIOR FILING DATE: 2000-03-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-16
---NDIRAWMGDFSQIKNVAKYAARLGQSFGSSRETLSVLR--
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard
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US-09-815-242-11609
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LENGTH: 897
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                                 Gaps
                                                                                                                                   ----SQLRD--NSVWMFASRPGLTANDIRAWMGDFSQIKNVAKYAARLGQSFGSSRET 501
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                                                                                                                                                        KEYGFISTLRDLENSPFIVENVPILNSTPI---LDNTPALDNAPKKSRMI---VLESAEP
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                                                                                                                                                                                                                                                               548 TPSAFQIRYGGYKGVVGVDPDSSMKLSLRKSMSKYESDNIKLDVLGWSKYQPCYLNRQLI
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                               Indels 270;
 Length 897;
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                                                               KLYSTDLLPKASTGSGVRTNIYERILSTLRKGFVIGDKKFEFL--AFSS-
Ouery Match 1.7%; Score 102; DB 10; Best Local Similarity 18.8%; Pred. No. 1.6; Matches 140; Conservative 104; Mismatches 229;
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Milne, Todd
No. US20020128250Alman, Thea
Royer, John
Salama, Sofile
Sherman, Amir
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Patent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
APPLICANT: Hocht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
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APPLICANT:
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APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 10972-147
CURRENT FILE OF DATE: 2001-03-07
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR PILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
LENGTH: 1331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDQWVRTTDFPPSWIGLSSSLCLQFRRGV-RLP---NFEESFFHYAERENNITLQTGFTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 1.7%; Score 102; DB 10; Length 1331;
Similarity 18.8%; Pred. No. 3;
28; Conservative 170; Mismatches 413; Indels 404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae
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; ORGANISM: Saco
US-09-801-368-370
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Matches 228;
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DSLKAQEALELMSPGENTNILKAMLNCGYKPDAEPFLSMMLQTFRASKLLDLRTRSRIFI 696
                                                                          RNPROMGKVLDAT --- DQGNKYLLSLASSLSNVS ------MRWQKRSFIGGGTFGQVY
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                                                                                                    VAKNPCLHPGDIRVLKAVNVRALHHMVDCVVFPQKGKR-----PHPN--ECSGSDLDG
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Search completed: November 6, 2002, 03:47:45 Job time : 22 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

November 6, 2002, 03:43:53 ; Search time 25 Seconds (without alignments) 4283.750 Million cell updates/sec Run on:

US-09-782-874-2 5864 1 MGKTIQVFGFPYLLSAEVVK......RPVLNLSSLRAQLSHRLVLK 1114 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 283224 seqs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		RNA-directed RNA p	RNA-directed RNA p	-dire	RNA-	hypothetical prote	_	_	_	hypothetical prote	protein M01G12.12	hypothetical prote	Ω	cytotoxin L - Clos	hypothetical prote	⊐	hypothetical prote	~~	DNA-directed RNA p	hypothetical prote	_	lysine-tRNA ligase	₽	anthranilate phosp	TOG protein - huma	hypothetical prote	д	hypothetical prote		
SUMMARIES	CI	T30819	T30828	T01920	T11660	T20695	T21381	F84582	H84582	G84582	F87936	T23669	T40928	I40884	T22298	S37972	F83928	H86430	RNBY2L	T12827	T11681	AC3572	AF3286	T48366	S68176	T21251	DECHE	S50580	T15921	052
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ALIGNMENTS

RESULT 1 730819 RADirected RNA polymerase (EC 2.7.7.48) - tomato C; Species: Lycoperation esculentum (tomato) C; Date: 22-0ct-1999 #sequence_revision 22-0ct-1999 #text_change 21-Jul-2000 C; Accession: T30819 R; Schiebel, W ; Pelissier, T:; Riedel, L.; Thalmeir, S.; Schiebel, R.; Kempe, D.; Lot Plant Cell 10, 2087-2102, 1998 R; Schiebel, W ; Pelissier, T:; Riedel, L.; Thalmeir, S.; Schiebel, R.; Kempe, D.; Lot Plant Cell 10, 2087-2102, 1998 R; Schiebel, W ; Pelissier, T: Riedel, L.; Thalmeir, S.; Schiebel, R.; Kempe, D.; Lot R; Schiebel, W ; Pelissier, 20885; MUD:99055198; PMID:9836747 A; Accession: T30819 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Residues: 1-1114 <sch> A; Residues: 1-1114 <sch> A; Residues: 1-1114 <sch> A; Rosidues: BmBL:Y10403; NID:94038591; PIDN:CAA71421.1; PID:94038592 C; Genetics: A; Note: RdRP C; Superifamily: Arabidopsis probable RNA-directed RNA polymerase C; Keywords: nucleotidyltransferase</sch></sch></sch>	Query Ma Best Loc Matches	OY 1 MGKTIOYOFOFPILASAEVIKSFLEKYTGTGTVCALENYOSKOGSRAPANYOSADNISADK 60	QY 121 IQFGIGLKKFFFFLSSGSADYKLQLSYENIMQVVLHRPYGQNAQFLLIQLFGAPRIYKRL 180 Db 121 IQFGIGLKKFFFFLSSGSADYKLQLSYENIMQVVLHRPYGQNAQFLLIQLFGAPRIYKRL 180 QY 181 ENGCYSFFKETPDDQWVRTTDFPPSWIGLSSSLCLQFRRGYRLPNFEESFFHYAERENNI 240 Db 181 ENGCYSFFKETPDDQWVRTTDFPPSWIGLSSSLCLQFRRGYRLPNFEESFFHYAERENNI 240 LB 111111111111111111111111111111111111	QY 241 TLQTGFTFFVSQKSALVPNVQPPEGISIPYKILFKISSLVQHGCIPGPALNVYFFRLVDP 300 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OY 361 LVTPCKVYFCGPEVNVSNRVLRNYSEDIDNFLRVSFVDEEWEKLYSTDLLFKASTGSGVR 420
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                                                                                                                             ENSCYSFFKETPDDOWVRTTDFPPSWIGLSSSLCLQFRRGVRLPNFEESFFHYAERENNI
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C; Species: Nicotiana tabacum (common tobacco)
C; Date: 22-Oct.1999 #text_change 20-Jun-2000
C; Date: 22-Oct.1999 #sequence_revision 22-Oct.1999 #text_change 20-Jun-2000
C; Accession: T30828
R; Schiebel, W; Pelissler, T; Riedel, L.; Thalmeir, S.; Schiebel, R.; Kempe, submitted to the RMBL Data Library, October 1998
A; Description: Isolation of an RNA-directed RNA polymerase-specific cDNA clone A; Reterence number: 220890
A; Accession: T30828
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-1116 <SCH>
A; Cross references: EMBL:AJ011576; PIDN:CAA09697.1
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Superfamily: Arabidopsis probable RNA-directed RNA polymerase
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probable RNA-directed RNA polymerase (EC 2.7.7.48) - fission yeast (Schizosaccharomyoc C; Species: Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999 (C; Accession: T11660 C; R: Barrell, B.G.; Rajandream, M.A.; Wood, V. A; Reference number: 217305 
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16.2%; Score 948; DB 2; Length 12
Best Local Similarity 31.3%; Pred. No. 4.3e-56;
Matches 243; Conservative 155; Mismatches 316; Indels
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                                                                                                                                                    Probable RNA-directed RNA polymerase (EC 2.7.7.48) - Arabidopsis thaliana
NyAlternate names: protein T22B4.110
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 10-Dec-1999
C.Accession: T01920; T06192
C.Accession: T01920; T06192
R.Strony, C.; Graves, T.; Duckels, G.
Submitted to the EMBL Data Library, July 1998
A; Description: The sequence of A. thaliana F2P3.
A; Accession: T01920
A; Status: translated from GB/EMBL/DDBJ
A; Residues: 1-1133 <STR>
A; Coss-reference number: 214455
A; Cross-references: EMBL:AF080120; NID:g3600045; PID:g3600048
A; Residues: 1-1133 <STR>
A; Cross-references: EMBL:AF080120; NID:g3600045; PID:g3600048
A; Esterence number: 216098
A; Residues: 1-1133 <STR>
A; Residues: 1-1133 <STR
A; Residues: EMBL:ANO49876
A; Residues: 1-1134 SUR Columbia; BAC clone T22B4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPNFEESFFHYAERENNITLQTGFTFFVSQKSALVPNVQPP-EGISIPYKILFKISSLVQ 281
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A;Introns: 184/3; 820/2; 870/3
A;Note: F2P3-11; T22B4.110
C;Superfamily: Arabidopsis probable RNA-directed RNA polymerase C;Keywords: nucleotidyltransferase
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1081 CVYDQLIQIKKAKARRRPVPHLSSLGSQLSRKLVI 1115
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                                                                                                                                                                                                      GDFAHRVASKC-GLQYTPSAFQIRYGGYKGVVGVDPDSSMK-----LSLRKSMSKYESD
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                                                                                                       504 GGSDGFRNEKLYSRIQOLLIYGIKVGNQIYEFLAFGNSOLREHGAYFFASGSDLNAKQIR
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                                                                                                                                                                    473 AWMGDFSQIKNVAKYAARLGQSFGSSRETLSVLRHEIEVIPDVKVHGTSYVFSDGIGKIS
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IHIKKLYVTPTTLRIVEDSLEAGNRVIRNFKDFANRFMRVQITDEYYKQ--
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Introns: 23/2; 226/3; 305/2; 343/2; 462/3; 736/1; 922/2; 993/1; 1222/2; 1463/3; 161
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A;Cross-references: EMBL:266500; PIDN:CAA91312.1; GSPDB:GN00020; CESP:F10B5.7 A;Experimental source: clone T0Sc12 C;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Map postition: 2 A;Introns: 23/2; 226/3; 305/2; 343/2; 462/3; 736/1; 922/2; 993/1; 1222/2; 1463
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                                                                                                                                                                                                                                                                                                                                                                                      RIYKRL-ENSCYSFFK-----ETPDDQWVRTTDFP--------PSWIGLS 210
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                                                                                                                                                                                                                                                                                 FLVRGDFISQENTVCSVKLQSH------HNADASRENSSFKVAGSNKYLSYARFEHDK 378
                                                                                                                                                                                                                                                                                                                                                                                                                  HIMEGIPKNTIFHPSKSKVLNMET-CTEWTRVLSWPGDAEGRGVGCTSEAFSQSSWIRLT 493
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                                                                                                                                                                                                                                                        70 YFGSSYLKAWEMKTDIVQLRAYVDQMDGITLNFGCQISDDKFAVLGSTE------ 118
                                                                                                                                                                                                                                                                                                                        119 --VSIQFGIGLKKFFFFLSSG--SADYKLQLSYENIWQVVLHRPYGQNAQFLLIQLFGAP 174
                                                                                                                                                                                                                       LFSEFASSFTSRITGMLHDQVFLEVPKM---HTLFTKITPQHMDINISAIAIGNCPNSGL 326
                                                                                                                                                                                                                                                                                                                                                      RLAVVYFGVRLAE---FADDGLDHAGFRLNLYYNLFVRIVVDMSH-ETTNSIYIOMKNPP 434
                                                                                                                                                                                       14 LSAEVVKSFLEKYTG-YGTVCALEVKQSKGGSRAFAKV--QFAD-NISADKIITLANNRL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------QYDGYLKGRQPPKSPSITLDDGL-----VYVRRVLVTPCKVYFCGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLDAILHDSLKAQEALELMSPGENTNIL----KAMLNCGYKPDAEPFLSMMLQTFRASKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1045 IHHISKAKIFLPPSLGRSMYGVVDETGLLQYGQVFIQYS------PSIRQTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NDEDDDDDDDDTKKPMELVHEPLFLKLVRRGMKECSQATEETLEQLLNAFDERRQIDVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVNVSNRVLRNYSEDIDNFLRVSFVDEEWEKLYSTDLLPKASTGSGVRTNIYERILSTLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KISGDFAHRVASKCGLQYTPSAFQIRYGGYKGVVGVDPD----SSMKLSLRKSMSKY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---NVYFFRLVDPRRRNVAC---
                                                                                                                                                       296;
                                                                                                                        Length 1780;
                                                                                                                      Query Match
15.9%; Score 932; DB 2; Length 178
Best Local Similarity 25.1%; Pred. No. 9.8e-55;
Matches 322; Conservative 199; Mismatches 465; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MR-----KDDDNDSVSSTQLMDIVTRLSA-----
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Db 1998 LNEQHWKNFLEIIIWYFNDNQLCEAALEDLVHLIDGRRF-IGSILKCLDKICQKRE-VM 2055 Qy 324 DPVRWLTEQYDGYLKGRQPPKSPSITLDDGLVYFRVLVTPCKVYFCGPEVNVSNRVL 381	Qy 631 LDAILHDSIKAQEALELMSPGENTNILKAMLNGGYKDDAEPFELSML 677 1 1 1 1 1 1 1 1 1	RESULT 7 F84581 hypothetical protein At2g19910 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
Db 1091 NRPILKTGKVLITKNPCHVPGDVRVFDAVWQPALAHLVDVVVFPQHGPRPHPDEMAGSDL 1150 Qy 803 DGDIYFVCMDQDMIPPRQVQPMEYPPAPSIQLDHDVTLEEVEEYTTXTVNDSLGIIANA 862 1151 DGDEYSIIMDQEMLLDYNEEAMYPPSSSAAEEDKEPTTDDMVEFFLRYLQQDSIGRMSHA 1210 Qy 863 HVVFADREPDMAMSDPCKKLAELFSIAVDFPKTGVPAEIPSQLRPKEY-PDFMDKPDKTS 921 11 HLAYADLHGLFHENCHALAKCAVAVDFPKSGVPAEPLSSFEQCEMTPDYMSGGRPM 1268 Qy 912 YSERVIGKLFRKYKDKAPQASSIATFTRDVARRSYDADMEY-DGFEDYIDEAPD 975 1	FESULI 6 Table 1 Ta	OY 271

C; Accession: F84582 R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D., Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-769, 1999 A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Accession: As 44582 A; Status: preliminary A; Molecule type: DNA	DD 877 NQLTNEVIQRYKQDFYGAAGFEDSNKS
A; Residues: 1-966 <sto> - A; Cross - references: GB: AE002093; NID: q3687227; PIDN: AAC62125.1; GSPDB: GN00139 - C; Genetics: A; Gene: At2g19910 A; Map position: 2</sto>	RESULT 8 H84582 hypothetical protein At2g19930 [imported] - Arabidopsis thaliana
Query Match 6.2%; Score 362; DB 2; Length 966; Best Local Similarity 22.0%; Pred. No. 2.9e-16; Matches 198; Conservative 136; Mismatches 306; Indels 262; Gaps 42;	C;Species: Aradiadopsis thallana (mouse-ear cress) C;Decies 20-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: H84582 C;Accession: F84582 R;Lin, X; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
QY 323 YDPVRWLIEQYDGYLKGRQPPKSPSITLDDGLV-YVRRVLVTPCKVYFCGPEVNVSNR 379	M.; KOO, H.; MOITEL, N.S.; CIOUIN, D.A.; SHEN, M.; VANAREN, S.D.; UMAYEM, D.; ALLION, BOLS, D.; NIERMAN, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thallana.
QY 380 VLRNYSEDIDNFLRVSFVDEBWEKLYSTDLLPKASTGSGVRTNIYERILSTLRKGFVIGD 439	A; Reference number: A84420; MUID:20083487; PMID:10617197 A; Accession: H84582 A; Status: preliminary A; Molecule type: DNA
OY 440 KKFEFLAFSOSQLEDNSVMMFASRPGLJANDIRAW 474 1 1 1 1 1 1 1 1 1	A; Mesidues: 1-929 < SFU> A; Mesidues: 1-929 < SFU> C; Genetics: GB: AE002093; NID: 93687225; PIDN: AAC62123.1; GSPDB: GN00139 C; Genetics: At2919930 A; Gene: At2919930
Qy 475 MGDFSQIKNVAKYAARLGQSFGSSRETLSVLRHEIEVIPDVKVHGTSYVFSDGIGKISGD 534 :::	A; Map postilon: 2 Query Match Query Match Best Local Similarity 22.6%; Profession No. 1.0-15; Matches 170: Conservative 128: Mismatches 279; Indels 207; Gaps 39;
QY 535 FAHRVASKCGLQYTPSAFQIRYGGYKG 561 : :	RVSEVDEEWEKLYSTDLLPKASTGSGVRTNIYERILSTLRKGFVIGDKRFEFLAF
Qy 562VVGVDPDSSMKLSLRKSMSKYESDNIKLDVLGWSK-YQPCYLNRQLITLLSTLG 614	448SSSQLRDNSVWMFASRPGLTAND 1. :: :: :: 1 :: :: 1 :: ::
Qy 615 VKDEVLEQKQKEAVDQLDAILHDSLKAQEALELMSPGENTNILKAMLNCGYKPDA 669 ::::	487
OY 670EPFLSMMLQIFRASKLLDLRTRSRIFIPNGRIMMGCLDESRILEYGQVFV 719	519 IMARCOLL DRINILLY DATA TO THE STATE OF THE STATE OF THE STANDARD TO THE STANDARD
OY 720 GFTGAGHGEFSDDLHPFNNSRSTNSNFILKGNVVVAKNPCLHPGDIRVLKAVNVRALHHM 779 1	578 DEARWACE INTERCRETE STATES THE STATES OF
OY 780 VDCVVFPQKGKRPHPNDCSGSDLDGDIXFVCWDQDMIPPRQVQPME	642 QEALELMSPGENTNIL ::: :: 476 ONAAOMILVGIPLD
OY 826 -YPPAPSIQLDHDVTIEEVEEYFTNYIVNDSLGIIANAHVVFADREPDWAMSDPCK 880 :	702 MMGCLDESRTLEYGYEVQFT 702 MMGCLDESRTLEYGYEVQFT 702 IMGTUTDTGAIREDEVCYILE
OY 881KLAELFSIAVDFPRIGVPAEIPSOLRPKEYPDFMDKPDKISVISERVIGKL 931	762 PGDIRVLKAVNVRALHHMVDCVVFPOKGKRPHPNECSGSDLDG
Qy 932 FRKVKDKAPQASSIATFTRDVARRSYDADMEVDGFEDYIDEAFDYKTEVD 981	818
Qy 982 NKLGNLMDYYGIKTEAEILSGGIMKASKTFDRRKDAEAISVAVRALRKEARAWF 1035	9

QY 864 VVFADR	OY 688 LRTRSRIFIPNGRTMMGCLDESRTLEYGQVFVQFTGAGHGEFSDDLHPFNNSRSTN 743 Db 592 LEKDDLKAGKLPIDESYZLMGTVDPT
RESULT 9 G84582 hypothetical protein At2g19920 [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C:Accession: G84582 R:Lin, X.: Kaul, S.: Rounsley, S.D.: Shea, T.P.: Benito, M.I.; Town, C.D.: Fujli, M.: Koo, H.; Mcffat, K.S.: Cronin, L.A.; Shen, M.; VanAken, S.E.: Umayam, L.; Ta euss, D.; Nierman, W.C.: White, O.; Eisen, J.A.; Salzberg, S.L.: Fraser, C.M.; Valure 402, 761-768, 1999 A;Itle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; FMID:10617197 A;Relection: DNA A;Relection: DNA A;Relection: CSTO> A;Cross references: GB:AE002093; NID:93687226; PIDN:AAC62124.1; GSPDB:GN00139 A;Cross references: A;Gene: At2919920 A;Map position: 2	RESULT 10 F87936 protein M01G12.12 [imported] - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10- C; Accession: F87936 C; Accession: F87936 Illon, L. R; Anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998 A; Title: Genome sequence of the nematode C. elegans: a platform for A; Reference number: A75000; MUID:99065613; PMID:8851916 A; Note: published errata appeared in Science 283, 35, 1999; Science A; Motes: prellminary A; Motestions: prellminary A; Motestions: prellminary A; Motestions: Te604 cSTO> A; Cross-references: GB:Chr_I; PIDN:CABO4618.1; PID:93878658; GSPDB: A; Note: CDNA EST yk406h6.5 comes from this gene
Query Match Best Local Similarity 24.2%; Pred. No. 1.7e-14; Matches 173; Conservative 98; Mismatches 234; Indels 211; Gaps	A/Gene: MULLI.1.2 A/Map position: 1 Query Match 3.4; Core 222.5; DB 2; Length 604;
OY 351 DDGLVYVRRVLVTPCKVYFCGFEVNVSRRVLRNYSEDIDNFLRVSFVDEEWEKLY 405 1	Indels 177; Gaps 2 (TDIVQLRA 90
QY 406 STDLLPKASTGSGVRTNIYERILSTLRKGFVIGDKKFEFLAFSSQLRDNSVW 458	E H
QY 504 VLRHEIEVIPDVKVHGTSYVFSDGIGKISGDFA	Db 185 RKDTIRRIIVDPQVDMNKTRIHFELNCPPLIRQGSVDDDKPSTQKPFYKRTNRYSCIG-T 243 Qy 189 KETPDDQWVRTTDFPPSWIGLSSSLCLQFRRGVRLPNFEE- 228
434 SNNIQGTC-VQEPPLLIQIRMFNDGSAVKGIFLLNKNLPPQTVQVRP-SMIKVYKDKNLS	229
QY 581 KYESDNIKLDVLGWSK-YQPCYLNRQLITLLSTLGVKDEVLEQKQKEA 627 :: : : : :	Db 304 DVPIGKVYPYLRYPTSSKSYAFECFIYNCFPSKMKIIDAQSINENDGRQFAITYLIECLL 363 Qy 281 QHGCIPGPALNVYFFRLVDPRRRNVACIEHALEKLYYIKE 320
QY 628 VDQLDAILHDSLKAQEALELMSPGENTNILKAMLNCGYKPDAEPFLSMMLQTFRASKLLD 687	Db 364 SRGAIVRDQVLTDEICWGQFLGIITHYYLENDKLCEAALEDLIYLIDGRKRIG 416 Qy 321CCXDDVRWLTEQYDGYLKGRQPPKSPSITLDDGLVYVRRVLYFPCKYVFCGPEVN 375

	Q Q	: : : : : : : : : : : : : : : : : : : : : : : : :	Db 514	LEHGIVVANRDFGFLGCSSSQMRD
-	oy Db	376 VSNRVLRNYSBDIDNFLRVSFVDEBWEKLYSTDLLFKASTGSGVRTNIYERILST 430	Oy 475 Db 572	5 MGDFSQIKNVAKYAARLGQSFGSSI : : :
	Qy Db	1 LRKGFVIGDKKFEFLAFSSSQLRDNS : ::	RESULT 12 T40928 conserved	RESULT 12 140928 conserved hypothetical protein SPC
	Qy Db	475 MGDFSQIKNVAKYAARLGQSFGSSR 499 : : : : 572 LGNFLQIENIPKLMARLGQCFTQSR 596	N, Alterna C, Species C, Date: 2 C, Accessi	N.Alternate names: conserved nypot. C.Species: Schizosaccharomyces pom C.Date: 20-0cf-2000 #sequence_revil C.Accession: T40948
	RESULT T23669		R;Lyne, N submitted A;Referer	M.; Rajandream, M.A.; Barri d to the EMBL Data Library nce number: Z21958
	hypoth C; Spec C; Date	etical protein M01G12.12 - Caenorhabditis elegans (fragment) ies: Caenorhabditis elegans :: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 sequents.	A; Accessi A; Status: A; Molecul A; Residue	ion: T40928 : translated from GB/EMBL/ le type: DNA es: 1-549 <lin></lin>
	R; Lenr submit A; Refe	and, N. ted to the EMBL Data Library, November 1996 stence number: 219779	A; Experin R; Lucas,	references: EMBL:AL121807; mental source: strain 972h M.; Gaillardin, C.; Lyne,
	A; Acce A; Stat A; Mole	sssion: T23869 .us: preliminary; translated from GB/EMBL/DDBJ coule type: DNA	Submitted A; Referer A; Accessi	u to the Embi Data bibialy nce number: 221959 ion: T40948
	A; Res. A; Cros A; Expe	dues: 1-604 <wil> s-references: EMBL:281571; PIDN:CAB04618.1; GSPDB:GN00019; CESP:M01G12.12 rimental source: clone M01G12</wil>	A;Status: A;Molecul A;Residue	: translated Ifom GB/EMBL/. le type: DNA es: 374-1021 <luc> references: EMBL:AL035259;</luc>
	C;Gene A;Gene A;Map A;Inti	C, Generics: A, Generics: A, Map Position: 1 A, Introns: 35/3; 88/3; 183/3; 224/3; 273/3; 331/3; 420/3	A; Genetic	mental source: strain 972h cs: spbm:sPCC132.01c; SPDB:SPC
	Que Best Matc	Query Match 3.8%; Score 222.5; DB 2; Length 604; Best Local Similarity 20.7%; Pred. No. 4.6e-07; Matches 117; Conservative 74; Mismatches 197; Indels 177; Gaps 20;	Query Match Best Local S	Match 2.4%; Match 21.3%; ocal Similarity 21.3%; ocal 713%. Conservative 93
	QJ Dp	43 GSRAFAKVQFADNISADKIITLANNRLYFGSSYLKAWEMKTDIVQLRA 90	Qy 567	MKLSLRKSMS :
	Qy Dp	91YVDQMDGITLNFGCQISDDKFAVLGSTEVSIQFGIGLKKFFFFLSSGSADYKLQL 145 		6 LITLLSTLGVKDEVLE
	. 60 t	SYENIMOVVLHRPYGONAQFLLIQLFGAPRIYKRLEN-SCYSFF	Db 129 Qy 658	129 LLDGHYKILSLLRVVTFDKDQVYA 658 KAMLNCGYKPDAEPFLS :: :
	DP QY		Db 186	6 LDEISTAYASPTSINEPLFDQQLS 1 TLEYGOVFYOFTGAGHGEFSDDLH
	OD			
	Qy Db	229SFFHYAERENNITLQTGFTFFVSQKSALVPNVQPPEGISIPYKILFKISSLV 280 :	Oy 771	1 VNVRALHHMVDCVVFPQ
	Qy Db	281 QHGCIP320 		
	y do	321CCYDPVRWLTEQYDGYLKGRQPPKSPSITLDDGLVYVRRVLVTPCKVYFCGPEVN 375		
	oy B	376 VSNRVLRNYSEDIDNFLRVSFVDEBWEKLYSTDLLPKASTGSGVRTNIYERILST 430		RKVKDKAPQASS
	ογ	LRKGFVIGDK	Db 428	18 OSOKRRSPVAAAIQIPLKLIKNAV

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CCC132.01c [imported] - fission yeast (Schizosaccharo thetical protein SPCC1322.17c
                                                                                                                                                                                                                                                                                                                                                                                                                                 ); PIDN:CAA22870.1; GSPDB:GN00068; SPDB:SPCC1322.17c2.17c cosmid c1322
                                                                                                                                                                                                                                                                                                    7; PIDN:CAB58128.1; GSPDB:GN00068; SPDB:SPCC132.01c
2h-; cosmid c132
3, M.; Rajandream, M.A.; Barrell, B.G.
cy, January 1999
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                                                                                                                                                                               ision 03-Nov-2000 #text_change 03-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 138; DB 2; Length 1021;
Pred. No. 0.61;
13; Mismatches 215; Indels 146; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LHPFNNSRSTNSNFILKGNVVVAKNPCLHPGDIRVLKA 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POKGKRPHPNECSGSDLDGDIYFVCWDQDMIPPRQVQP 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (FINYIVNDSLGIIANAHVVFADREPDMAMSDPCKKLA 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPKEY---PDFMDKPDKTSYISERV-----IGKLF 932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMMLQTFRASKLLDLRTRSRIFIPNGRIMMGCLDESR 710
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ODIGAYEMVKNTDNRHKNACKMNSKFKPNI--DSVRNQ 571
                                                                                                                                                                                                            rell, B.G.; Aert, R.; Volckaert, G.
y, October 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cc1322.17c
                                          /DDBJ
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OY 983 KLGNLMDYYGIKTEAEILSGGIMKASKTFDRRKDAEAISVAVRALRKEAR 1032 OH 10	Db 656LBTILNLAK 683
1033 AWEKRRNDIDDMLPKASAWYHVIYHPTYWGCYNGG 1067	ADISPKYIEINLIGCNKFSYSISAEETYPGKLLLKIKDRVSELMPSI
u;	Qy 706 LDESRTLEYGQVFVQFTGAGHGEFSDDLHPFNNSRSTNSNFILKGNVVVAK 756
RESULT 13 14.0884 Cytotoxin L - Clostridium sordellii C; Species: Clostridium sordellii	Qy 757 NPCLHPGDIRVLKAVNVRALHHWVDCVVFPQKGKRPHPNECSGSDLDGDIYFVCW 811 :
5-0ct	OY 812 DQDMIPPRQVQPMEYPPAPSIQLDHDVTIEEVEEYFTUYIVNDSLGIIANAHVVFA 867 ::
A,Title: Cloning and characterization of the cytotoxin L-encoding gene of Clostridium sq. A,Reference number: 140884; MUID:95369733; PMID:7642137 A,Rocession: 140884 A,Status: preliminary; translated from GB/EMBL/DDBJ	Qy 868DREPDMAMSDPCKKLAELFSIAVDFPKTGVPAEIPSQLRPK 908
A;Molecule type: DNA A;Residues: 1-2364 <res> A;Cross-references: EMBL:X82638; NID:g1000694; PIDN:CAA57959.1; PID:g1000695 C;Superfamily: cpl repeat homology</res>	OY 909 EYPDFWDKPDKTSYISERVIGKLFRKVKDKAPQASSIATFTRDVARRSYDADMEVDGFED 968
C;Keywords: cytotoxin Query Match	Qy 969YIDBAFDYKTEYDNKLGNLMDYYGIKTEABILLSGGIMKASKTFDRRKDABAISVAVRA 1026
FAKVQFADNISADKIITLA 	Qy 1027 LRKEARAWFKRRNDIDDMLPKAS 1049 Db 1016
Qy 104 CQISDDKFAVLGSTEVSIQFGIGLKKFFFFLSSGSADYKLQLSYENIWQVVLHR 157	RESULT 14 122298 hypothetical protein F46C3.3 - Caenorhabditis elegans
QY 158 PYGQNAQFLLIQLFGAPRIYKRLENSCYSFFKETPDDQWVRTTDPPPSWIGLSSSLCLQF 217 Db 294QPDLFKSINKPDSITNTSWEMIKLEAIMKY 323	C;Species: Caenorhabdilis elegans C;Date: 15-oct-1999 #sequence_revision 15-oct-1999 #text_change 18-Feb-2000 C;Accession: T2228 R;Cottage, A.
OY 218 RRGVRLPNPEESFFHYAERENNITLQTGFTFFVSQKSALVPNVQPPEGISIPYKILF 274 1 :	submitted to the EMBL Data Library, November 1995 A;Reference number: 219543 A;Accession: T22298 A;Accession: T22298 A;Status: preliminary; translated from GB/EMBL/DDBJ
QY 275 KISSLVQHGCIPGPALNVYFFRLVDPRRRNVACIEHALEKLYYIKECCYDPVRWLTEQYD 334	A; Molecule type: DNA A; Residues: 1-2810 - WIL> A; Cross-references: EMBL: 266563; PIDN: CAA91469.1; GSPDB: GN00028; CESP: F46C3.3 A; Experimental source: clone F46C3
QY 335 GYLKGRQPPKSPSITLDDGLVYVRRVLVTPCKVYFCGPEVNVSNRVLRNYSEDIDNFLRV 394	C;Genetics: A;Gene: CESP:F46C3.3 A;Map position: X A:Introns: 67/2; 172/3; 204/2; 310/3; 366/2; 431/2; 684/3; 739/3; 786/3; 823/2; 880/ 1958/3; 1999/1; 2078/1; 2117/3; 2159/2; 2220/1; 2269/3; 2306/1; 2399/2; 2444/1; 2488
QY 395 SFVDEEWEKLYSTDLLPKASTGSGVRTNIYERILSTLRKGFVIGDKKF 442 : :	Query Match 2.3%; Score 133; DB 2; Length 2810; Best Local Similarity 17.7%; Pred. No. 6.7; Matches 169; Conservative 141; Mismatches 303; Indels 344; Gaps 46;
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QY 500 ETLSVLRHELEVIPDVKVHGTSYVFSDGIGKISGDFAHRVASKCGLQYTPSAF 552 : : :: : : : :	295
QY 553 QIRYGGYKGVVGVDPDSSMKLSLRKSMSKYESDNIKLDVLGWSKYQ 598	351 DDGLVYVRRVLVTPCKVY : : : OQS DVKVAVTELARIWPIV
OY 599 PCYLNROLITLESTLGVKDEVLEQKQKEAVDQLDAILHDSLKAQEALELMSPGENTNILK 658 ; ; ; : : ; ;	394

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Keuchel, H.; Hollenberg, C.P.
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NyAlternate names: protein YKL143w; protein YKL2
C.$Fectes: Saccharomyces cerevisiae
C.$Fectes: Saccharomyces cerevisiae
C.Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 06-Feb-1998
C;Accession: S37972; S38997; S22275
R;Ramezani Rad, M.; Xu, G.; Kirchrath, L.; Fritz, C.; Keuchel, H.; Hollenberg, C submitted to the Protein Sequence Database, March 1994
A;Reference number: S37953
A;Accession: S37972
A;Accession: S37972
A;Accession: S37972
A;Reference smbl: 228143; NID:9486244; PID:9486245; MIPS:YKL143w
A;Residues: 1-463 <ARAM>A;Residues: 1-463 <ARAM>A;Residues: 1-463 <ARAM>A;Reference number: S38996
A;Reference number: S38996
A;Reference number: S38996
A;Rocession: S38997
A;Recession: S38997
A;Recession: S38997
A;Recidues: 1-134, 'ATCVSKRBGKA', 146-463 <ABR>
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A;Cross-references: EMBL:225464; NID:9396434; PID:9396436
R;Abraham, P.R.; Mulder, A.; van't Riet, J.; Planta, R.J.; Raue, H.A.
Yeast 8, 227-238, 1992
A;Title: Molecular cloning and physical analysis of an 8.2 kb segment of chromosome 3
A;Title: Molecular cloning and physical analysis of an 8.2 kb segment of chromosome 3
A;Reference number: S22274; MUID:92245761; PMID:1574929
A;Accession: S2275
A;Molecule type: DAA
A;Residues: 1-134, ArcvskrbckA, 146-313, 'LSKTKARRGRRKERAVKKRA', 334-363, 'SSMVTKL' <ABZ
A;Cross-references: GB:S97962
C;Genetics:
C;Genetics:
A;Cross-references: SGD:S0001626; MIPS:YKL143w
A;Map position: 11L
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Best Local Similarity 18.0%; Pred. No. 0.52;
Matches 96; Conservative 75; Mismatches 155; Indels 206;
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November 6, 2002, 03:40:53 ; Search time 15 Seconds (without alignments) 3080.309 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

criptí	P34078 saccharomyc	P04050 saccharomyc							Q8rah4 thermoanaer							Ŋ		P53599 saccharomyc		bos tauru		saccharon	Ţ						saccharom		P52519 human herpe		P04933 plasmodium
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POL_COXMV RPOB_PSEAE YBA4_PEAST TOP1_THEACT TOP1_THEAC	ALIGNMENTS	PRT; 46	ed) sequence update) annotation updat rotein LTV1.	cer's yeast Saccharom (cetaceae;	929; T Riet J., al analysi s cerevisi	L., Fritz C., 1 . EMBL/GenBank/I SPAC3F10.17.	pyright. It is e of Bioinfor Institute. utions as lor is not removagreement (§ eisb-sib.ch).	LPVFORGMAKP ->	Score 131; Pred. No. 5; Mismatc	FQIRYGGYKGVVGVDFDS: : : : : :: YDYTQHLKPIGLDPEN	TLGVKDEVLEQ : : RDEI	FLSMMLQTFRA : :
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FEMS MICTOBIOL. Lett. 130:221-230(1995).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                         815
                                                                                                                                                                                                                                                  ------FDEWDIDN 239
                                                                                                                                                                                                                                                                                                               871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 KKKRKSRQKKGAMSDVSGFSMSSAIARTETMTVLDDQYDQIINGYENYEEELEEDEEQN 382
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----EDEAYVVNDDVVVEDISK 194
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THIS SUBUNIT IS THE LARGEST COMPONENT OF RNA POLYMERASE II.
-1. SUBCELLULAR LOCATION: Nuclear.
-1. PTM; THE TANDEM 7 RESIDUES REPEATS CAN BE HIGHLY PHOSPHORYLATED.
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PP04050; 012364; 092315;
01-NOV-1996 (Rel. 03, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 36, Last annotation update)
16-JUL-1999 (Rel. 36, Last annotation update)
16-JUL-1999 (Rel. 36, Last annotation update)
16-JUL-1999 (Rel. 36, Last annotation update)
17-JUL-1999 (Rel. 36, Last annotation update)
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                                                            SRTLE---YGQ-----VFVQFTGAGHG----EFSDDLHPFNNSRSTNSNFILKGNVVVA
                                                                                                                                                                                         756 KNPCLHPGDIRVLKAVNVRALHHMVDCVVFPQKGKRPHPNECSGSDLDGDIYFVCWDQDM
                                                                                                                                                                                                                                                                                                               816 I----PPRQVQPMEYPPAPSIQLDHDVTIEEVEEYFTNYIVNDSLGIIANAHVVFADREP
                                                                                                                                                                                                                                                                                                                                                                           240 VENFEDENYVKEM-----AQFDNIENLEDLEN-------IDYQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              973 --AFDY---KTEYDNKLGNIMDYYGIKTEAEILSGG--IMKASKTFDRRKDA 1017
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TATAIN=2288C / FY1679;
MEDLINE-217326; PubMed=8972577;
WOelfil S., Haneman V., Saluz H.P.;
"Analysis of a 26,756 bp segment from the left arm of yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        930 KLFRKVKDKAPQASSIATFTRD---VARRSY-----DADMEVDGFEDYIDE-
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                                                                                                     150 HQQDTTDEIR----GFKPDMNPALREVLEAL-----
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MEDLINE=95377607; PubMed=7649444;
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DR EMEL; X03162; CAA25619.1; --

EMEL; X04063; CAA2694.1; --

DR EMEL; 277162; RABZ01.

DR EMEL; 277162; RABZ01.

DR InterPro; IPR000064; RNA_POLII_repeat.

DR InterPro; IPR0001879; RNA_POL_A2.

DR InterPro; IPR0001879; RNA_POL_A3.

DR Pfam; PP00187; RNA_POL_A3.

DR Pfam; PP00187; RNA_POL_A3.

DR Pfam; PP0187; RNA_POL_A3.

DR Pfam; PP018
                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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-!- MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE FOUND IN BURARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE II FOR 5S AND TRNA GENES.

-!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 AVLGSTEVSIQFGIGLKKFFFFLSSGSADYKLQLSYENIW-----QVVLHRPYGQNAQ 164
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Q14008; Q14668;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OUT-2001 (Rel. 40, Last annotation update)
CH-TOG protein (Colonic and hepatic tumor over-expressed protein).
ASRPGLTAND--IRAWMGDFSQIKNVAKYAARLGQSFGSSRETLSVLRHEIEVIPDVKVH
                                                                    ----ETGYIQRRLVKALEDIMVH
                                                                                                                                     -----GISYVF---SDGIGKISGDFAH-RVASKCGLQYTPSAFQIRYGGYKGVVGV
                                                                                                                                                                                       852 YDNTTRNSLGNVIQFIYGEDGM-----BAAHIEKQSLDTIGGSDAAFEKKY----RVDLL
                                                                                                                                                                                                                                                                                                                                           903 NIDHTLDPSLLESGSEILGD-LKLQVLLDEEYKQLVKDRKFLREVFVDGEANWPLPVNIR
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Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                          DPDSSMKLSLRKSMSKYESDNIKLDVLGWSKYQPCYLNRQLITLL-
                                                                ----GLTPOEFFFHAMGGREGLIDTAVKTA--
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
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SEQUENCE FROM N.A.
TISSUE-Bone marrow;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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HEAT 3.
HEAT 4.
HEAT 5.
HEAT 6.
HEAT 7.
HEAT 9.
MISSING (IN REF. 1).
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ve 66; Mismatches 146;
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EMBL; D43946; BAAC7892.2; ALT_INIT.
InterPro; IPR000357; HEAT_REPEAT.
PROSITE; PS50077; HEAT_REPEAT; 1.
MEDLINE=95308325; PubMed=7788527;
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                  -----MMHLGYEKMAKATGKLKP 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----FQIRYGGYKG-----VWGVDPDSSMKLSLRKSMSKYESDNIKLDVLG 593
 667
                                                                                                                                                             GLUD.
Gallus gallus (Chicken).
Eukaryota: Metazoa: Chordata; Craniata: Vertebrata: Euteleostomi;
Archosauria: Aves: Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                VDPRRRNVACI-----EHALEKLYYIKECCYDPVRWLTEQYDGYLKGRQPPKSPSITL 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351 DDGLVYVRRVLVTPCK-----VYFC------GPEVNVSNRVLRNYSEDIDNFL 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 ASTIGHYDINAHACVTKPGISQGGIHGRISATGRGLFGHIENFIENASYMSILGMTPGFG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RETLSVLRHEIEVIPDVKVHGTSYVFSDGIGKISGDFAHRVASKC------GLQYTPSA 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 MEORRHRVRGILRIIKPCNHVLSVSFPIKR---DDGZW--EVIEGYRAQHSHQRTP---C 92
  ---KP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVSFVDEEWEKL---YSTDLLPKASIGSGVRINIYERILSTLRKGFVIGDKKFEFLA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FSSSQLRDNSVWMFASRPGLTANDIRAWM-----GDFSQIKNV---AKYAARLGQSFGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 DKTFAV-----OGFGNVGLHSMRYL------HRFGAKCVAVGEFDGSIWNPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.0%; Score 118.5; DB 1; Length 5
19.2%; Pred. No. 1.5;
Live 67; Mismatches 147; Indels
KQKEAVDQLDAILHD - - - - SLKAQEALELMSPGENTNILKAMLNCGY - -
                                                                                                                                                                                                                                                                                                                                                                                                                            129
55711 MW; 340DDB45BB0A5B04 CRC64;
                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Glutamate dehydrogenase (EC 1.4.1.3) (GDH).
                                                                                                       503 AA.
                                                                                                                                                                                                                                                                                                                                      PIR, A00380; DECHE.
HSSP; P00366; 11WX.
InterPro; IPRO01625; GLFV_Dh.
Pfam; PF00208; GLFV_dehydrog.N; 1.
Pfam; PF002812; GLFV_dehydrog.N; 1.
PRINTS; PR00082; GLFDHDRGNASE.
PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
OX140areductase; NADP; Mitochondrion.
BINDING 30
                 ----CVPHLYSCLEDRNGDVRKKAQDALPFF----
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                                                                                                                                                                                                                                  SEQUENCE, AND ACTIVE SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 19.2'
Matches 83; Conservative
                                                                                                       STANDARD;
                                                        1064 TSKDQVLAMLE 1074
                                    DAEPFLSMMLQ 678
                                                                                                                                                                                                                                                                                                                                                                                                                            129 1
503 AA;
                                                                                                                                                                                                              NCBI_TaxID=9031;
                                                                                                                                                                                                                                           TISSUE=Liver
                                                                                                     DHE3_CHICK
P00368;
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SEQUENCE
623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   630 QLDAILHDSL-KAQEALELMSPGENTNILKAMLNC-------GYKPDAEPFL 673
                                                                                                                   | :| : : | : : | : : | : : | : : | EGANGPTTPQADKIFLERNIMVIPDLYLNAGGVTVSAFZZKNLNHVSYGRLTFKYERDSN 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     407 TDLLPKASTGSGV-------RTNIYERILSTLRKGFVIGDKKFEFLAFSSS 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 KRROLKKLOKTAYPKDQAFHI---LRKFHKINNEALADTKLGPTSOSDLKFLSLTKDKRL 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 -LKTI--DSLCDKNELTEI----EYNTALAALINCIDETLVFKLLNKKCPGLKKDSITYT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAINS-SEBEC / ABB72;
STRAINS-SEBEC / ABB72;
Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.
Chung E., Duncan M., Guzman E., Hartzell G., Huncke-Smith S.,
Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
Taylor P., Wei Y., Yellon M., Botstein D., Davis R.W.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
289 IDPKELEDYKLOHGTIMGFPKAOKLEGSILETDCDILIPAASEKOLTKANAHKVKAKIIA
                                                                   594 WSKYQP-----CYLNRQLITL----LSTLGVKDEVLEQKQKEAVD-----QLDAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               451 QLRDNSVWMFASRPGLTANDIRAWMGDFSQIKNVAKYAARLGQSFGSSRETLSVLRHEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 FYTILGVNGEQLRDSKLIANDVQKFLKRG-----OLEKAVFLARLAKKKGVVG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 TRMLPRINTAINLTEHLLRRSFHSLTNLOKTOVKERLHELERHGFILNKTSKOLERINSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      511 VIPDVKVHGTSYVFSDGIGKISGDFAHRVASKCGLQYTPSAFQIRYGGYKGVVGVDPDSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomyceties;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical 79.5 kDa protein in PTP3-SER3 intergenic region.
YER077C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 688;
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SEQUENCE 688 AA; 79547 MW; 44C9EDC2E3D24E4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.0%; Score 117; DB 1; Lv
ilarity 22.2%; Pred. No. 3.1;
Conservative 51; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     688 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S0000879; YER077C.
                                                                                                                                                                                                             646
                                                                                                                                                                                                                                                                                409 YHLLMSVQESLE 420
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es 78; Conserv
                                                                                                                                                                                                             LHDSLKAQEALE
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Matches
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481 IKN-----
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                                                                                                                                                                                                                                                                                                                                                                                      AND MEDIATE
                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID-6239;
                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable pre-mRNA splicing factor AIP-dependent RNA helicase mog-5 (Sex determination protein mog-5) (Masculinization of germ line
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-20202625; PubMed-10737793;
Puoti A., Kimble J.;
Figh hermaphrodite sperm/oocyte switch requires the Caenorhabditis elegans homologs of PRP2 and PRP22.";
Proc. Nati. Acad. Sci. U.S.A. 97:3276-3281(2000).
                                                                                                                                                                                                                                                                                                                                                            Length 1200;
674 SMMLQTFRASK-----LLDLRTRSRIFIPNGRTMMGCLDESRTLEYGQV 717
                LISCTRIADEKRFMVVLNDLMNK----IPD----YCVDSKLLFEYCEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        023C46E494D7F44F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00690; DEAH_ATP_HELICASE; 1.
PROSITE; PS50126; S1; 1.
mRNA processing; mRNA splicing; Helicase; ATP-binding;
Nuclear protein; Developmental protein.
DOMAIN 176 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.0%; Score 116.5; DB 1;
llarity 18.8%; Pred. No. 7.9;
Conservative 137; Mismatches 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP (POTENTIAL).
DEAH BOX.
                                                                                1200
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                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WOINDED; EEDB.5; CE01889.
InterPro; IPR001410; DEAD.
InterPro; IPR001464; DEAL_box.
InterPro; IPR001650; Halicase_C.
InterPro; IPR003029; S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135759 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF286899; AAG01332.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam: PF00271; helicase_C; 1.
Pfam: PF00275; S1: 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U23484; AAC46765.1; -. HSSP; P05055; 1SRO.
                                                                                STANDARD;
                                                                                                                                                                                           Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                   STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                  protein 5)
MOG-5 OR EEED8.5
                                                                               MOG5_CAEEL
Q09530:
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SITE
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                                                         RESULT 6
MOG5_CAEEL
                       313
δ
                       g
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44;

Gaps

247;

Indels

Best Local Sim Matches 166;

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----KLGNLMDYYGIKTEAEILSGGIMKASKTFDRRKD---AEA 1019
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                                                  340 WMNPEASGVGQG-----PSTSIGGGKARVR--ISTPERWELROMOGAGVLTATDMPDFD 391
                                                                                                             425
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09BXW6; Q9NW87; Q9BEF5;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
0xysterol binding protein-related protein 1 (OSBP-related protein 1)
                                                                                                                VSNRVLRNYSEDID-NFLRVSFVDEEWEKLY----STDLLP----KASTGSGVRTNIYE
                                                                                                                                                      ||||| :: | :: |:: |:: |:: |:: |
EEMGVLRNYDDESDGEDIEIELVEDEPDFLRGYGKGGAEIEPVKVVKNPDGSLAQAALMQ
                                                                                                                                                                                                                                                                       502 DRNNKWKEMPEWLKHVTAGGKATYGRRTNLSMVEQRESLPIFALKKNLMEAMIDNQI--L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKYESDNIKLDVLGWSKYQPCYLNRQLITLLSTLGVKDEVLEQKQKEAVDQLDAILHDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MLDEAHERTI---HTDVLFGLLKAAARKRPELKLIITSATLDSVKFSEYFLEAPIFTIPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     742 IHLTEPPGDVLVFLTGQEEID-----TSCEVLYERMK-----SMGPDVPELI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              812 DQDMIP----PRQVQPMEYPPAPSIQLDHDVTIEEVEEYFTNYIVNDSLGIIANAHVVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADREPDMAMSDPCKKLAELFSIAVDFPKTGVPAEIPSQLRPKEYPDFMDKPDKTSYISER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        871 -PGKCYRLYTERAFRDEMLPTPVPEIQRTNLASTLLQLKAMGINNLIDFDFMDAPPLDSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            930 ITALNILHILSALDGDGLLIKLGRRMAEFPLEP------SLSKLLIMSVDLGCSEE
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                                                                                                                                                                                                                                    RILSTLRKGFVIGDKKFEFL----AFSS-SQLRDNSVWMFASRPGLTANDIRAWMGDFSQ
                                                                                                                                                                                                                                                                                                                                                  SYVFSDGIGKISGDFAHRVASKCGLQYTPSAFQIRYGGYKGVVG-VDPDSSMKLSLRKSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           560 VVVGETGSGKTT------QMTQYAIEAGL-GRRGKIGCTQPRRVAAMSVAKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEEYGCKLGTDVGYTIRFEDCTSQDTIIKYMT----DGML---LRECLIDPDLSGYSLI
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WLTEQYDGYLKGRQPPKSPSITLDDGLVYVRRVLVTP-----CKVYFCG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1078 WCVYDQLIQIKKDKARNRPVLNLSSLRAQL----SHRLVL 1113
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OSBPL1 OR ORP1 OR OSBP8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50088; ANK_REPEAT; 3.
PROSITE; PS50297; ANK_REP_REGION; 1.
PROSITE; PS01013; OSBP; 1.
PROSITE; PS01003; PH_DOMAIN; 1.
Lipid transport; Transport; ANK repeat; Repeat; Alternative splicing.
REPEAT 47 76 ANK 1.
REPEAT 80 109 ANK 2.
                                                                                                                                                     MEDLINE-21601154; PubMed-11735225;
Jaworski C.J., Moreira B., Li A., Lee R., Rodriguez I.R.;
A family of 12 human genes containing oxysterol-binding domains.";
Genomics 78:185-196(2001).
                                                                                                                                                                                                                                                                                                                                                        Xu Y., Liu Y., Riddway N.D., McMaster C.R.;
Novel members of the human oxysterol.binding protein family bind
phospholipids and regulate vesicle transport.";
J. Biol. Chem. 276:18407-18414(2001).
            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ehnholm C.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM C).
MEDLINE-21376257; PubMed=11483621;
Lehto M., Laitinen S., Chinetti G., Johansson M.,
Staels B., Ikonen E., Olkkonen V.M.;
"The OSBP-related protein family in humans.";
J. Lipid Res. 42:1203-1213(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SINTIARITY: BELONGS TO THE OSBP FAMILY. SIMILARITY: CONTAINS 3 ANK REPEATS. SIMILARITY: CONTAINS 1 PH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 514-790 FROM N.A. (ISOFORM A).
                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS A AND B).
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InterPro: IPR001849; Cxysterol_BP.
InterPro: IPR001849; PH.
Pfam; PF00023; ank; 4.
Pfam; PF00169; PH; 1.
Pfam; PF00127; Cxysterol_BP; 1.
SMART; SM00248; ANK; 3.
SMART; SM00233; PH; 1.
                                                                                                                                                                                                                                                                                                                                      MEDLINE=21264638; PubMed=11279184;
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EMBL; AF392450; AAL40663.1; --
EMBL; AF274714; AAK15154.1; --
EMBL; AF33726; AAG53407.2; --
EMBL; AK001079; BAA91496.1; --
Genew; HGNC:16399; OSBPLIA.
                                                                                                                                                                                                                                                                              [2]
SEQUENCE FROM N.A. (ISOFORM A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rissue=Embryo;
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               TEW BRANCH BRANC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .003 -GIMKASKTFDRRKDAEA-----ISVAVRALRKEARAWFKRRNDIDDMLPKASAWYHV 1054
                                            L (IN ISOFORM
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                                                                                                                                                                                                                                           592 LGWSK-YQPCYL-NRQLITLLSTLGVKDEVLEQKQKEAVDQLDAILHDSL---KAQEALE 646
                                                                                                                                                                                                                                                                                                                                          LLEYNADITIVNGSGQTAKEVTHAEBIRSMLEAVERTQQRKLEELLLAAARBGKTTEL-- 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1988 (Rel. 07, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
18A1 protein [Includes: dlutamine-dependent carbamoyl-phosphate
synthase (EC 6.3.5.5); Aspartate carbamoyltransferase (EC 2.1.3.2)].
URA2 OR YII130C OR J0686.
Saccharomyces Cerevisiae (Baker's yeast).
Bukaryota; Fungl; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  838 VIIEEVEE---YFTNYIVNDSLGIIANAHVVFADREPDMAMSDPCKKLAELFSIAVDFPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIEKAQSCQQRLDREISNFL-KMIKECDMAKEMLPSFLQKVEVVSEASRETCVALTDCLN
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                                                                                                                                                                                                                                                                     LGWTPLHLACYFGHRQVVQDLLKAGAEVNVLN-----DMGDTPLHRAAFTGRKELVML
                                                                                                                                                                                                                                                                                                                                                                                                            158 TALLINRPNPPDVNCSDQLGNTPLHC --- AAYRAHKQCALKLIRSGADPNLKNKNDQKPLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                               NSRSTNSNFILKGNVVVAKNPCLHPGDI------RVLKAVNVRALHHMV-----
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                                                                                                                                                                                                                                                                                                                ----LKAMLNCGYKPDAEPFLSMMLQTFRASKLLDLRT
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                                                                                                                                                                           Score 116; DB 1; Length 950;
Pred. No. 6;
                                                                               --> A (IN REF. 4).
-> P (IN REF. 1; AAL40663).
-> S (IN REF. 1; AAL40662).
-> G (IN REF. 1; AAL40662).
CDDA26CA27865F63 CRC64;
                                                                                                                                                                                  Query Match
2.0%; Score 116; DB 1; Length 950
Best Local Similarity 18.9%; Pred. No. 6;
Matches 116; Conservative 101; Mismatches 234; Indels
                                               ٨
                            MISSING (IN ISOFORM A).
FUPLLGETYELVRDDLGFRLISEQ ->
C).
T -> A (IN REF. 4).
S -> P (IN REF. 1; AAL40665
P -> S (IN REF. 1; AAL40665
A -> G (IN REF. 1; AAL40665
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 ANK 3.
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P07259;
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ALGASE (ASPARTATE TRANSCARBAMYLASE).

GATASE (BY SIMILARITY).

GATASE (BY SIMILARITY).

GATASE (BY SIMILARITY).

H -> D (IN REF. 2).

R -> A (IN REF. 2).

ELKVVPWN -> RIESCSMD (IN REF. 1 AND 2).

GA -> VQ (IN REF. 1 AND 2).

GI -> FF (IN REF. 1 AND 2).

GI -> FF (IN REF. 1 AND 2).

GI -> FF (IN REF. 1 AND 2).

I -> T (IN REF. 1 AND 2).

I -> T (IN REF. 2).

I -> Y (IN REF. 2).

I -> Y (IN REF. 2).

I -> Y (IN REF. 2).

A -> G(IN REF. 1).

D -> V (IN REF. 1).

EV -> S (IN REF. 1).

EV -> S (IN REF. 1 AND 3).

V -> G (IN REF. 1 AND 3).

V -> G (IN REF. 1 AND 3).

V -> G (IN REF. 1 AND 3).

Y -> G (IN REF. 3).

H -> L (IN REF. 3).
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DOMAIN 1400 GATASE (GLUTAMINE AMIDOTRANSFERASE).
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Pfam; PF02142; MGS; 1.
Pfam; PF02729; OTCace_N; 1.
Pfam; PF02789; CPSase_L_D3; 3.
PRINTS; PR00100; AOTCASE.
PRINTS; PR00099; CPSGASE.
PRINTS; PR00099; CPSGATASE.
PRINTS; PR00096; GTAASE.
TIGRPAMS; TIGR00670; asp_carb_tr; 1.
PROSITE; PS00049; CARBAMOTIRRNSFERASE; 1.
PROSITE; PS00046; CPSASE_1; 2.
PROSITE; PS000866; CPSASE_1; 2.
PROSITE; PS000866; CPSASE_1; 2.
                                                                                                                                                                       InterPro; IPR002029; Asp/orn_Cotranf.
InterPro; IPR002039; Asp_carbinItransf.
InterPro; IPR001317; CPS_GATase.
InterPro; IPR0013474; CPSase_an_chain.
InterPro; IPR002474; CPSase_an_chain.
InterPro; IPR002195; Dihydrooratase.
InterPro; IPR002195; Dihydrooratase.
InterPro; IPR004382; MS_like.
Pfam; PP00117; GATase; 1.
Pfam; PP00118; OTCace; 1.
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ALT_INIT.
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Dihydroorotase; 1.
CPSase_sm_chain; 1.
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              EMBL; X05553; CAA290681; EMBL; J04711, AA351981; EMBL; 249405; CAA89425.1; EMBL; X87371; CAA60825.1; EMBL; D28129; BAA05680.1; PIR; S05767; QDSVU2.
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2214 AA;
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PF00744;
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Souciet J.-L., Nagy M., le Gouar M., Lacroute F., Potier S.;
"Organization of the yeast URA2 gene: identification of a defective
dihydroorotase-like domain in the multifunctional carbamoylphosphate
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1268-2214 FROM N.A.
MEDLINE-8925278, PubMed-2498313;
MAGY M., le Gouar M., Potier S., Souciet J.-L., Herve G.;
"The primary structure of the aspartate transcarbamylase region of the primary structure of the Aspartate transcarbamylase region of the primary structure of the conformation of the URA2 gene product in Saccharomyces cerevislae. Features involved J. Blol. Chem. 264:8366-8374(1989).

    -!- SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.

                                                                                                                                                                                                         SEGUENCE OF 1-510 FROM N.A.
MEDLINE-87286375; PubMed=3039294;
Souciet J.-L., Potier S., Hubert J.-C., Lacroute F.;
"Nucleotide sequence of the pyrimidine specific carbamoyl phosphate synthetase, a part of the yeast multifunctional protein encoded by the URA2 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=S2886 / FY1679;

BDDLINE=97103775; PubMed=8948101;

Cziepluch C., Kordes E., Pujol A., Jauniaux J.-C.;

Cziepluch C., Kordes E., Pujol A., Jauniaux J.-C.;

Sequencing analysis of a 40.2 kb fragment of yeast chromosome X reveals 19 open reading frames including URA2 (5' end), TRK1, PBS2, SPT10, GCD14, RPS1, PHO86, NCA3, ASF1, CCT7, GZF3, two tRNA genes, three remnant delta elements and a Ty4 transposon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -I FUNCTION: THIS PROTEIN IS A "FUSION" PROTEIN ENCODING THREE ENZYMATIC ACTIVITIES OF THE PYRIMIDINE PATHWAY (GATASE, CPSASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Katsoulou C., Tzermia M., Tavernarakis N., Alexandraki D.; "Sequence analysis of a 40.7 kb segment from the left arm of chromosome X reveals 14 known genes and 13 new open reading including homologues of genes clustered on the right arm of
                                                                                                                                                       synthetase-aspartate transcarbamylase complex.";
Gene 79:59-70(1989),
                                                                                                                                                                                                                                                                                                                                   Gen. Genet. 207:314-319(1987)
                                     SEQUENCE FROM N.A.
STRAIN-ATCC 28583 / FL100;
MEDLINE-89378778; PubMed-2570735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 175-2214 FROM N.A.
STRAIN-S288c / FY1679;
MEDLINE-96408771; PubMed-8813765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-276 FROM N.A.
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Yeast 12:787-797(1996).
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enzyme

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43;
                                                        Gaps
                                                        Indels 273;
K (IN REF. 3)
CRC64;
                                  Length 2214;
           4CA58304DAECAD21
                                  DB 1;
                                                        267;
                                 2.0%; Score 114.5;
18.8%; Pred. No. 28;
1ve 119; Mismatches
                                                          Conservative 119;
                                                 Local Simi
nes 153;
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Matches
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-IDEAFDYK-----TEYD----NKLGNLMDY-----YGIKTEAEILSGGIMKAS 1008
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine--tRNA ligase) (AlaRS).
ALAS OR TTE1248.
                                                                                                                                                                                                                                                                                                                                                                             ------QVLVEKSMKGWKEVEYEVRDAFDNCITVCNMENFDPLGIHTGDSIVVA
                                                                                                                                                                                                                                                                                                                                                                                                                     KNPCLHPGDIRVLKAVNVRALHHM--------VDCVVFPQKGKRPHPNECS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IANAHVVFADREPDMAMSDPCKKLAELFSIAVDFPK-----IGVPAEIPSQLRPKEYPD
----LPKASIGSGVRTNIYERILST
                   :: |: | :: | :: | :: | : | : | : | 347 FAVDVDTLTSGWKPLFVNANDDSNEGIYHSELPYFSVQFHPESTPG------PRDTEF
                                                        LRKGFVIGDKKFEF-----LAFSSSQLRDNSVWMFASRPGLTANDIRA-WMGDFSQIKN
                                                                                     LFDVFIQAVKEFKYTQVLKPIAFPGGLLEDN----VKAHPRIEAKKVLVLGSGGLS----
                                                                                                                     VAKYAARLGOSFGSSRETLSVLRHE----IEVIPDVKVHGTSYVFSDGI--GKISGDFAH
                                                                                                                                         ----IGQAGEFDYSGSQAIKALKEEGIYTILINPNIATIQTSKGLADKVYFVPVTAEFVR
                                                                                                                                                                             RVASKCGLQYTPSAFQIRYGGYKGV-VGVDPDSSMKLSLRKSMSKYESDNIKLDVLGWSK
                                                                                                                                                                                                YQPCYLNRQLITLLST-----LGVKDEVLEQKQK-EAVDQLDAILHDSLKAQEALELMS
                                                                                                                                                                                                                                                          550 PGENTNILKAM----LNCGYKPDAEPFLSMMLQTFRASKLLDLRTRSRIFIPNGRTWMG
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Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
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 YSEDIDNF ---- LRVSFVDEEWEKLYSTDL --
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SEQUENCE FROM N.A.
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OBRAH4;
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SYA_THETN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            441
                                                                                                                                                                                                                                                              PROSITE; PS50860; AA_TRNA_LIGASE_II_ALA; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Complete proteome.
SEQUENCE 878 AA; 98363 MW; F2CE98288DC2A244 CRC54;
                                                                                                                                                                                                                                                                                                                                                                                                                                         403
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                                                                                                                                                                                                                                                                                                                                                               308;
                                                                                                                                                                                                                                                                                                                                     Query Match
1.9%; Score 113.5; E
Best Local Similarity 19.4%; Pred. No. 7.9;
Matches 180; Conservative 113; Mismatches
                                                                                                                                                                                                                                                           EMBL; AE013087; AAM24472.1; -
STRAIN-MB4 / JCM 11007;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DV-ARRSYDADMEVDGFEDYIDEAFDYKTEYDNKLGNLMDYYGIKTEAEILSGGIMKASK 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Expression of the xylulose 5-phosphate phosphoketolase gene, xpkA, from Lactobacillus pentosus MD363 is induced by sugars that are fermented via the phosphoketolase pathway and is repressed by glucose mediated by CcpA and the mannose phosphoenolpyruvate
                            641
                                                       907
                                                                                                              908 ------KEYPDFMDKPDKTSYISER-VIGK---LFRKVKDKAPQASSIATFTR 950
                                                                                                                                         695 IEALTGIEAIKYLNEQKEILDRVSETLKAQEKEVVSKIENLQOSLKDKEREIEGLKTKIA 754
                                                                                                                                                                                                 755 SILAETLIDSAISVDGVKVIASRVEDYDMEALKTLGDIL-----KDRLKSAAVILASS 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Posthuma C.C., Bader R., Engelmann R., Postma P.W., Hengstenberg W.,
                                                                           809 VCWDQ------DMIPPRQVQPMEYPPAPSIQLDHDVTIBEVEEYFTNYIVNDSL--GI
                         589 VAYDRLRFDFSHYQAVSKEELKKIEERVNEKIYEQLPVVVEE-----KNY--EDALKEGA
                                                      859 IANAHVVFADREPDMAMSDPCKKLA------ELFSIAVDFPKTGVPAEIPSQLRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   650-658,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        787 AA; 88573 MW; B049F3DB932DFEB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
XYlulose-5-phosphate phosphoketolase (EC 4.1.2.9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., SEQUENCE OF 1-31; 477-488 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      787 AA.
                                                                                                                                                                                                                            1010 TFDR------RKDAEAISVAVRALRKE 1030
                                                                                                                                                                                                                                                       SKDKALFVGMATKDAVEKGVNMGAVIKE 835
                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                             Lactobacillus pentosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=11823225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pouwels P.H.;
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                                                                                                                                                                                                                                                                                                                            XPKA_LACPE
0937F6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372 PEVNVSNRVLRN---YSEDIDNFLRVSFVDEEWEKLYSTDLLPKASTGSGVRTNIYERIL 428
                                                                                                                                                                   | :|: : | : | : | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                                                                                                             STLRKGFVIGDKKFEFLAFSSSQLRDNS----VW---MFASRPGLTANDIRAWMGDFSQ 480
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                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          PALAKAM---DEAVEKIKAIQKNARENDDATLPVWPMIVFRAPKGWTGP--KSWDGD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DREPDMAMSDPCKKLAELFSIAVDFPKTGVPAEIPSQLRPKEYPDFMDKPDKTSYISERV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGKLFRKVKDKAPQASSIATFTRDVARRSYDADMEV----DGFEDYIDEAFDYKTEYDNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FVCWDQDMIPPRQVQPMEYPPAPSIQLDHDVTIEEVEEYFTNYIVNDSLGIIANAHVVFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---- DWASTDQGSEPDIVFAAAGTEPTLETLAAI--QLLHDSFPDM-----KIRFVN--V
                                                                                                                                                                                                                                                                                                                                                                    481 IKNVAKYAARLGQSFGSSRETLSV----LRHEIEVIPDVKVHGTSYVFSDGIGKISGDFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HRVASKCGLQYTPSAFQIRYGGYKGVVGVDPDSSMKLSLRK----SMSKYESDNIKLDVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WSKYQPCYLNRQLITLLSTLGVKDEVLEQKQKEAVDQLDAILHDSLKAQ-EALELMSPGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLKAVNV-----PALHHMYDCVVFPQKGKRPH-----PNECSGSDLDGDIY
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Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Hypothetical 196.1 kDa protein in RPS3-PSD1 intergenic region.
WNL172W OR N1677.
Length 787;
                                                                Indels
   1.9%; Score 113; DB 1; L. L. L. 19:1%; Pred. No. 7.2; Conservative 113; Mismatches 270;
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      Query Match
Best Local Similarity
Matches 139; Conserv
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SEQUENCE FROM N.A.
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P53886;
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134 LSSGSADYKLQLSYENIWQVVLHRPYGQNAQFLLIQLFGAPRIYKRLENSCYSFFKETPD 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 LVPNVQPPEGISIPYKILFKISSLVQHGCIPGPALNVYFFRLVDPRRRNVACIEHALEKL 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 475 LILVSEGONKEEVKACLYDP-----FVKITSPSKNISEELTKONSLPSLOKLFPY 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       600 CYLNRQLITLLSTLGVKDEVLEQKQKEAVDQLDAILHDSLKAQEALELMSPGENTNILK 658
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15-JUN-2002 (Rel. 41, Last annotation update)
Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGQSFGSSRETLSVLRHEIEVIPDVKVHGTSYVFSDGIGKISG------DFAHRVA--S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              316 YYI-----KECCYDPVRWLTEQYDGYLKGRQPPK--SPSITLDDGLVYVRRVLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-----CKVYFCGPEVNVS-----NRVLRNYSEDIDNFLRV----SFV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         585 LLILPIPSSSAQEYQEYKEIYERDLFQHLKQDSEITSSVLPRIVIGLHLIREEYSLNVLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----VIGDKKFEFLAFSSQLRDNSVWMFASRPGLTANDIRAWMGDFSQIKNVAKYAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              645 RNEHALLG----QFLRFATAAMGWPDLWQSYYVPKMDSE---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---DEEWEKLYSTDLLPKASTGSGVRTNIYERI---LSTLRKGF ----
                                                                                                                                                                                                                                                                                                                                                                                                                                    19.4%; Pred, No. 24;
vative 79; Mismatches 157; Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 1748;
rmaier B., Piravandi E., Rinke M., Domdey H.;
nitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
SIMILARITY: TO A.NIDULANS BIME AND MOUSE TSG24.
                                                                                                                                                                                                                                                                                                                                                                      1748 AA; 196142 MW; 34BC9212020BB2B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                  1.9%; Score 113; Di
9.4%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TERT_SCHPO STANDARD; P 013339; 013338; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequin-15-JUN-2002 (Rel. 41, Last anno-
                                                                                                                                                                                                                                                             EMBL; Z71448; CAA96060.1; -.
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TRT1 OR SPBC29A3.14C.
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SEQUENCE FROM N.A.
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                       Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                   RAY WOOD V., GWilliam R., Rajanderilb99300, A. Bakhan D., Bowman S., Ray Bacous J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Rayles J., Parker S., Basham D., Bowman S., Rayles J., Parker S., Churcher C.M., A. Collias M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Collias M., Connor R., Cronin A., Davis P., Fidurell T., Fraser A., Rayles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones M., Leather S., McDonald S., McLean J., Raylor K., Jones M., Leather S., McDonald S., McLean J., Raylor K., Jones M., Squares R., Squares K., Stevens K., Stevens K., Autherford K., Taylor R.G., Tivey A., Walsh S., Stevens K., Autherford K., Taylor R.G., Tivey A., Walsh S., Stevens K., Hibbert B., Modward J., Volckaert G., Aert R., Robben J., Grymonprez B., Modward J., Volckaert G., Aert R., Robben J., Grymonprez B., Modward J., Volckaert G., Aert R., Robben J., Grymonprez B., Reger M., Schaefer M., Meller H., Manbut R., Pohl T.M., Rabel C., Fuchs M., Wedler H., Reinhardt R., Pohl T.M., Agal D., Limmenn M., Wedler H., Reinhardt R., Pohl T.M., Rabel C., Fuchs M., Rochet M., Gallardt S., Moccobet M., Gallardt V., Mottier S., Ragan L., Dreano S., Gloux S., Lelaure V., Mottier S., Radalibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Rochet M., Galllardin C., Jamene J., Sanchez M., del Rey F., Bentto J., Moreno S., Gloux S., Lelaure V., Mottier S., Ragan R.R., Cruzado L., Jimene J., Sanchez M., del Rey F., Bentto J., Moreno S., Gloux S., Calle R., Raster R., Barsell B.G., Nurse P., Rather R., Reinhardt R., Pottshir M., Rainhert E., Breyence G., Schlack R., Raster Benzone Sequence of Schizosaccharomyces pombe. The Redictor Reparts TO CHROMSOME ENDS BY COPYING A TEMPLATE SIGNERASE TELOMERASE IT R. RADERINIAR PRODUCTS: TWO ISOFORMS ARE PRODUCED BY ALTERNATIVE TWO THE REPLEMBATIVE TWO ISOFORMS ARE PRODUCED BY ALTERNATIVE
                                                                       Nakamura T.M., Morin G.B., Chapman K.B., Weinrich S.L., Andrews W.H., Lingner T., Harley C.B., Cech T.R., "Telomerase catalytic subunit homologs from fission yeast and human."; Science 277:955-959(1997).
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-i- SIMILARITY; BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
TELOMERASE SUBFAMILY.
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116328 MW; AB2DC7030228F443 CRC64;
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1.9%; Score 112.5; DB 1;
Best Local Similarity 18.2%; Pred. No. 11;
Matches 128; Conservative 109; Mismatches 258;
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EMBL; AF015783; AAC49803.1; -.
EMBL; AL022299; CAA18391.1; -.
InterPro; IPR000477; RYTSe.
InterPro; IPR003545; Telomerase_RT.
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Transferase; RNA-directed DNA polyn
DNA-binding; Alternative splicing.
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MEDLINE=21848401; PubMed=11859360;
STRAIN=972;
MEDLINE=97400623; PubMed=9252327;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DR HSSP; P19821; ITAU.

BR TIGR; HP1470; -: FAUCOSJU: ALILINIT.

BR TIGR; HP1470; -: FR002261; 3_5_exonuclease.

BR TIGR; HP1470; -: FR002421; 5_3_exonuclease.

BR InterPro; IPR001299; DNA_pol.

BR InterPro; IPR001399; DNA_pol.

BR InterPro; IPR001394; HHH_2.

BR Ffam; PR00476; DNA_pol.

BR Ffam; PR00689; DNAPOLI.

BR SWART; SW00479; BHH2; 1.

BR SWART; SW00479; DOLAC; 1.

BR SWART; SW00479; DOLAC; 1.

BR SWART; SW00779; HH2; 1.

BR SWART; SW00479; DOLAC; 1.

BR SWART; SW00479; DNA_pollymerase; DNA replication; DNA repair; WHY HYDISSE; Exonuclease; DNA-bollyming; Complete proteome.

SQUENCE 891 AA; 101975 MW; 3D6E7D8FF613EB88 CRC64;
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-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                       EXHIBITS 3' TO 5' AND 5' TO 3' EXONUCLEASE ACTIVITY, THIS DNA POLYMERASE EXHIBITS 3' TO 5' AND 5' TO 3' EXONUCLEASE ACTIVITY (BY
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                          "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 PLLKIKDELKEYGFISTLRDLENSPTPLILDNAPLLDNTPALDNTPKKSCM-----IV
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                                                                                                                                                                                                                                                                 + {DNA}(N)
-:- SUBUNIT: SINGLE-CHAIN MONOMER WITH MULTIPLE FUNCTIONS
-:- SIMILARITY: BELONGS TO THE DNA POLYMERAGE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE000647; AAD08510.1; ALT_INIT
                                                           pylori.";
Nature 388:539-547(1997)
Venter J.C.
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Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Binding to cells via a high affinity receptor, laminin is thought to mediate the attachment, migration, and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.
                                                                                                                                              685
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                                    714 YGQV-----SRSTNSNFI 747
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Richards A.J., Al-Imara L., Carter N.P., Lloyd J.C., Leversha M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Fetal lung;

BEDLINE=25300971, PubMed=7781776;

Ityanainen A., Sainio K., Sariola H., Tryggvason K.;

"Primary structure and expression of a novel human laminin alpha 4
536 VLERQILELIGVDFNLNSPKQLSEVLYDKLGLPKNKSHSTDEKSLLKILDKHPSIALILE
                                                                                                      748 LKGNVVVAKNPCLHPGDIRVLKAVNVRALHHMVDCVVFPQKGKRPHPNECSGSDLDGDIY
                                                                                                                                                                            808 FVCWDQDMIPPRQVQPMEYPPAPSIQLDHDVTIEEVEEYFTNYIVNDSLGIIANAHVVFA
                                                                                                                                                                                                                ----DKDLM-------EAFLKGRDIHLETSKALFGEYLAKEKRSIAKSINF---
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                                                                                                                                                                                                                                                                                  726 ----GLVYGMGSKKLSETLNISLNEAKSYIEAYF-----KRFPSIKD-----YLN---
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                                                                                                                                                                                                                                                                                                                                                         767 -----RMKEEILKTSK--AFTLLGRYRVFD----FTGANDYVKG--NYLREGVNAI---
                                                                  596 YRELNKLFNTYTTPLLRLKDKDDKIHTTFIQ-TGTATGRLSSHSPNLQNIPVRSPKGLLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Richards A.J., Luccarini C., Pope F.M.; The structural organisation of LAMA4, the gene encoding laminin
                                                                                                                               || : :| || ; :| || 655 RKGFIASSKEYCLLGVD---YSQIELRLLAH-----FSQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMA4_HUMAN STANDARD; PRT; 1816 AA. 016365; 015335; 014735; 090E18; 090UN9; 01-NOV-1997 (Rel. 35, Created) EJUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                             988 MDYYGIKTEAEILSGGIMKASKTF 1011
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Mammalia; Eutheria;
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Q16363; Q15:
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C. -- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
MEMBRANES (MAJOR COMPONENT).
C. -- TISSUE SPECIFICITY: IN ADULT, STRONG EXPRESSION IN HEART, LUNG,
OVARY SMALL AND LARGE INTESTINES, PLACENTA, LIVER; WEAK OR NO
C. EXPRESSION IN SKELETAL MUSCLE, KIDNEY, PANOREAS, TESTIS, PROSTATE,
BRAIN, HIGH EXPRESSION IN FETAL LUNG AND KIDNEY. EXPRESSION IN
FETAL AND NEWBORN TISSUES IS OBSERVED IN CERTAIN MESENCHYMAL CELLS
IN TISSUES SUCH AS SMOOTH MUSCLE AND DERMIS.
C. -- DOMAIN THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
C. -- DOMAIN: CONTAINS 3.5 LAMININ GF-LIKE DOMAINS.
C. -- SIMILARITY: CONTAINS 5 LAMININ GF-LIKE DOMAINS.
C. -- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
C. -- CAUTION: GENE LAMA4 WAS FORMERY CALLED LAMA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
SUBUNIT: Laminin is a complex glycoprotein, consisting of three different polypeptide chains (alpha, beta, gamma), which are bound to each other by disulfide bonds into a cross-shaped molecule comprising one long and three short arms with globules at each
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00053; laminin_G5; 6.
Pfam; PF00054; laminin_G5; 6.
SWART; SW00180; EGF_Lam; 3.
SWART; SW00282; LamG; 5.
PROSITE; PS00022; EGF_L1; UNKNOWN_1.
PROSITE; PS00248; LAMININ_TYPE_EGF; 3.
PROSITE; PS50025; LAM_G_DOMAIN; 5.
PROSITE; PS50025; LAM_G_DOMAIN; 5.
LAMININ_TYPE_EGF; 3.
LA
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LAMININ G-LIKE 1.
LAMININ G-LIKE 1.
LAMININ G-LIKE 3.
LAMININ G-LIKE 3.
LAMININ G-LIKE 4.
LAMININ G-LIKE 4.
LAMININ G-LIKE 5.
COLLED COLL (POTENTIAL).
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LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4 (INCOMPLETE).
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EMBL; X91171; CAA62596.1; --
EMBL; X14240; CAA74636.1; --
EMBL; X16939; CAA54253.1; --
EMBL; Z99289; CAB1653.1; --
HSSP; PO0468; 1KLO.
Genew, HGNC: 6484; LAMA4.
NIN; 600133; --
InterPro; IPR0020561; EGF-like.
InterPro; IPR002059; Laminin_EGF.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR002049; Laminin_GF.
Pfam; PF00053; laminin_GG.
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DMLPKAS------AWYHVTYHPTYWGCYNQGLKRAHFISFPWCVYDQLIQIKKDKAR 1093
                                   673 QAKAESSSDEAVADTSRRVGGALARKSALKTR-----LSDAVKQLQAAERGDAQQRLGQS 727
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                                                                                      NLTEVVPQLLDQLRTVEQKRPASNVSA 806
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MEDLINE-92107656; PubMed-1762905;
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MEDLINE=94077736; PubMed=8255785;
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P32372;
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(POTENTIAL)
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L -> F (IN REF. 1).
G -> GMOCPTIS (IN REF. 4).
D -> A (IN REF. 4).
T -> P (IN REF. 2 AND 3).
T -> P (IN REF. 1).
SGR -> GGP (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                -> GGP (IN REF. 4).
04E9AF379A0F4A4D CRC64;
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INTERCHAIN (PROBABLE).
INTERD (GLCNAC...)
INTERED (GLCNAC...)
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.5%; Pred. No. 33;
BB; Mismatches 228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1993 (Rel. 27, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
S-M checkpoint control protein rad4 (Protein cut5) (P74).
RAD4 OR CUT5 OR SPAC23C4.18C.
                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
NCBL_TaxID-4896;
648 AA.
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Search comp
Job time :
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                                                                                                                MEDLINE-55045426; PubMed=7957098;

MEDLINE-55045426; PubMed=7957098;

Saka Y., Fantas P., Sutani T., McInerny C., Creanor J., Yanagida M.;

"Fission yeast cut5 links nuclear chromatin and M phase regulator in
the replication checkpoint control.";

EMBO J. 13:5319-5329(1994).

-I- FUNCTION: ESSENTIAL COMPONENT FOR DNA REPLICATION AND ALSO THE
CHECKPOINT CONTROL SYSTEM WHICH COUPLES S AND M PHASES. MAY
DIRECTLY OR INDIRECTLY INTERACT WITH CHROMATIN PROTEINS TO FORM
THE COMPLEX REQUIRED FOR THE INITIATION AND/OR PROGRESSION OF DNA
SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 WIPVLYESWVQGED-----LDDGLLVDKHFLPTLFKCRVCLTNIGQPERSRIENYVL 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : : : : : : 126 KHGGTFCPDLTRDVTHLIAGISSGRKYEYALKWKINVVCVEWLMQSIQRNAVLEPQYFQL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WLTEQYDGYLKGRQPPKSPSITLDDGLVYVRRVLVTPCKVYFC----GPE-VNVSNRVL 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DMPAEKIGLGA----YVRLDPNTTEAKSYSENQKISKNKEKSGQSLAALAEEADLEPVIM 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----KFEFLAFSSSQLRDNSVWMFASRP----GLTANDIRAWMGDF 478
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NUCLERA LOCALIZATION SIGNAL (POTENTIAL)
NUCLERA LOCALIZATION SIGNAL (POTENTIAL)
C14EC1EC26868BEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 KRGKKRDRSILWEELNNGKFEF----SSRSEENSVLLDDFTPETVQPLEENELDTEL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQIKNVAKYAARLGQSFGSSRETLSVLRHEIEVIPDVKVHGTSYVFSDGIGKISGDFAHR
Lehmann A.R.; "Duplicated region of sequence similarity to the human XRCC1 DNA repair gene in the Schizosaccharomyces pombe rad4/cut5 gene."; Nucleic Acids Res. 21:5274-5274(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 272;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   409 LLPKASTGSGVRTNIYERI--LSTLRKGFVIGDK-------------
                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: SOME, TO HUMAN XRCCI.
SIMILARITY: CONTAINS 4 BRCT DOMAINS.
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Pfam; PF00533; BRCT; 4.
SMART; SM00292; BRCT; 4.
PROSITE; PS50172; BRCT; 4.
DNA replication; Nuclear protein; Repeat.
DOMAIN
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BRCT 3.
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249
648
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PIR; S22584; S22584.
PIR; A40727; A40727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             648 AA;
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582 YESDNIKLDVLGWSKYQPCYLNRQLITLLSTLGVKDEVLEQKQKEAVDQLDAILHDSLKA 641
                                                                                                       396 YFN-----GLS-----IHLIGERGEELSH-LKKALTILGAVVHEFLGV 432
                                                                                                                                                                                                                                                                                                                      MMGCLDESRILEYGQVFVQFTGAG-----HGEFSDDLHPFNNSRSIN---SNFILKGN 751
                                                                                                                                                                                                                                                                                                                                                                                    -----QHATEWN---VRVVGVAWLWNIIQSGKFIDQVSPWAIDKKENQEIKKFTNQNN 503
LSSTIDFVVIPHYFPVDELPIFSFPTVNEWWIERCLYYKKIFGIDEHALAKPFFRPSLVP 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                         VV-------VAKNPCLH--PGDIRVLKAVNVRALHHM-------VDCVV 784
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Search completed: November 6, 2002, 03:45:17 Job time: 27 secs

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092EEX4 001869 001869 0082190 0082189 00941V6 00941V6 0097266 009707

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SEQUENCE FROM N.A.
STRAIN-RUTGERS;
MEDLINE-99055198; PubMed-9836747;
Schiebel W., Pelissier T., Riedel L., Thalmeir S., Schiebel R.,
Rempe D., Lottspeich F., Sanger H.L., Wassenegger M.;
"Isolation of an RNA-directed RNA polymerase-specific cDNA clone from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGKTIQVFGFPYLLSAEVVKSFLEKYTGYGTVCALEVKQSKGGSRAFAKVQFADNISADK 60
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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Plant Cell 10:2087-2102(1998).
Plant Cell 10:2087-2102(1998).
EMBL, Y10403; CAA71421.1;
InterPro: IPR000504; RNA_rec_mot.
InterPro: IPR000355; RRM_2.
Pfam; PF00076; rrm; 1.
SMART; SM000362; RRM_2! 1.
Nucleotidyltransferase; RNA-directed RNA polymerase; Trassguence 1114 Aa; 126807 MW; B6D30ACD41DB37FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
RNA-directed RNA polymerase (EC 2.7.7.48).
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1114; Conservative 0; Mismatches
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Q9zry7 nicottana t
Q9zrx3 petunia the
Q9zrx3 petunia hyb
Q9zrs5 arabidopsis
Q9zrs5 arabidopsis
Q9zrs6 arabidopsis
Q91kp0 arabidopsis
Q91k2 neurospora
Q8ty4 diaporthe a
Q8ty4 diaporthe a
Q8x1c2 phomopsis s
O14zz7 schizosacch
Q12z8 caenorhabdi
Q9bh5 caenorhabdi
Q9bh5 caenorhabdi
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(without alignments)
5738.412 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                     1 MGKTIQVFGFPYLLSAEVVK.....RPVLNLSSLRAQLSHRLVLK 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                       GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Listing first 45 summaries
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092RX7
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ALIGNMENTS

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DB 10; Length 1114; 0; Indels

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HTLNFGCQISDDKFAVLGS 	PYGQNAQFLLIQLFGAPR PYGQNAQFLLIQLFGAPR	'RRGVRLPNFEESFFHYAE 	KISSLVQHGCIPGPALNVYFFRLVD 	KGRQPPKSPSITLDDGLVYVRRV 	SFVDEEWEKLYSTDLLPKAST 	WMFASRPGLTANDIRAWMGDFSQ 	SGDF	YESDNIKI 	SLKAQEALELMSPGENTN 	EYG	MGCLDESRTLE SDIRVLKAVNV		PPRQVQPMEYPPAPSIQLDHI	KKLAELFSIAVDFPKT	LAELFSIAVDFPKT	KAPQASSIATFTRDVARR: 	EILSGGIMKASKTFDRRKD	ILSGGIMKASE	YHPTYWGCYNQGLKRAHFISE	PTYWGCYNQGLKRAHFIS	14	14	
EMKTDIVQLRAYVDQMDC EMKTDIVQLRAYVDQMDG	SADYKLQLSYENIWQVVLHRI SADYKLQLSYENIWQVVLHRI	PPPSWIGLSSSLCLOF 	SIPYKILE SIPYKILE	CIEHALEKLYXIKECCYDPVRWLTEQYDGYLKGRQPPR: 	/lrnysedidnelry /////////////	RKGFVIGDKKFEFLAFSSSQLRDNSVWMFASRPGLTAND: 	SRETLSVLRHEIEVIPDVKVHGTS 	MKLSLRF MKLSLRF	LEQKQKEAVDQLDAILHD 	FLSMMLQTFRASKLLDLRTRSRIFIP	KIKSKIF	SRSTNSNFILKGNVVVAKNPCLHP	SDLDGDIYFVCWDQDMII 	ADREPDMAMSI	AHVVEADREPE	TSYISERVIGKLFRKVKDKAPQ 	ONKLGNLMDYYGIKTEA	YDNKLGNLMDYYGIKTEA	EARAWFKRRNDIDDMLPKASAWYHVTYH	IDDMLPKASAWYHVT	SSLRAQLSHRLVLK 11	SSLRAQLSHRLVLK 11	
IITLANNRLYFGSSYLKAWI IITLANNRLYFGSSYLKAWI	IQFGIGLKKFFFFLSSGSA 	ENSCYSFFKETPDDQWVRTTD 	TLQTGFTFFVSQKSALVPNVQPPEGI: 	RRRNVACIEHALEKLYYIK 	LVTPCKVYFCGPEVNVSNR\ LVTPCKVYFCGPEVNVSNR\	TNIYERILSTLRKGFVIGD	IKNVAKYAARLGQSFGSSR. 	_ წ – წ	TTLLSTLC	NCGYKPDAEF	SIRPDAEF AGHGEFSD	FTGAGHGEFSDDLHPFNNS	DCVVFPQKGKRPHPNECSG	EVEEYFTNY IVNI	EYFTNYIVN	IPSQLRPKEYPDFMDKPDKTS IPSQLRPKEYPDFMDKPDKTS	EDYIDE	DYIDEAFDYKTE	SVAVRALRKEARAWFKRRN	SVAVRALRKEARAWFKRRN	YDQLIQIKKDKARNRPVLNL:	POLIQIKKDKARNRPVLN	
61	121	181 181	241 1	301 F	361 I 361 I	421 T	481 1	541 8	601 1			721 E	781	41	41	901	961	961 N	1021	1021	81	1081	
Qy Dp	QY	Qy Db	Qy Db	QY	Oy Dp	Qy Db	Qy Dp	Q Q	VQ d	i o	g &	qq	δλ Q	οy	qq	Oy Dp	QY	Dp	δλ	QQ	δλ	Q D	

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[1]
SEQUENCE FROM N.A.
STRAIN-CV. PETIT HAVANA SRI; TISSUE-LEAF;
SCHAIN-CV. PETIT HAVANA SRI; TISSUE-LEAF;
SCHiebel W., Pelissier T., Riedel L., Thalmeir S., Schiebel R.,
Schiebel W., Delissier T., Saenger H.L., Wassenegger M.;
Kempe D., Lottspeich F., Saenger H.L., Wassenegger M.;
Isolation of an RNA-directed RNA polymerase-specific cDNA clone from
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                                                                                                             RDRP.
Nicotiana tabacum (Common tobacco).
Nicotiana tabacum (Common tobacco).
Nicotiana tabacum (Common tobacco).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
Asteridae, euasterids I; Solanales; Solanaceae; Nicotiana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1116;
                                                                                                                                                                                                                                                                                                                                       Tomato.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ011576; CAA09697.1; -.
RNA-directed RNA polymerase.
SEQUENCE 1116 AA; 127553 MW; 8D9B89DA826D31DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                  01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RNA-directed RNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.5%; Score 5070; DB 10;
86.0%; Pred. No. 0;
Live 67; Mismatches 87;
PRT; 1116 AA
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    PRELIMINARY;
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                                                                                                   868
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Petunia hybrida (Petunia).
Petunia hybrida (Petunia).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Solanales; Solanaceae; Petunia.
                                                                                                            AMINCGYKPDAEPFLSMMLQTFRASKLLDLRTRSRIFIPNGRIMMGCLDESRTLEYGQVF
         VQFTGAGHGEFSDDLHPFNNSRSTNSNFILKGNVVVAKNPCLHPGDIRVLKAVNVRALHH
                                         WVDCVVFPQKGKRPHPNECSGSDLDGDIYFVCWDQDMIPPRQVQPMEYPPAPSIQLDHDV
                                                                         TIEEVEEYFTNYIVNDSLGIIANAHVVFADREPDMAMSDPCKKLAELFSIAVDFPKTGVP
                                                                                                                                    AEIPSQLRPKEYPDFMDKPDKTSYISERVIGKLFRKVKDKAPQASSIATFTRDVARRSYD
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                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                 CVYDQLIQIKKDKARNRPVLNLSSLRAQLSHRLVL 1113
                                                                                                                                                                                                                                                                                                                                           (Fragment).
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87.0%;
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775 AA;
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675; Conserv
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TISSUE=LEAF;
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EDYIDEAFDYKTEYDNKLGNLMDYYGIKTEAEILSGGIMKASKTFDRRKDAEAISVAVRA 1026
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chāo Q., Siinn P., Dunn P., Buehler E., Kahn S., Kim C., Walker M., Williams S., Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen N.F., Huizar L., Kremenetskala I., Lenz C., Li J., Liu S., Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskala V., Yu G., Davis R.W., Federspiel N.A., Theologis A., Ecker J.R., "Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRKEARAWFKRRNDIDDMLPKASAWYHVTYHPTYWGCYNQGLKRAHFISFPWCVYD 1082
                                                                                                              ITLLSTLGVKDEVLEQKQKEAVDQLDAILHDSLKAQEALELMSPGENTNILKAMLNCGYK
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                          YAARLGOSFGSSRETLSVLRHEIEVIPDVKVHGTSYVFSDGIGKISGDFAHRVASKCGLQ
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
F10B6.19.
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SEQUENCE FROM N.A.
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GLKRAHFISFPWCVYDQLIQIKKDKARNR 1095
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STRAIN-CV. COLUMBIA;
Strong C., Graves T., Duckels G.;
                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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Submitted (SEP-1998) to
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Submitted (MAR-2000)
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STRAIN-CV. COLUMBIA;
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                                                   SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
Theologis A., Ecker J.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AC006917; AAF79241.1; -.
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                                   to the EMBL/GenBank/DDBJ databases,
                                                                                                                                                                                                1 50.2%; Score 3532; DB 10; Similarity 62.4%; Pred. No. 8.6e-246; Conservative 160; Mismatches 225;
                         Ecker J.R.;
Submitted (MAY-1999)
            SEQUENCE FROM N.A.
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Matches 692;
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
02-MAR-2002 (TrEMBLrel. 20, Last annotation Arabidopsis thaliam (Monse-ear cress).
03-MAR-2004: Viridiphantae; Streptophyta; Embryophyta; Tracheophyta;
03-MAR-2004: Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
04-MAR-2004: Reassicales; Brassicaceae; Arabidopsis.
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826
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                                                                                                                                                                                           SIAVDFPKTGVPAEIPSQLRPKEYPDFMDKPDKTSYISERVIGKLFRKVKDKAPQASSIA
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                                                  PPAPSIQLDHDVTIEBVEZYFTNYIVNDSLGIIANAHVVFADREPDMAMSDPCKKLAELF
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the EMBL/GenBank/DDBJ databases.
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Mayer K.F.X., Schueller C.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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Waterston R.;
Waterston (JUL-1998) to the EMBL/GenBank/DDBJ databases
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Submitted (SEP-1998) to the EMBL/GenBank/DDBJ
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                                                           Query Match 34.0%; Score 1995.5; DB 10; Length 1133; Best Local Similarity 40.1%; Pred. No. 7e-135; Matches 459; Conservative 214; Mismatches 389; Indels 83;
EMBL; AE080120; AAC35535.1; -.
EMBL; AL049876; CAB43048.1; -.
EMBL; AL161531; CAB81214.1; -.
Nucleotidyltransferase; RNA-directed RNA polymerase; TransEquence 1133 Aa, 129323 MW; 32872C4E429B20B9 CRC64;
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Kempe D., Lottspeich F., Saenger H.L., Wassenegger M.;
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EMBL; AJ011977; CAA09884.1; -.
RNA-directed RNA polymerase.
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SEQUENCE 513 AA; 57802 WW; 924FDA2B70EDAE0E CRC64;
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MEDLIN-20306668; PubMed=10850495;

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R EMBL; AL329646, CAP71285.1;

R EMBL; AR239718; AAF73959.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M., Mewes H.W., Lencke K., Mayer K.F.X., Quetier F., Salanoubat Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                            FTRDVARRSYDADMEVDGFEDYIDEAFDYKTEYDNKLGNLMDYYGIKT
                                                                                                                                                                                                                                                               Putative RNA-directed RNA polymerase.
T1G12.20 OR T9C5.95.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryots Vildiplinae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core everosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                        (TrEMBLrel. 13, Last sequence update) (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA-directed RNA polymerase.
SEQUENCE 1196 AA; 136927 MW; 812DEB9CEDC82C8F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.6%; Score 1621; DB 10;
llarity 34.6%; Pred. No. 8.2e-108;
Conservative 191; Mismatches 414;
                                                                                                                                                                                                    PRT; 1196
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01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRKVF-----EETIPDHENLSEEEKNILYEKKASAWYHVTYHPE-WVKKSLELQDPDES
194 KLELLVRDIQTV---RQYKTLHGFVLILQLASSPRVWYRTADD--DIYDTVPGDLLDDDD
                                                                                                                        SQKSALVPN---------VQPPEGISIPYKILFKISSLVQHGCIPGPALNV
                                                                                                                                                                                                       293 YFFRLV--DPRRRNVACIEHALEKLYYIKECCYD-PVRWLTEQYDGYLK------GRQ
                                                                                                                                                                                                                                                                                      PPKSPSITLDDGLVYVRRVLVTPCKVYFCGPEVNVSNRVLRNYSEDIDNFLRVSFVDEEW
                                                                                                                                                                                                                                                                                                                                                                       EKLYSTDL-----LPKASTGSGV--RTNIYERILSTLRKGFVIGDKKFEFLAFSSSQLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              516 DRSAWFFAEDGKTRVSDIKTWMGKFKD-KNVAKCAARMGLCFSSTYATVDVMPHEVDTEV
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                                         QWVRTTDFPPSWIGLSSSLCLQFRRGVRLPNFEESFFHYAERENNITLQTGFTFF-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         453
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                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).

Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEPHAFVHFAVFESAGRAMDAAGOCNLILDGQPLKVSLGPKNPYSLNORRRTTVPYKLAG 134
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                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-20306669; PubMed-10850496; MEDLINE-20306669; PubMed-10850496; Dalmay T., Hamilton A., Rudd S., Angell S., Baulcombe D.C.; and RNA-dependent RNA polymerase gene in Arabidopsis is required for posttranscriptional gene silencing mediated by a transgene but not t a virus."; 23-253(2000)
Cell 101:543-553(2000)
Cell 101:543-553(2000)
EMBL, AF268093; AAF74208.1; -. RNA-directed RNA polymerase.

RNA-directed RNA polymerase.

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                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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27.5%; Score 1610; DB 10;
Best Local Similarity 34.6%; Pred. No. 5.1e-107;
Matches 431; Conservative 188; Mismatches 417;
                                              1196 AA
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                                                                                                                                                                                         RNA-dependent RNA polymerase.
                                                    PRELIMINARY;
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Q9LKP0;
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                                                                                                                                                                                                                                             LGIIANAHVVFADREPDMAMSDPCKKLAELFSIAVDFPKTGVPAEIPSQLRPKEYPDFMD 915
                                                                                                                                                                                                                                                                                              KPDKTSYISERVIGKLFRKVK----DKAPQASSIATFTRDVARRSYDADMEVDGFEDYIDE 972
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                                                                                                                                                                                                                                                                                                                                                               1031 ARAWEKRRNDIDDMLP-------KASAWYHVTYHPTYWGCYNQGLK----
                                                                                                                                                                                                                                                                                                                                                                                                               RTRSRIFIPNGRTMMGCLDESRTLEYGQVFVQFT------GAGHGEFSDDLHPFN
                                                                                                              NSRSTNSNFILKGNVVVAKNPCLHPGDIRVLKAVNVRALHHMVDCVVFPQKGKRPHPNEC
-- MKLSLRKSMSKYESDNIKLDVLGWSKYQPCYLNRQLITLLSTLGVKDEVLEQKQKEAV
                                             DQLDAILHDSLKAQEALELMSPGENTNILKAMLNCGYKPDAEPFLSMMLQTFRASKLLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 1638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                1070 -RAHFISFPWCVYDQLIQIK-----KDKARNRPVLNLSSLRAQ 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Shiu P.K.T., Raju N.B., Metzenberg R.L.;
Shiu P.K.T., Raju N.B., Metzenberg R.L.;
"Meiotic Silenciling of Unpaired DNA.";
"Metotic Silenciling of Unpaired DNA.";
Submitted (SFR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY029284; AAK31733.1;
"InterPro. IPR000504; RNA_rec_mot.
Pfam; PF00075; rrm;
SEQUENCE 1638 AA; 184233 MW; 7BC58EA66373D9BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Suppressor of ascus dominance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.2%; Score 1068.5; D. ilarity 28.2%; Pred. No. 1e-67; Conservative 184; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Simi
Matches 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
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RESULT 10

QY Dp	141	YKLQLSYBNIWQVVLHRPYGQNAQFLLIQLFGAPRIYKRLENSCYSFFKEPPDDQ	195 332
VQ 4	196	WVRITDEPERMICLSSSLCLQFREGVRLFNFEESFFHYAERENNITLQTGFTFFVSOK	
δ	254	dōvng	262
a	375	 STRVWDQVQQYLLDWNLRTKLTVFPEPLPNQKFKVWDFLDDRYGHDIQQVSSRSWSNDFS	434
δλ	263	PEGISIPYKILEKISSLVQHGCIPGPALNVYFFRLVDPRRRNVACIEHALEKLY	316
СС	435	FDVRYQLEVCISQGIINEHNI	472
ζ ς	317	YIKECCSPEVRWLIEGYDGYLKGRQPPKSPSITLDDGLV H	ro c
3 8	2 4	VITED BY THE CONTROL CANDERFORM THE PROPERTY OF THE PROPERTY O	750
g 8	533	INTERPRETATION OF THE STATE OF	413 590
ōλ	414	STGSGVRINIXERILSTLRKGFVIGDKKFEFLAFSSSQLRDNSVWMFASRPGLTANDIRA	473
Op	591	:	641
δō i	474	WMGDFSQIKNVAKYAARLGQSFGSSRETLSVLRHEIEVIPDVKVHGTSYVFSDGIGKISG	533
g	64.2	WMGRFSHIKVIAKYAARLGQCFSTTRLVPGIPAPRIVTIPDVEKDGFCFTDGVGKISP	669
yo 4	534	DFAHRVASKGGLQYTPSAFQIRYGGYKGVVGVDPD-SSMKLSLRKSMSKYESDNIKLDVL	6
a :	0 0	DEATH VARIOWSIDFFFSAIGE KMGGCKGVLVIWFDVKGMEVHIRKSQEKFVAEFNGLEVV	n
25 25	760	GWENTER-CITEMENTERSTERVENDENTERVENDENTERDENTERDENTERSFG :: : : : : : : :	651 819
οy	652	ENTNILKAMLNCGYKPDAEPFLSMMLQTFRASKLLDLRTRSRIFIPNGRTMMGCLDESRT	711
qq	820		879
Οy	712	LEYGQVFVQFTGAGHGEFSDDLHPFNNSRSTNSNF-ILKGNVVVAKNPCL	760
g	880	LKGHMKVIEDWKDVSSEKLPQIFLQIPDDVNGGYRVITGTCVVGRNPSL	928
δλ	761	HPGDIRVLKAVNVRALHHMVDCVVFPQKGKRPHPNECSGSDLDGDIYFVCWDQDMIP-PR	819
qq	929	HPGDIRVVEAVDVPALRHLRDVVVFPLTGDRDVPSMCSGGDLDGDDFFVIWDPLLIPPKER	986
δλ	820	OVQPMEYPPAPSIQLDHDVTIEEVEEVFTNYIVNDSLGIIANAHVVFADREPDMAMSDPC	879
q	686	SHPPMISEPIAGKELATEPTVNNLITFFVLYMKYNNLPLIAHAHLATADAEVEGVKSPKC	1048
δλ	880	KKLAELFSIAVDFPKTGVPAEIPSQLRPKEYPDFMDKPDKTSYISERVIGKLFRKVKDKA	939
QΩ	1049	LELASLESMANDYVKTGVAABFPRRLDPKTWPHFMEK-NRHTYHSVTALGKLYDMYKRET	1107
ζ	940	PQASSIATFTRDVARRSYDADMEVDGFEDYIDBAFDYKTEYDNKLGNLMDY	066
g	1108	FDMKENYQLPFDNRILKHTKCRALRDGTLAKARRIKSQYDTAMRRVMCQ	1156
δ	991	YGIKTEAEILSGGIMKASKTFDRRKDAEAISVAVRALRKEARAWFKRRNDIDDMLPKASA	1050
QQ	1157	Ž2:	1215
δý	1051	WYHVIYHPIWGCYNQGLKRAHFISFPWCVDDLIQIKK 108	61
Q _O	1216	MYRVTYEEVRIALFEAKQPHVRPDGRLGTRKITPKTMPLVSFPWLFWDKLGELAR 127	0

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29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 352 YGRLPVSHDDEQTLWQEW--DLWARQTNISSEMHKLRDLPAKLEKQTWKSIEFGRWTT-- 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225 NFEESFFHYAERENNITLOTGFFFFVSQKSALVPNVQPPE----GISIPYKIL----- 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        461 LELLGSTQSYHLDFPVRYQLEVCISHGLLSEYGVNAQFLEKLISFETDRARMMLEGVAEA 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     312 LEKLYYIKECCYDPVRWLTEQYDGYLKGRQPPKSPSITLDDGLVYVRRVLVTPCKVYFCG 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372 PEVNYSNRVLRNYSEDIDNFLRVSFVDE-EWEKLYSTDLLPKASTGSGVRTNIYERILST 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      620 MQNGVIIGDRHYKFLAFSNSQFRENGAFFFCETDHVTCASIRNWGDFRHIRSVGKFAAR 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            491 LGQSFGSSRETLSVLRHEIEVIPDVKVHGTSYV--FSDGIGKISGDFAHRVASKCGLQYT 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  728 EFSDDLHPFNN------SRSTNSNFILKGNVVVAKNPCLHPGDIRVLKA 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 EVSIQFGIGLKKFFFFLSSGSADYKLQLSYENIWQVVLHRPYGQNAQFILLIQLF-GAPRI 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 QFELQFTVNLGRY-----GCKAFKSQIDFSHPTKIIWGR--RENGAWALAMLLPSPPKL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 YKRL---ENSCYSFFKETPDDQWVRTTDFP------PSWIGLSSSLCLQFRRGVRLP 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRKGFVIGDKKFEFLAFSSSQLRDNSVWMFASRPGLTANDIRAWMGDFSQIKNVAKYAAR 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      680 MGQCFTTTROVNGISIPKIRQIGDIQRRSGDNIWNFTDGVGKISVFFARMIASERDLPET 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         549 PSAFQIRYGGYKGVVGVDPD-SSMKLSLRKSMSKYESDNIKLDVLGWSKYQPCYLNRQLI 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      608 TLLSTLGVKDEVLEQKQKEAVDQLDAILHDSLKAQEALELMSPGENTNILKAMLNCGYKP 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               668 DAEPFLSMMLQTFRASKLLDLRTRSRIFIPNGRTMMGCLDESRTLEYGQVFVQFTGAGHG 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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17.6%; Score 1031; DB 3; Length 1484;
Best Local Similarity 27.9%; Pred. No. 4.5e-65;
Matches 300; Conservative 196; Mismatches 410; Indels 168;
                                                                                                                                                                                                                                                                                                                     Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Diaporthales, Valsaceae, Diaporthe.
NCBI_TaxID=186170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Presists 0., Wingfield M.J.;
Putative fungal RNA-dependent RNA polymerase.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; 74468822; AAI/78034.1; -.
RNA-directed RNA polymerase.
SEQUENCE 1484 AA; 167213 MW; 57E0AFB8D12547BD CRC64;
                                                                          01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative RNA-dependent RNA polymerase RDP-1.
        PRT; 1484 AA
PRELIMINARY;
                                                                                                                                                                                                                                                                                  Diaporthe perjuncta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CMW3407;
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                                           ACCOORDING THE REPORT OF THE T
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Db 909	9 ODTEG-KGFNNIESLPQIFLQVPIEGSDGKSTINYEVITGICVVGRNPALHPGDVRVVEA 967	AC	367 VYFCGPEV
Qy 771		; a	
Db 968	8 VDVPELRHLKNVVVFPKTGDRDVPSMCSGGDMDGDDYFVYWDERLIPSEWDHPPLD 1023	: ^O	
Oy 829	9APSIQLDHDVTIEEVEEYFTNYIVNDSLGIIANAHVVFADREPDMAMSDPCKKL 882 : : :	7 dg	
·	AELFSIAVDFPKTGVPABIPSGLRPKEYPDFMDKPDKTSYISBRVIGKLFRKVKDKAPQA	Qy da	486 KYAARLGC : : 676 KFAARMGC
Db 1084	4 AKLHSKAVDYIKSGKPAVMKRHLQPRNWPHWMERDKKSSYHSRGALGQIYDRIKIEEFHA 1143	ò	544 GLQYTPSP
Qy 943	3 SSIATE-TRDVARRSYDADMEVDGFEDYIDEAFDYKTEYDNKLGNLMDYYGIK-TEAEIL 1000 **SENATE-TRDVARRSYDADMEVDGFEDYIDEAFDYKTEYDNKLGNLMDYYGIK-TEAEIL 1000 **SENATEPOTATIONON	ପୁ	
	RIEMSFUIKLLSKIUULE EUILMARASEIRMALUIMAKKIUGENKKII OGGEGERFYIEFELM 1103 SGGIMKASKTFDRRKDAEAISVAVRALRKEARAWFKRRNDIDDMLPK 104	ò t	603 NRQLITLE
Db 1196	: : : : : :	a è	663 CGYKPDAF
Qy 1048	8ASAWXHVTXHPTYWGCYNQGLKRAHFISFPWCVYDQLIQI 1087	୍ ପ	
Db 1256	6 DRFVAAMYTVTHNEVRAAVRERSKPRPDDEGDLEEIQMPLISFPWLYHRELARV 1309	QY	713EN
RESULT 11	1	qa —	916 RDNNIESI
OSPOULE ID OSE	b OGGULG PRELIMINARY; PRT; 1483 AA.	Qy	767 VLKAVNVI
	(TrEMBLrel. 19,	අ	965 VVEAVDAI
DT 01.	01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 1-UN-2002 (TrEMBLrel. 21, Last annotation update) 5-1-4-1-1-4-0-0-0-1-1-1-1-1-1-1-1-1-1-1-1	03	826 -YPP
	oative and dependent and polymetase.	a a	1019 УНРРГОНІ
	Diaporthe ambigua. Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;	δδ	877 DPCKKLAI
	porthales; Valsaceae; Diaporthe. N_TaxID=73123;	qu	1079 PKCIELA
	11) STATE OF THE CONTRACTOR OF	QY	937 DKAPQAS
	STRAIN=CRWSZ8/) Proisig O., Wingfield M.J.;	q _O	1139 ІЕЕГНАА
	itative ingal KNA-dependent kNA polymerase; nmitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.	δ	996 EAEILSG
DR EM	EMBL; AY049072; AAX95829.1; RNA-directed RNA polymerase.	ව	1192 EFEIWST
	16658U MW; 4246FAGIDEICSES	οy	1040 DIDDMLP
Query Best	uery Match lest Local Similarity 26.8%; Pred. No. 1.8e-62; Lethon 703. Concentation 107. Mismatched A76: Todale 176. Gans 27:	q _O	1252 NLEKLDR
Σ	295; COMBELVALLYE 197; MISMIGLOMES 420; INDOLES 170; ORFS ORESPONDED TO COMPUTE 1700VI, HEDVIOLDED 170; 170	QY	1089 KDKARN-
. E	GREDIGEKVNVGRYGLKVFKMQVDFNHPTKIIWGTRKNGAWGLAMLL	đ	1312 LGRGGDV
0y 1	171 FGAPRIYKBLENSCYSFFKETPDDOWVRTTDFPPSWIGLSSSLCLOFR 218	RESULT	RESULT 12 OBX102
Dp 3	348 PSPPKLYGRLPVSHDDDQSLWQEWDLWARQTHISGELHKIKGIPARLEKPAGQSVDFG 405	A H	08X1C2 08X1C2;
Qy 2		TO	01-MAR-2002 01-MAR-2002
Db 4	406 RWTTYYFDLDSFLSEWGSVCTYLADYNVKIVQVDRFELVNPDSTNAWKLLD 456	DE	01-MAR-2002 Putative RNA
	268DPYKILEKISSLVQHGCIPGPALNVYFF-RLVDPRRRNVA 306	GN OS	RDP-1. Phomopsis sp Eukarvota: F
	STDLTLELLGSTDAYHLDFPVRYQLEVCISHGLLDEISIGAQF LGKLISF DIDRAKMLLE		Diaporthales
Oy 3	307 CIEHALEKLYYIKECCYDPVRWLTEQYDGYLKGRQPPKSPSITLDDGLVYVRRYLVTPCK 366 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	RR	SEQUENCE FRO

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GGIMKASKTFDRRKDAEAISVAVRALRKEARA---------WFKRRN 1039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----APSIQLDHDVTIEEVEEYFTNYIVNDSLGIIANAHVVFADREPDMAMS 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSIATETRDVARRSYDADMEVDGFEDYIDEAFDYKTEYDNKLGNLMDYYGIK-T 995
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                                                                                              APQIRYGGYKGVVGVDPD-SSMKLSLRKSMSKYESDNIKLDVLGWSKYQPCYL 602
                                                                                                                                                                                                                                            LSTLGVKDEVLEQKQKEAVDQLDAILHDSLKAQEALELMSPGENTNILKAMLN 662
                                                                                                                                                                                                                                                                                                                   SYGQVFVQFTGAGHGEFSDDLHPFNNSRSTNSNFILKGNVVVAKNPCLHPGDIR 766
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                                                                                                                                              QSFGSSRETLSVLRHEIEVIPDVKVHGTSYV--FSDGIGKISGDFAHRVASKC
                       KGFVIGDKKFEFLAFSSSQLRDNSVWMFASRPGLTANDIRAWMGDFSQIKNVA
                                                                                                                                                                                                                                                                                                                                                             ABPFLSMMLQTFRASKLLDLRTRSRIFIPNGRTMMGCLDESRTL------
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ingl, Ascomycota; Pezizomycotina; Sordariomycetes;
is; Valsaceae; mitosporic Valsaceae; Phomopsis.
179291;
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(TIEMBLIE). 20, Last sequence update)
(TIEMBLIE). 20, Last annotation update)
(A-dependent RNA polymerase (Fragment).
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VRPLQN 1323
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OM N.A.

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                                                                                                                                                                                                                                                                                               FEFLAFSSSQLRDNSVWMFASRPGLTANDIRAWMGDFSQIKNVAKYAARLGQSFGSSRET
                                                                                                                      104;
                                                                                               Length 1122;
                                                                                            16.8%; Score 987; DB 3; Length 112
llarity 30.3%; Pred. No. 4.2e-62;
Conservative 160; Mismatches 349; Indels
                                                                     1122 AA; 126794 MW; 27D672BA58E0CCBE CRC64;
          TYWGCYNQGLKRAH------FISFPWCVYDQLIQI 1087
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Matches 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-972;
Badcock K., Churcher C.M., Barrell B.G., Rajandream M.A., Wc Badcock K., Churcher C.M., Barrell B.G., Rajandream M.A., Wc Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: SOME, TO C.ELEGANS F10B5.7, F26A3.3 AND P.CHRYSOSPORIUM HYPOTHETICAL 109.5 KDA PROTEIN (Q01869).
EMBL: Z99E33; CABAll093.1;
-Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 16.2%; Score 948; DB 3; Length 12 Local Similarity 31.3%; Pred. No. 3.2e-59; les 243; Conservative 155; Mismatches 316; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .1 protein.
1215 AA; 139476 MW; 389B95C8217CB05C CRC64;
                                                                                             01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 06, Last annotation update)
Hypothetical 139.5 kDa protein C6F12.09 in chromosome:
SPAC6F12.09.
                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases
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1269 YYSTRLNGQLHRKAR-KVEBVLEEFETRGSVFEREYDKLICPEDVDVFFGNEIKLVQTLT 1327
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                  QLDAILHDSLKAQEALELMSPGENTNIL----KAMLNCGYKPDAEPFLSMMLQTFRASKL
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01-JUN-2001 (TrEMBLrel. 17, C.
01-JUN-2001 (TrEMBLrel. 17, L.
01-JUN-2001 (TrEMBLrel. 17, L.
M01G12.12 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SFFHYAERENNITLQTGFTFFVSQKSALVPNVQPPEGISIPYKILFKISSLV 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281 QHGCIP------GPALNV---YFFRLVDPRRRNVACIEHALEKLYYIKE----- 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 25.1%; Pred. No. 2e-55;
Matches 317; Conservative 196; Mismatches 449; Indels 302;
                                                                                                            "Genome sequence of the nematode C.elegans: A platform for investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                              Lennard N.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; AL132848; CAC35915.1;
EMBL; Z81571; CAC35915.1; JOINED.
EMBL; Z81571; CAC35914.1;
EMBL; AL132848; CAC35914.1;
EMBL; AL13284
                                                         MEDLINE=99069613; PubMed=9851916;
[2]
SEQUENCE FROM N.A.
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1035 DDATGEMIPPE-RAERVPDYHVGSDHMPKYVSPRLCGKLFREFQG-IDNAMKISEEKSEQ 1092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     953 ARRSYDADMEVDGFEDYIDEAFDYKTEYDNKLGNLMDYYGIKTEAEILSGGIMK-ASKTF 1011
                                                                                                                                                                                                                849 NYIVNDSLGIIANAHVVFADREPDMAMSDPCKKLAELFSIAVDFPKTGVPAE----- 900
675 MMLQT---FRASKLLDLRTRSRIFIPN--GRTMMGCLDESRTLEYGQVFVQFTGAGHGEF 729
                                                                                                                          790 KRPHPNECSGSDLDGDIYFVCWDQDMIPPRQVQPMEYPPAPSIQLDHDVTIEE-VEEYFT
                 SLVKASIKFAITKQL---FKEQIQIPSELGRSMLGVVDETGILQYGQVFVQYT-KNHRNI
                                                                                    1039 NDIDDMLPKASAWYHVTYHPTYWGCYN--QGLKRAHFISFPWCVYDQLIQIKKDKARNRP
                                                             SDDLHPFNNSRSTNSNFILKGNVVVAKNPCLHPGDIRVLKAVNVRALHHMVDCVVFPQKG
                                                                                                                                                                                                                                                         -----IPSQLRPKEYPDF-MDKPDKTSYISERVIGKLFRKVKDKAPQASSIATFTRDV
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92.517 Million cell updates/sec
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1114
1 MGKTIQVFGFPYLLSAEVVK......RPVLNLSSLRAQLSHRLVLK 1114
                                                                                                            6, 2002, 03:37:53; Search time 167 Seconds
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                      90412 seqs, 13869272 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Listing first 50 summaries
                                                                          using sw model
                                                                                                                                                                                                                                                                                  Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
                                                                        protein search,
                                                                                                              November
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                                                                                                                                                                                    Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                          Word size :
                                                                        OM protein
                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                              Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1: //ggn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
2: //ggn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: //ggn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
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14: //ggn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*

Published_Applications_AA:*

Database :

Result Ouery Duery Duery Duery Description Description Duery
Sequence 11987, A	148	, App	19,	e 137	e 138	ednence 4	Sequence 10841, A		'n	e 195,	e 29, A	7, Appl	e 12, A	e 19, A	equence 129,	90, A	equence 101,	equence 43391	e 14,	ednence 3	equence 13,	45443,	410	47440,	equence 810, Ap	eguence 45869,	284,	equence 36412,	e 4051	œ œ	
US-09-815-242-11	US-09-801-36	us-09-870-3	890-086	US-09-925-301-13	US-09-815-24	US-09-815-242-497	US-09-815-242-10	0-50	-910-386A-	US-09-771-16	-Sn	-910-386A-	US-09-872-34	US-09-124-280A	US-09-765-527-12	US-09-881-490-9	8-60-SD	US-09-864-761-	US-09-860-793-1	US-09-864-761-3	US-09-860-19	US-09-864-76	US-09-864-761-4108	US-09-864-761-47	US-09-764-869-81	US-09-864-761-458	US-09-864-761-46	8-60-SD	us-	us-	
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ALIGNMENTS

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US-09-782-874-2

Sequence 2, Application US/09782874

Sequence 2, Application US/09782874

Sequence 2, USZ0010023067a1

GENERAL INFORMATION:

Riedel, Leonhard

Schiebel, Winfried

ADDRESSE:

CORRESPONDENCE ADDRESS:

SCHWEEF 1251 Avenue of the Americas

CITY: New York

COUNTRY: USA

CONFUTE: 100-

CONFUTE: 100-

CONFUTE: BM PC compatible

COMPUTER: DATE: Now NATH:

SCHING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURSSIFICATION NUMBER: US/09/782,874

FILING DATE: 05-MAR-1997

ATTORNEY-AGENT INFORMATION:

NAME: Haley, James F.

RECISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: 27,794
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Wed

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ACTIVITY OF
EEVEEYFTNYIVNDSLGIIANAHVVFADREPDMAMSDPCKKLAELFSIAVDFPKTGVPAE 900
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                                                                                                   MEVDGFEDY IDEAFDYKTEYDNKLGNLMDYYGIKTEAEILSGGIMKASKTFDRRKDAEAI
                                                                                                                                                                                       1021 SVAVRALRKEARAWFKRRNDIDDMLPRASAWYHVTYHPTYWGCYNQGLKRAHFISFPWCV
                                                                 901 IPSQLRPKEYPDFWDKPDKTSYISERVIGKLFRKVKDKAPQASSIATFTRDVARRSYDAD
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                                  IPSQLRPKEYPDFMDKPDKTSYISERVIGKLFRKVKDKAPQASSIATFTRDVARRSYDAD
                                                                                                                                961 MEVDGFEDYIDEAFDYKTEYDNKLGNLMDYYGIKTEAEILSGGIMKASKTFDRRKDAEAI
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Sanger, Heinz
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
POLYPEPTIDES HAVING THE ENZYMATIC
RNA-DIRECTED RNA POLYMERASE (RGRP)
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llarity 100.0%; Pred. No. 2.4e-206;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                      YDQLIQIKKDKARNRPVLNLSSLRAQLSHRLVLK 1114
                                                                                                                                                                                                                                                        1081 YDQLIQIKKDKARNRPVLNLSSLRAQLSHRLVLK 1114
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FILING DATE: 05-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,874 FILING DATE: 08-Feb-2001
CLASSIFICATION: <a href="https://doi.org/10.1007/10.1007/">CLASSIFICATION</a>: <a href="https://doi.org/">CURNOWN></a>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MPG-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
                                                                                                                                                                                                                                                                                                           RESULT 2
US-09-782-874-3
; Sequence 3, Application US/09782874
; Patent No. US20010023067A1
; GENERAL INFORMATION:
; APPLICANT: Wassenegger, Michael
; Riedel, Leonhard
; Schliebel, Winfried
Schliebel, Winfried
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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RADRESSEE: F1SH & NEAVE
STREET: 1251 Avenue of t
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TYPE: amino acid
STRANDEDNESS: <Unknown>
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COUNTRY: US:
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Best Local Similarity
Matches 218; Conserv
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                                                                                                                                  ID NO:
              INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1114 amino acids
212-596-9000
                                                                        TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-782-874-2
TELEPHONE:
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COUNTRY:
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Best Local Simi
Matches 14;
                    RESULT 4
US-09-782-874-10
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US-09-782-874-11
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                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
POLYPEPTIDES HAVING THE ENZYMATIC ACTIVITY OF AN
RNA-DIRECTED RNA POLYMERASE (RARP)
                                                                         LHPGDIRVLKAVNVRALHHMVDCVVFPQKGKRPHPNECSGSDLDGDIYFVCWDQDMIPPR 819
                                                                                                                      QVQPMEYPPAPSIQLDHDVTIEEVEEYFTNYIVNDSLGIIANAHVVFADREPDMAMSDPC 879
Gaps
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COMPUTER READABLE FORM:
MEDIUW TEPE: Ploppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/782,874
FILING DATE: 08-Eb-2001
CLASSIFICATION CURNOWN>
PRIOR APPLICATION OFFA:
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FILING DATE: 05-MAR-1997

ATTONNEY, AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794

REGISTRATION NUMBER: 27,794

REGISTRATION INFORMATION:
TELEPHONE: 212-596-9000

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/09782874
Patent No. US20010023067A1
GENERAL INFORMATION:
APPLICANT: Wassenegger, Michael
Riedel, Leonhard
Schiebel, Winfried
Sanger, Heinz
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STRANDEDNESS: <Unknown>
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Best Local Similarity 100.
Matches 17; Conservative
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US-09-782-874-12
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Schiebel, Winfried
Sanger, Heinz
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
POLYPEPTIDES HAVING THE ENZYMATIC ACTIVITY OF AN
RNA-DIRECTED RNA POLYMERASE (RGRP)
                                                                                                                                                                           POLYPEPTIDES HAVING THE ENZYMATIC ACTIVITY OF AN RNA-DIRECTED RNA POLYMERASE (RGRP)
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Similarity 100.0%; Pred. No. 5.7e-07;
14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/811,583
FILING DATE: 05-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIble
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,874
FILING DATE: 08-Feb-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-782-874-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: MPG-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFRX: 212-596-9090
INFORMATION FOR SEQ ID NO: 10:
                                                              APPLICANT: Wassenegger, Michael
Riedel, Leonhard
Schiebel, Whifried
Sanger, Heinz
TITLE OF INVENTION: NUCLEIC ACID D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Haley, James F. REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wassenegger, Michael
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Sequence 10, Application US/09782874 Patent No. US20010023067A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                   CITY: New York
STATE: New York
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us-09-782-874-2.oli.rapb

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NAME/KEY: SITE LOCATION: (252)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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COATION: (265)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-846-220
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MAME/KEY: SITE
LOCATION: (158)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Patent No. US20020102638A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT212

CURRENT APPLICATION NUMBER: US/09/764,846

CURRENT APPLICATION OF EMPLOYER CONSULT PALM OF file wrapper

NUMBER OF SEQ ID NOS: 348

SEQ ID NO 220

LENGTH: 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 0.9%; Score 10; DB 10; Length 13
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 10; Conservative 0; Mismatches 0; Indels
                          APPLICATION DAMER: US 08/811,583
FILING DATE: 05-MAR-1997
ATTORNEY, AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
RELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9090
INFORMATION FOR SEQ 1D NO: 13:
SEQUENCE CHRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: Linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-782-874-13
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US-09-764-846-140
Sequence 140, Application US/09764846
Patent No. US20020102638A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 13 amino acids
          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 0.7
Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             784 VFPQKGKRPH 793
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US-09-764-846-220
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                                    CITY.
STATE: New .
COUNTRY: USA
ZUDE: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBD PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
STILING DATE: 08-Feb-2001
CLASSIPTCATION NUMBER: US/09/78,874
FILING DATE: 08-Feb-2001
STILING DATE: 08-Feb-2001
APPLICATION NUMBER: US 08/811,583
FILING DATE: 05-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: MEG-1
TATION NUMBER: MEG-1
TATION INFORMATION:
TA
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Riedel, Leonhard
Schiebel, Winfried
Sanger, Heinz
TILE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
COMPUTER: 10020
COMPUTER: TOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPATIBLE
COMPUTER: DATE: OP-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,874
FILING DATE: 08-Feb-2001
CLASSIFICATION: <un continuous.
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ADDRESEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-782-874-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/09782874 Patent No. US20010023067A1 GENERAL INFORMATION:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of t
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 14 amino acids
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Matches 14; Conservative
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US-09-782-874-13
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IITLE OF INVENTION: HOMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL IITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.69
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 0.76
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.67
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.67
US-09-864-761-45788
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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Pred. No. 5.3;
0; Mismatches
                                                                                                                      TILE REFERENCE: Acomica X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR FILING DATE: 2001-05-24

PRIOR PELLING DATE: 2000-02-04

PRIOR PELLING DATE: 2000-03-04

PRIOR PLING DATE: 2000-03-06

PRIOR PELLING DATE: 2000-03-06

PRIOR PELLING DATE: 2000-03-06

PRIOR PELLING DATE: 2000-03-07

PRIOR PELLING DATE: 2001-03-07

PRIOR PELLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR PELLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR PELLING DATE: 2001-01-30

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; Scor.
100.0%; Pre
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                                      Wensheng
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 7; Conserv
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12 KLSLRKS 18
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US-09-864-761-46295
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272-147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
ENGINE DATE: 1999-10-20
SOFTWARE: PATENTIN VERSION 3.0
ENGINE DATE: 1000-1140
ENGINE DATE: 100
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT212
CURRENT APPLICATION NUMBER: US/09/764,846
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 348
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.7%; Score 8; DB 10; Length 506;
100.0%; Pred. No. 9.9;
iive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 9.4
Matches 8; Conservative 0; Mismatches
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US-09-864-761-45788
US-09-864-761-45788
Sequence 45788, Application US/09864761
Pacent No. US2002004876341
GENERAL INFORMATION:
APPLICANT: Penn, Sharton G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 214, Application US/09801368 Patent No. US20020128250A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
APPLICANT: Hockt, Peter
APPLICANT: Holtzman, Doug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.7
Best Local Similarity 100.
Matches 8; Conservative
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Sherman, Amir
                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-764-846-140
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Milne, Todd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Silva, Jeff
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-870-336
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Patent No. US20020061521A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007
CURRENT FILING DATE: 2001-01-17
FILE REPLICATION OF THE TENDER OF THE TENDER FILE THE TENDER OF THE TENDER THE THE TENDER THE THE TENDER TH
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US-09-925-299-1317
Sequence 1317, Application US/09925299
Fatent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
ITILE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 1999-03-12
NUMBER OF SED ID NOS: 1556
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 1317
LENGTH: 51
FILE REFERENCE: PT214
CURRENT APPLICATION NUMBER: US/09/764,870
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 336
LENGTH: 46
TYPE: PRT
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100.0%; Pred. No.
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Best Local Similarity 100.0
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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; ORGANISM: Homo sapiens
US-09-764-869-1017
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ORGANISM: Homo sapiens
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NAME/KEY: SITE
LOCATION: (39)
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US-09-764-869-1017
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                                           APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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Patent No. US20020042386A1
GENERAL INFORMATION:
APPLICANT: Rosen et al
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
US-09-864-761-46295
                                                                                                                                           FILE REFERENCE: AGENE EXPRESSION ANALYSIS BY MICKOA CURRENT APPLICATION NUMBER: US/99/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PLICATION NUMBER: US 60/207,066
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PLING DATE: 2000-10-30
PRIOR PLING DATE: 2001-01-30
PRIOR PRIOR DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DA
Hanzel, David K.
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ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity
Matches 7; Conserv
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US-09-764-870-336
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OTHER INFORMATION: EXPRESSED IN FFTAL LIVER, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN FORMATION, SIGNAL = 4.4

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96

OTHER INFORMATION: EXPRESSED IN PRAIN, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN PRAINC, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN ADULT LIYER, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN THE ADULT LIYER, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN ADULT LIYER, SIGNAL = 1.2

OTHER INFORMATION: SINISSPECT HIT: ODGS86, EVALUE 2.00e-44

OTHER INFORMATION: SINISSPECT HIT: ODGS86, EVALUE 2.00e-43
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Patent No. US2002022718A1
GENERAL INPORMATION:
APPLICANT: POSSYTH, R. Allyn
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
TITLE OF INVENTION: Proliferation of E. coli
FILE REFERENCE: ELITRA 009A
CURRENT APPLICATION UNMER: US/09/741,669
CURRENT FILING DATE: 2000-12-19
PRIOR FILING DATE: 1999-12-33
NUMBER OF SEQ ID NOS: 481
SEQ ID NO 427
LENGTH: 157
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LENGTH: 85
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                    PCT/US01/00668
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Best Local Similarity 100.
Matches 7; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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US-09-741-669-427
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David K.
APPLICANT: Rank, David K.
APPLICANT: Rank, David K.
APPLICANT: Rank, David K.
APPLICANT: Hansel, David K.
APPLICANT: Hansel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR FILL OF DATE: 2001-05-23
PRIOR PPLICATION NUMBER: US 60/280,312
PRIOR FILLING DATE: 2000-02-04
PRIOR FILLING DATE: 2000-05-26
PRIOR PLILOR DATE: 2000-06-03
PRIOR PLILOR DATE: 2000-09-03
PRIOR FILLING DATE: 2000-09-03
PRIOR FILLING DATE: 2000-09-03
PRIOR FILLING DATE: 2001-01-30
PRIOR PLILOR DATE: 2001-01-30
PRIOR PLILOR DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
                                                              JUGGATION: (2)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (3)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (5)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (14)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (16)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (16)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (28)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
LOCATION: (38)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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US-09-864-761-37705
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APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Raud, Vined
APPLICANT: Raud, Vined
APPLICANT: Raud, Vined
APPLICANT: Asundi, Vined
APPLICANT: Drmanac, Radoje T
APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLECTIDES
TITLE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLECTIDES
TILE REFERENCE: HYS-37CIP
CURRENT APPLICATION NUMBER: US/09/747,835A
CURRENT APPLICATION NUMBER: US 09/620,312
PRIOR PELING DATE: 2000-12-04
PRIOR PELING DATE: 2000-06-31
PRIOR PELING DATE: 2000-06-20
PRIOR PELING DATE: 2000-06-21
NUMBER OF SEQ ID NOMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 63
SOGTWARE: PATENTIN VERSION 3.0
SEQ ID NO 54
LENGTH: 322
LENGTH: 322
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APPLICANT: Cyskind, Judith W.
APPLICANT: Cyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Tranick, John D.
APPLICANT: Tammoto, Robert T.
APPLICANT: Vammoto, Robert T.
APPLICANT: Vammoto, Robert T.
APPLICANT: Xb, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: DANIER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/19,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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100.0%; Pred. No. 64;
tive 0; Mismatches C
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Patent No. US20020661569Al
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                      Sequence 54, Application US/09747835A Patent No. US20020146692A1 GENERAL INFORMATION:
                                                                                                                                            APPLICANT: Yamazaki, Victoria
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                     Zhou, Ping
Wang, Dunrui
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US-09-747-835A-54
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US-09-815-242-11987
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Patent No. US2002013716941

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BASTUCK, CHRISTINE
APPLICANT: BATHE, BELGITTE
APPLICANT: MOCKEL, BETTINE
APPLICANT: THIRBACH, GEORG
TITLE OF INVENTION: ACID OR NICOTINIC ACID DERIVATIVES
TITLE OF INVENTION: ACID OR NICOTINIC ACID DERIVATIVES
CURRENT APPLICANTON ACID OR NICOTINIC ACID DERIVATIVES
CURRENT APPLICATION NUMBER: US/09/789,582A
CURRENT APPLICATION NUMBER: DEL0055870.4
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
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SEQ ID NO 2
MUNDER DELOF THE NOS 3.0
SEQ ID NO 2
MUNDER DELOF THE NOS 3.0
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                                                                                   RESULT 17
US-09-205-658-309
Sequence 309, Application US/09205658
Fatent No. US20010029617A1
GENERAL INFORMATION:
APPLICANT: RUVKUN, GATY
APPLICANT: Ogy, SCOTT
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
FILE REFERENCE: 00786/3351004
CURRENT APPLICATION NUMBER: 08/09/205,658
CURRENT FILING DATE: 1998-12-03
EARLIER FILING DATE: 1997-05-15
EARLIER FILING DATE: 1997-05-15
SEALIER FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 328
SOFTWARE: FASSEQ for Windows Version 4.0
SEQ ID NO 309
LENGTH: 249
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Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT; ORGANISM: Caenorhabditis elegans
US-09-205-658-309
604 RQLITLL 610
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37 RQLITLL 43
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| 56 FRLVDPR 62
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US-09-789-582A-2
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APPLICANT: ADVANCED RESEARCH & TECHNOLOGY INSTITUTE
TITLE OF INVENTION: Compositions and Methods for Identifying
TITLE OF INVENTION: Agents Which Modulate PTEN Function and PI-3 Kinase Pathways
TITLE REFERENCE: ARTION GOAL-US
CURRENT APPLICATION NUMBER: US/09/870,379
CURRENT FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: RESEASEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 403
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Sequence 19, Application US/08980068B

Sequence 19, Application US/08980068B

Sequence 19, Application US/08980068B

Sequence 19, Application US/08980068B

GENERAL INFORMATION: A POLYPEPTIDE COMMON TO GLIAL CELLS MISSING (GCM)

TITLE OF INVENTION: PROTEINS (AS AMENDED)

TITLE OF INVENTION: PROTEINS (AS AMENDED)

FILE REFERENCE: 97-1513*/LC/00653

CURRENT APPLICATION UNBER: US/08/980,068B

CURRENT FILING DATE: 1997-11-26

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PATENTIN Ver. 2.0
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Sequence 1377, Application US/09925301

Sequence 1377, Application US/09925301

GENERAL INCEMATION:
APPLICANT: Rosen et al.
ITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05882

PRIOR FILING DATE: 2000-03-08

PRIOR PILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.6%; Score 7; DB 10; Length 403; 100.0%; Pred. No. 78;
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100.0%; Pred. No. 83;
:Ive 0; Mismatches
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Best Local Similarity luv...
For 7; Conservative
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Best Local Similarity 100.0
Matches 7; Conservative
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US-09-870-379-2
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LENGTH: 436
TYPE: PRT
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APPLICANT: Milne, Todd
APPLICANT: No. 0252020128250Alman, Thea
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Sherman, Amir
APPLICANT: Slava, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
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                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION WUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-33
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-6
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: 7333
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CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR PILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFWARE: ParentIn Version 3.0
LENGTH: 358
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 148, Application US/09801368
Patent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Gali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Hocht, Peter
APPLICANT: Madden, Kevin
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100.0%; Pre
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ORGANISM: Saccharomyces cerevisiae
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US-09-870-379-2
Sequence 2, Application US/09870379
Patent No. US20020150954A1
                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-11987
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Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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US-09-801-368-148
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; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-4978
                                                                                                      Ohlsen, Kari L.
Zyskind, Judith W.
                                                                         Haselbeck, Robert
               US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1030 EARAWFK 1036
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US-09-815-242-10841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13863, Application US/09815242

Batent No. US20020061569A1

GENERAL INCPEMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Trawick, Judith W.
APPLICANT: Trawick, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Wall, Howard
ITILE OF INVENTION: Identification of Essential Genes in
TILLE OF INVENTION: Prokaryotes
TILLE OF INVENTION: PROKARYOTES
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PLING DATE: 2000-05-21
PRIOR PLING DATE: 2000-05-28
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/25,931
PRIOR APPLICATION NUMBER: 60/25,931
PRIOR APPLICATION NUMBER: 60/25,931
PRIOR APPLICATION NUMBER: 60/25,931
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PRING DATE: 2001-02-17
PRIOR PRIOR DATE: 2001-02-17
PRIOR PRIOR DATE: 2001-02-17
PRIOR
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                                                                                                                                                                                                                                                  DB 10; Length 469;
                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                            Mismatches
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COCATION: (1)...(482)
COTHER INFORMATION: Xaa = Any Amino Acid
US-09-815-242-13863
                                                                                                                                                                                                                                                      Score 7;
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US-09-815-242-4978
; Sequence 4978, Application US/09815242
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100.0%; Pre
0;
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Best Local Similarity 100.0%; P. Matches 7; Conservative 0;
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1377
; LENGTH: 469
; TYPE: PRT
; CRGANISM: Homo sapiens
US-09-925-301-1377
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ORGANISM: Salmonella typhi
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Best Local Similarity 100.
Matches 7; Conservative
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US-09-815-242-13863
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Gaps
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APPLICANT: Zysking, Judiln W.

APPLICANT: Trawick, John D.

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Tamouto, Robert T.

APPLICANT: Yamomoto, Robert T.

APPLICANT: Yamomoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF. INVENTION: Identification of Essential Genes in

TITLE OF. INVENTION: Identification of Essential Genes in

TITLE OF. INVENTION: Identification of Essential Genes in

TITLE OF. INVENTION: DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-21

PRIOR FILING DATE: 2000-05-21

PRIOR FILING DATE: 2000-05-28

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-12-22

PRIOR FILING DATE: 2001-22-15

PRIOR FILING DATE: 2001-22-15

PRIOR FILING DATE: 2001-22-15

PRIOR FILING DATE: 2001-22-16

PRIOR FILING DATE: 2001-22-16
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Traniel, Daniel
APPLICANT: Traniel, John D.
APPLICANT: Tanamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: USOUGHOUS STATE CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-23
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-02-3
PRIOR PLILING DATE: 2000-02-3
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
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Sequence 2, Application US/08910386A Patent No. US20020092041A1 GENERAL INFORMATION:
                                                                                                       APPLICANT: Ronald, Pamela C. APPLICANT: Wang, Guo-Liang APPLICANT: Song, Wen-Yuang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.6
Best Local Similarity 100.
Matches 7; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1099 NLSSLRA 1105
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| US-99-815-3242 |
| US-99-815-3242 |
| Patent No. US200206156941 |
| GUREAL INPORMATION: |
| APPLICANT: Haselbeck, Robert |
| APPLICANT: Trawick, John D. |
| TITLE OF INVENITON: Identification of Essential Genes in TITLE OF INVENITON: PROARTY ON 10-3-21 |
| PRIOR PILING DATE: 2000-03-21 |
| PRIOR PILING DATE: 2000-05-26 |
| PRIOR PILING DATE: 2000-01-23 |
| PRIOR PILING DATE: 2000-10-23 |
| PRIOR PILING DATE: 2000-10-23 |
| PRIOR PILING DATE: 2000-10-24 |
| PRIOR PILING DATE: 2000-10-24 |
| PRIOR PILING DATE: 2001-02-16 |
| PRIOR PILING DATE: 2001-02-16 |
| PRIOR FILING DATE: 2001-02-16 |
| PRIOR
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0.6%; Score 7; DB 10; Length 563;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
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; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 10841
                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10841
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Best Local Similarity 100.
Matches 7; Conservative
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US-08-910-386A-2
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APPLICANT: Song, Wen-Yuang
APPLICANT: Hulbert, Scot
APPLICANT: Richter, Scot
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 53
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.6%; Score 7; DB 8; Length 612;
100.0%; Pred. No. 1.1e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                            COUNTRY: CALLLIANTS

ZIP: 9411-3834

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIDLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/910,386A

FILING DATE: 13-AUG-1997

CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 195, Application US/09771161A
Fatent No. US20020110811A1
GENERAL INFORMATION:
TILLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2000-01-26
PRIOR PRIOR APPLICATION NUMBER: 13676
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-06-15
SEQ ID NOS: 273
SOFWARE: Patentin version 3.0
SEQ ID NOS: 273
LENGTH: 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET WIMBER: 023070-058950US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 612 amino acid
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Sequence 19, Application US/09124280A
Sequence 19, Application US/09124280A
Sequence 19, Application US/09124280A
Setent No. US20020034520A1
GENERAL INFORMATION:
APPLICANT: PORTO: Massimo
TITLE OF INVENTION: VACCINES FOR PREVENTION OF GRAM-
TITLE OF INVENTION: NEGATIVE BACTERIAL INFECTIONS AND ENDOTOXIN RELATED DISEASE
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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US-09-872-349-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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0.5%; Score 6; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.5e+04;
Matches 6; Conservative 0; Mismatches 0; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,386A
FILING DATE: 13-AUG-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 023070-058950US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTER STICS:
LENTH: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 0.65
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-910-386A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1099 NLSSLRA 1105
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US-09-124-280A-19
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                                                                                                                                                                                                                                                                                         Sequence 29, Application US/09934909

Patent No. US20020058275a1

GENERAL INFORMATION:
APPLICANT: GRADIA, Scott

APPLICANT: GRADIA, Scott

APPLICANT: GRADIA, Scott

TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR EFFECTING ADENINE
TITLE OF INVENTION: NUCLECTIDE MODULATION OF DNA MISMATCH RECOGNITION
TITLE OF INVENTION: NUCLECTIDE MODULATION OF DNA MISMATCH RECOGNITION
TITLE OF INVENTION: NUCLECTIDE MODULATION OF DNA MISMATCH RECOGNITION
FILE REFERENCE: 9855-603

CURRENT APPLICATION NUMBER: US 60/093,935

PRIOR APPLICATION NUMBER: US 60/093,935

PRIOR PELING DATE: 1998-07-23

PRIOR FILING DATE: 1997-11-28

PRIOR PELING DATE: 1997-11-28

PRIOR PELING DATE: 1997-10-28

PRIOR FILING DATE: 1997-10-28

PRIOR FILING DATE: 1998-08-28

PRIOR FILING DATE: 1998-08-28

PRIOR FILING DATE: 1998-08-28

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 29
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US-08-910-386A-7
Sequence 7, Application US/08910386A
Fatent No. US20020092041A1
GENERAL INFORMATION:
APPLICANT: Wang, Guo-Liang
APPLICANT: Wang, Guo-Liang
APPLICANT: Hulbert, Scot
APPLICANT: Hulbert, Scot
TILLE OF INVENTION: Procedures and Materials for Conferring
TILLE OF INVENTION: Disease Resisitance in Plants
TILLE OF INVENTION: Disease Resisitance in Plants
TUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
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                                                  Query Match

0.6%; Score 7; DB 10; Length 737;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.6%; Score 7; DB 10; Length 834; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
CORGANISM: Homo sapiens
US-09-934-909-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        728 EFSDDLH 734
                                                                                                                                          647 LMSPGEN 653
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       US-09-771-161A-195
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US-09-934-909-29
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Sequence 90, Application US/09881490

Patent No. US2002077298A1

GENERAL INFORMATION:

APPLICANT Little II, Roger G.

Fadem, Mitchell B.

TITLE OF INVENTON: Anti-Fungal Peptides

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

STREET: 500 West Madison Street, 34th FloorDrive
CITY: Chicago

STATE: Illinois

COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION UNBER: US/09/881,490
FILING DATE: 14-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
0.5%; Score 6; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                  ) MAME/KEY: Modified-site
LOCATION: C-Terminus
) OTHER INFORMATION: /label= Amidation
//note= "The C-Terminus is Amidated."
) SEQUENCE DESCRIPTION: SEQ ID NO: 129:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAPLICATION NUMBER: 09/119,858
FILING DATE: <URKNOWN>
FILING DATE: <URKNOWN>
FILING DATE: 13.740.95
APPLICATION NUMBER: 08/306,473
APPLICATION NUMBER: 08/306,473
FILING DATE: 15.5EP-94
APPLICATION NUMBER: 08/273,540
FILING DATE: 11-0TU-94
APPLICATION NUMBER: 08/209,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 11-MAR-94
APPLICATION UNDBER: 08/183,222
PILING DATE: 14-JAN-94
APPLICATION NUMBER: 08/093,202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 15-JUL-93
APPLICATION NUMBER: 08/030,644
FILING DATE: 12-MAR-93
                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.250"
       TELECOMMUNICATION INFORMATION:
                                                                       INFORMATION FOR SEQ ID NO: 129: SEQUENCE CHARACTERISTICS: LENGTH: 14 amino acids TYPE: amino acids TOPE: Amino acids TOPE: TOPE: Innear MOLECULE TYPE: peptide
                              TELEPHONE: 312/474-630
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 LLIQLF 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                 FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 36
US-09-881-490-90
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Patent No. US20020006638A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Chicago
STATE: 111inois
COUNTRY: United States of America
COUNTRY: United States of America
COUNTRY: United States of America
COMPUTER: Eloppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: Parentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,527
FILING DATE: 18-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/621,803
FILING DATE: COUNCOND:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage COMPUTER: IBM PS/2
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.5%; Score 6; DB 10; Best Local Similarity 100.0%; Pred. No. 31; Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
                          Gibson & Costigan
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hedman, Glbson & Costigat
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: COSTIGAN, JAMES N.
REGISTRATION NUMBER: 25,669
REFERENCE/DOOKET NUMBER: 576-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 302-8998
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                           SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,280A
FILING DATE: July 29,1998
CLASSIFICATION: 424
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: circular
US-09-124-280A-19
                                                                                     : New York
RY: USA
10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 KKFFFF 133
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4 KKFFFF 9
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                                                                  CITY: Ner
STATE: Ne
COUNTRY:
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Sequence 43391, Application US/09864761

Sequence 43391, Application US/09864761

Sequence 43391, Application US/09864761

Sequence 43391, Application US/09864761

Sequence 43391, Devid R.

Sequence 64391, Devid R.

Sequence 6
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                                                          ATTORNEY AGENT INTORMATION:
NAME: MCNICHOLAS, Janet M.
RAGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 100-238/11021U501
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9155
TELEFAX: 312/707-9155
TELERA: 560 389-1248
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 6
OTHER INFORMATION: /label= N-methyl-L
/note= "Position 6 is N-Methyl-leucine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTETMING CTETMING
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Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches
                             APPLICATION NUMBER: 08/030,644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR PELICATION NUMBER: PCT/USO1/00664
PRIOR FILING DATE: 201.01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_fea
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 LLIQLF 171
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FIGH, MAICHELL B.

NUMBER OF SEQUENCES: 21

CORRESPONDENCES: 21

CORRESPONDENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th FloorDrive
CITY: Chloago
STATE: 1111nois
COMPUTR: United States of America
2 IP: 60661

COMPUTR: IBM PC Compatible
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: 05/09/881,490

FILING DATE: 14-Jun-2001
PRIOR APPLICATION NUMBER: 09/119,858
FILING DATE: 13-JAN-95
APPLICATION NUMBER: 08/302,473
FILING DATE: 13-JAN-95
APPLICATION NUMBER: 08/203,540
FILING DATE: 11-JUL-94
APPLICATION NUMBER: 08/203,540
FILING DATE: 11-JUL-94
APPLICATION NUMBER: 08/183,222
FILING DATE: 11-JUL-94
APPLICATION NUMBER: 08/183,222
FILING DATE: 11-JUL-94
APPLICATION NUMBER: 08/183,222
FILING DATE: 11-JUL-93
FILING DATE: 11-JUL-93
FILING DATE: 11-JUL-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.5%; Score 6; DB 10; Length 14; Best Local Similarity 100.0%; Pred. No. 41; Matches 6; Conservative 0; Mismatches 0; Indels
NAME: MCNICholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET WINDER: 100-238/11021US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELERAX: 312/707-8889
TELERAX: 512/707-8889
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COCATION: CTERMING
CTHER INFORMATION: /label= Amidation
SEQUENCE DESCRIPTION: SEQ ID NO: 90:
US-09-881-490-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.250"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 101, Application US/09881490
Patent No. US20020077298A1
GENERAL INFORMATION:
APPLICANT: Little II, Roger G.
Lim, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 14 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ropology: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 LLIQLF 171
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RESULT 40

15 Sequence 3999, Application US/09864761

26 APPLICAMIT: Hancel, David R.

26 APPLICAMIT: Hancel, David R.

27 APPLICAMIT: Hancel, David R.

28 APPLICAMIT: Hancel, David R.

29 APPLICAMIT: Hancel, David R.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: MAP TO 283844.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
OTHER INFORMATION: SWISSPROT HIT: P55194, EVALUE 2.00e-01
US-09-864-761-38599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             566 DPDSSM 571
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Patent No. US20020136734A1
GENERAL INFORMATION:
APPLICANT: Pruett, John H
APPLICANT: Temeyer, Kevin B
APPLICANT: Temeyer, Kevin B
APPLICANT: Temeyer, Kevin B
APPLICANT: Fisher, William F
TTLE OF INVENTION: Vaccines for the Protection of Cattle from Psoroptic
TTLE OF INVENTION: Vaccines for the Protection of Cattle from Psoroptic
TILE REFERENCE: Docket 0047.99
FILE REFERENCE: Docket 0047.99
CURRENT APPLICATION NUMBER: US/99/860,793
CURRENT FILING DATE: 2001-05-18
FRIOR APPLICATION NUMBER: 09/366,603
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 23
TYPE: PRE
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PREADURE:
PREATURE:
OTHER INFORMATION: MAP TO AC006385.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.85
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 0.87
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN BOULE MARROW, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN BOULE MARROW.
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PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR PILICATION NUMBER: PCT/US01/00668
PRIOR PLICATION NUMBER: PCT/US01/00663
PRIOR PLICATION NUMBER: PCT/US01/00663
PRIOR PLICATION NUMBER: PCT/US01/00663
PRIOR PLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PLICATION NUMBER: DCT/US01/00661
PRIOR PLICATION NUMBER: US 60/234,687
PRIOR PLICATION NUMBER: US 00/704,687
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-05-31
PRIOR FILING DATE: 2000-05-30
PRIOR FILING DATE: 2000-05-30
PRIOR FILING DATE: 2000-05-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 43391
LIBNGTH: 20
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Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches
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US-09-864-761-41081

Sequence 4.081, Application US/09864761

Fatent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Henn. Sharron G.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR THE DEPART CANNON NUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US 60/180,312

PRIOR PLING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PLING DATE: 2000-00-04

PRIOR PLING DATE: 2001-01-04

PRIOR PLING DATE: 2001-01-04

PRIOR PLING DATE: 2001-01-130

PRIOR PLING DATE: 2001-01-130

PRIOR PLING DATE: 2001-01-130

PRIOR PLING DATE: 2001-01-30

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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.94
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.82
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.94
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.84
US-09-864-761-45443
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0.5%; Score 6; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels
                                           PRIOR FILLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR PLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-06-30
PRIOR PLICATION NUMBER: US 09/608,408
PRIOR PLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NOS: 49443
LENGTH: 27
   FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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Sequence 4544.3 Application US/09864761

Factor No. US20020048763A1

GENERAL INFORMATION:

APPLICAMT: Bean, Sharron G.
APPLICAMT: Penn, Sharron G.
APPLICAMT: Hancel, David R.

APPLICAMT: Hancel, David R.

APPLICAMT: Hancel, David R.

APPLICAMT: Hancel, David R.

APPLICAMT: GENE EXPRESSION NUCLEIC ACID PROBES USEFUL FOR ITLE OF INVENTION: HUMBAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITLE OF INVENTION: HUMBAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR STATE OF INVENTION: HUMBAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR STATE 2001-05-20.

FRIOR PELICAMION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-06

PRIOR FILING DATE: 2000-05-07

PRIOR PELICAMION NUMBER: US 60/207,456

PRIOR PELICAMION NUMBER: PCT/US01/00666

PRIOR PELICAMION NUMBER: PCT/US01/00667

PRIOR PELICAMION NUMBER: PCT/US01/00669

PRIOR PELICAMION NUMBER: PCT/US01/00669

PRIOR PELICAMION NUMBER: PCT/US01/00668

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100.0%; Pred. No. 70;
iive 0; Mismatches
                                                                                                                                                        Sequence 13, Application US/09860793 Patent No. US20020136734A1
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Best Local Similarity 100.
Matches 6; Conservative
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; ORGANISM: Psoroptes ovis
US-09-860-793-13
20 DPDSSM 25
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21 YTGYGT 26
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US-09-864-761-45443
                                                                                         RESULT 41
US-09-860-793-13
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US-09-764-869-810
Sequence 810, Application US/09764869
Patent No. US20020061521A1
GENERAL INFORMATION:
APPLICAMT ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007
CURRENT FILING DATE: 2001-01-17
CURRENT FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 2442
SEQ ID NOS: 2442
SEQ ID NO 810
LENGTH: 38
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.51

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.52

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.44

OTHER INFORMATION: SWISSPROT HIT: P77891, EVALUE 4.90e+00
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                                                                  PRIOR APPLICATION UNDBER: PCT/USO1/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION UNDBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR FILING DATE: 2001-01-30
PRIOR FLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR PLICATION NUMBER: US 60/234,687
PRIOR PLICATION NUMBER: US 09/608,408
PRIOR PLILING DATE: 2000-09-21
PRIOR PLILING DATE: 2000-09-21
PRIOR PLILING DATE: 2000-09-21
PRIOR PLILING DATE: 2000-09-21
PRIOR PLILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 47440
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Best Local Similarity 100.0%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches
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ilarity 100.0%; Pred. No. 97;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-09-764-869-810
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Best Local Similarity
Matches 6; Conserv
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21 RVLRNY 26
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US-09-864-761-45869
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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Anazel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMBA GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: HUMBER: US 0/9/864,761
CURRENT PELING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PRING DATE: 2000-05-06
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-010-04
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-07
PRIOR PRILOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2001-01-03
PRIOR FILING DATE: 2001-01-30
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN HEARY, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN HEARY, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN FEARL LIVER, SIGNAL = 3.8
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100.0%; Pred. No. 84;
Live 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: PCT/USO1/00668

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/USO1/00662

PRIOR APPLICATION NUMBER: PCT/USO1/00661

PRIOR APPLICATION NUMBER: PCT/USO1/00661

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2000-01-31

PRIOR FILING DATE: 2000-05-31

PRIOR FILING DATE: 2000-09-31

PRIOR FILING DATE: 2000-09-31

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine vers: 1.1

SEQ ID NO 41081
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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US-09-864-761-47440
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OTHER INFORMATION: MAP TO AC008045.5

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4

OTHER INFORMATION: EST_HUMAN HIT: BE348399.1, EVALUE 9.00e-07

US-09-864-761-46284
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                                                                      Sequence 46284, Application US/09864761 Patent No. US20020048763A1
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Sequence 42869, Application US/U9864761

Special No. USGONDONGSTRAIN
GENERAL INFORMATION:
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OTHER INFORMATION: MAP TO ACO16948.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN LUNE, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNE, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN LUNE, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.93
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.93
US-09-864-761-45869
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Pred. No. 99;
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100.0%; Pre
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ORGANISM: Homo sapiens
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Best Local Similarity
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LSVLRH 24
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.1
Length 44;
                                                                   Indels
   0.5%; Score 6; DB 10; Let 100.0%; Pred. No. 1.1e+02; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                    Sequence 40514, Application US/09864761 Patent No. US2020048763A1 GENERAL INFORMATION: APPLICANT: Penn, Sharron G.
   Query Match 0.5
Best Local Similarity 100.
Matches 6; Conservative
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ORGANISM: Homo sapiens
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US-09-864-761-40514
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                                                                                                                                                  N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
N: EXPRESSED IN ADDLT LIVER, SIGNAL = 1.5
N: EXPRESSED IN BAT44, SIGNAL = 1.7
N: EXPRESSED IN BRAIN, SIGNAL = 1.3
N: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
N: EXPRESSED IN LUNG, SIGNAL = 1.5
N: EXPRESSED IN PLACENTA, SIGNAL = 1.5
N: EXPRESSED IN HELIOO, SIGNAL = 1.5
N: EXPRESSED IN HELA, 
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC008045.4
OTHER INFORMATION: EXPRESSED IN FETAL L
OTHER INFORMATION: EXPRESSED IN BT474.
OTHER INFORMATION: EXPRESSED IN BT474.
OTHER INFORMATION: EXPRESSED IN BT474.
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OTHER INFORMATION: SYNESSED OTHER INFORMATION: SYNESSED
                                                                                                       Sequence 36412, Application US/09864761
Patent No. US20020048763A1
                                                                       US-09-864-761-36412
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CTHER INFORMATION: MAP TO AL137853.3

COTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.56

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.56

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.73

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.46

COTHER INFORMATION: EST_HUMAN HIT: BE733841.1, EVALUE 4.00e+00

US-09-864-761-45158
                                                                                              0.5%; Score 6; DB 10; Length 45; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
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                                                                                                 Query Match 0.5
Best Local Similarity 100.
Matches 6; Conservative
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Job time : 175 secs
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     CTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.2

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.5

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.2

OTHER INFORMATION: EST_HUMAN HIT: BF061077.1, EVALUE 1.00e-10

US-09-864-761-40514
                                                                                      Query Match

0.5%; Score 6; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
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ORGANISM: Homo sapiens
FEATURE:
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29 LSAEVV 34
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US-09-864-761-45158
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November 6, 2002, 03:35:08 ; Search time 81 Seconds (without alignments) 1322.145 Million cell updates/sec
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1114
1 MGKTIQVFGFPYLLSAEVVK.....RPVLNLSSLRAQLSHRLVLK 1114
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                          283224 seqs, 96134422 residues
                                                                  OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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1: pir1:*
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	results pred to the scor	מוסי פווס דס	SUMMARIES	Ę	1	T30819	T30828	T01920	H69165	T22/03	2000 K	A78874	H97272	S51436	\$69045	G28771	T04848	D70116	G70951	534230	T27121	AB0717	A5/125	AB23/1	AD1030	T46384	T07231	S14355	AG2329	D97840	AC21/2	*0 / T96
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ribosomal protein ribosomal protein	outer membrane pro hypothetical prote Ig heavy chain pre	glutathione peroxi hypothetical prote probable glutathio	glutathione peroxi probable glutathio	B12 B12 B12	ப	hypothetical prote ribosomal protein ribosomal protein hypothetical prote
	H82567 B89929 A60943	S75019 H64930 F83541	T14262 D84722		HAH	F83815 JC2368 S23753 T22984
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ALIGNMENTS

RESULT 1 T30819 RNA-directed C; Species: 0. C; Date: 22-0. C; Accession: R; Schiebel: R; Schiebel: R; Accession: A; Reference: A; Reference: A; Residues: A; Residues: C; Genetics: A; Note: RdRP: C; Superfamil: C; Keywords:	RESULT 1 T30819 RNA-directed RNA polymerase (BC 2.7.7.48) - tomato C.\$pecias: Lycopersicon esculentum (tomato) C.\$pecias: Lycopersicon esculentum (tomato) C.\$pecias: Lycopersicon esculentum (tomato) C.\$Accession: T30819 RS.\$Chiebel, W.; Pelissier, T.; Riedel, L.; Thalmelr, S.; Schlebel, R.; Kempe, D.; Lof RS.Schlebel, W.; Pelissier, T.; Riedel, L.; Thalmelr, S.; Schlebel, R.; Kempe, D.; Lof Plant Cell 10, 2087-2102, 1998 A.; Title: Isolation of an RNA-directed RNA polymerase-specific cDNA clone from tomato A.; Retence number: Z20885; MUID:99055198; PMID:9836747 A.; Scatus: preliminary; translated from GB/EMBL/DDBJ A.; Status: preliminary; translated from GB/EMBL/DDBJ A.; Status: EMBL:Y10403; NID:94038591; PIDN:CAA71421.1; PID:94038592 C.; Generion: RGRP C.; Superfamily: Arabidopsis probable RNA-directed RNA polymerase C.; Keywords: nucleotidyltransferase
Quer)	Query Match 100.0%; Score 1114; DB 2; Length 1114;
Best	Best Local Similarity 100.0%; Pred. No. 0;
Match	Matches 1114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ςς	1 MGKTIQVFGFPYLLSAEVVKSFLEKYTGYGTVCALEVKQSKGGSRAFAKVQFADNISADK 60
Op	
oy	61 IITLANNRLYFGSSYLKAMEMKTDIVQLKAYVDQMDGITLNFGCQISDDKFAVLGSTEVS 120
Db	
Oy	121 IQFGIGLKKFFFFLSSGSADYKLQLSYENIWQVVLHRPYGQNAQFLLIQLFGAPRIYKRL 180
Db	
Qy	181 ENSCYSFFKETPDDQWYRTTDFPPSWIGLSSSLCLQFRKGVRLPNFEESFFHYAERENNI 240
Db	
oy	241 TLQTGFTEFVSQKSALVPNVQPPEGISIPYKILFKISSLVQHGCIPGPALNVYFFRLVDP 300
Og	
Oy	301 RRRNVACIEHALEKLYYIKECCYDPVRMLTEQYDGYLKGRQPPKSPSITLDDGLYYVRRV 360
Db	

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hypothetical protein MTH500 - Methanobacterium thermoautotrophicum (strain Delta H) (Species: Methanobacterium thermoautotrophicum (strain Delta H) (Species: Methanobacterium thermoautotrophicum (Space: Space: 1997 #sequence_revision 05-Dec-1997 #text_change 04-Mar-2000 (Space: O5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 04-Mar-2000 (Space: O5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 04-Mar-2000 (Space: O5-Dec-1997 #text_change 04-Mar-2000 (Space: Of-Dec-1997 #text_change of-Dec-1997 #te
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A. Molecule type: DNA
A. Residues: 1-1133 <STR>
A. Residues: 1-1133 <STR>
A. Foresolves: 1-1133 <STR>
A. Foresolves: 1-113 <STR>
B. Street ences: EmBL: AF080120; NID: 93600045; PID: 93600048
A. Experimental source: cultivar Columbia
R. Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Sch. Submitted to the Protein Sequence Database, May 1999
A. Reference number: 216098
A. Accession: 108192
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                                                                                                                                                                                                                                                                                                                                                                              Probable RNA-directed RNA polymerase (EC 2.7.7.48) - Arabidopsis thaliana NyAlternate names: protein T2284.110 (c) Species: Arabidopsis thaliana (mouse-ear cress) (c) Abet: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 10-Dec-1999 (c) Accession: T01920; T08192 R; Strong, C.; Graves, T.; Duckels, G. submitted to the EMBL Data Library, July 1998 A; Description: The sequence of A. thaliana F2P3. A; Reference number: 214452 A; Accession: T01920
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C;Superfamily: Methanobacterium thermoautotrophicum hypothetical
   Length 1116;
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A;Note: F2P3.11; T22B4.110
C:Superfamily: Arabidopsis probable RNA-directed RNA polymerase
C;Keywords: nucleotidyltransferase
                                                                           Indels
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A; Molecule type: DNA
A; Residues: 1-1133 <= EEV>
A; Residues: 1-1133 <= EEV>
A; Cross references: EMBL; AL049876
A; Experimental source: cultivar Columbia; BAC clone T22B4
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   DB 2; Le
4.3e-36;
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1.3%; Score 14; DB 2; L.
Best Local Similarity 100.0%; Pred. No. 9.8e-06;
Matches 14; Conservative 0; Mismatches 0;
                                                                                                                                       979 EYDNKLGNLMDYYGIKTEAEILSGGIMKASKTFDRRKDAEAI
Ouery Match 3.8%; Score 42; DB Best Local Similarity 100.0%; Pred. No. 4.3 Matches 42; Conservative 0; Mismatches
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C; Jaces 14. Aug 2001 #Sequence_revision 24-Aug 2001 #text_change 30-Sep-2001
C; Jacessian: A95395
R; Barnett, M.J; Fisher, R.F; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; E
r; Kalman, S.; Keating, D.H; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, R
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A; Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli
A; Reference number: A95262; MUID:21396509; PMID:11481432
A; Recession: A95395
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-286 cKUR>
A; Reterences: GB:AE006469; PIDN:AAK65723.1; PID:914524217; GSPDB:GN00165
A; Remain R: W; Jones, T:
Cowie, A.; Public, A.; Ralman, S.; Reating, D.H.; Kiss, E.; Romp, C.; Lelau hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S; Relis, D.H.; Wong, K.; Yeh, A; Reference number: A96039; MUID:21368234; PMID:11474104
A; Contents: annotation
C; Genetics: annotation
C; Genetics: annotation
C; Revised Reliation
C; Revised Reliation
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A; Experimental source: strain 972h-; cosmid c4G9
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C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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                                                           A;Map position: 15R
C;Superfamily: Saccharomyces hypothetical protein YOR220w
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100.0%; Pred. No. 11;
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Best Local Similarity 100.0%; Pred. No. 8.7
Matches 8; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 9.3
Matches 8; Conservative 0; Mismatches
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A;Map position: 1
A;Introns: 5/1; 48/3
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A;Genome: plasmid
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A. Accession 56097; 567113; 571722

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Cipacies: Caenoriabditis elegans
Cipacies: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 15-0ct-1999
Cipacies: 17-2763
R; McMurray, A.
B; McGerence number: 219612
A; Reference number: 219612
A; Reference number: 219612
A; McGerence number: 219612
A; McGerence number; A; McGerence number; A; McGerence number: 219612
A; McGerence number; A; McGerence number; A; McGerence number; A; McGerence number; A; McGerence number; A; McGerence number; Mc
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                                                           Length 583;
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                                           0.8%; Score 9; DB 2;
100.0%; Pred. No. 1.4;
tive 0; Mismatches
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100.0%; Pred. No. 7.7;
ive 0; Mismatches
Ouery Match
Best Local Similarity 100..
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221 SPSITLDDG 229
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Matches 8; Conserv
                                                                                                                                                                                                                                                  345 SPSITLDDG 353
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A; Introns: 65/2; 97/3
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A;Gene: CESP:F56A8.2
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A; Accession: B48069
A; Molecule type: DNA
A; Residues: 1-251, (%', 253-506 < IRI>
A; Cross references: EMBL:D13785; NID:g218442; PIDN:BAA02933.1; PID:d1003439; PID:g218
A; Note: sequence extracted from NCBI backbone (NCBIP:129897)
C; Genetics: MKK2; SSP33
A; Genes: SGD:S0006061; MIPS:YPL140c
A; Map position: 16L
C; Function:
                                                                                                                                                                               A;Accession: S69045
A;Molecule type: DNA
A;Cross-references: 1-506 (HAL>
A;Cross-references: EMBL:U43703; NID:91244769; PIDN:AAB68220.1; PID:91244775; MIPS:YP
B;Irie, K.; Takase, M.; Lee, K.S.; Levin, D.E.; Araki, H.; Matsumoto, K.; Oshima, Y.
Mol. Cell. Biol. 13, 3076-3083, 1993
A;Title: MKX1 and MKX2, Which encode Saccharomyces cerevisiae mitogen-activated prote
A;Reference number: A48069; MUID:93233668; PMID:8386320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Description: phosphotransferase, serine/threonine-specific protein kinase; involved C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases, protein kinase hom C; Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase; signal F; 212-481/Domain: protein kinase homology <KIN>F; 220-228/Region: protein kinase ATP-binding motif F; 342/Active site: ASP #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the photosynthetic reaction.
                        C; Species: Saccharomyces cerevisiae
C; Species: Saccharomyces cerevisiae
C; Date: 2.2-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 24-Sep-1999
C; Accession: S69045; B48069; S30786
R; Hall, J; DePaulo, T; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, Submitted to the EMBL Data Library, December 1995
A; Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.
A; Reference number: S69040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein C2814 (photosynthetic gene cluster) - Rhodobacter capsulatus C; Species: Rhodobacter capsulatus C; Species: Rhodobacter capsulatus C; Species: Rhodobacter capsulatus C; Species: 18-0ct-1989 #sequence_revision 18-0ct-1989 #text_change 04-Sep-1998 C; Accession: G28771 R; Youvan, D.C.; Bylina, E.J.; Alberti, M.; Begusch, H.; Hearst, J.E. Cell 37, 949-957, 1984 A; Title: Nucleotide and deduced polypeptide sequences of the photosynthetic reacting A; Reference number: A90850; MUID:84259352; PMID:6744416
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N/Alternate names: protein F16G20.10; protein F21P8.200
C.Species: Arabidopsis thaliana (mouse-ear cress)
C;bate: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 17-Mar-2000
    protein
    N;Alternate names: mitogen-activated protein kinase kinase homolog;
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Similarity 100.0%; Pred. No. 15;
8; Conservative 0; Mismatches
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100.0%; Pred. No. 19;
iive 0; Mismatches
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A; Residues: 1-641 <</u>
Cross-references: GB:K01183
C; Superfamily: hypothetical protein C2814
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Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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NyAlternate names: hypothetical protein L9470.1
C.Species: Saccharomyces cerevisiae
C.Species: Saccharomyces cerevisiae
C.Species: Saccharomyces cerevisiae
C.Species: Saccharomyces cerevisian 12-May-1995 #text_change 06-Feb-1996
C.Accession: S51436
R:Wohldmann, P.
R:Wohldmann, P.
R:Wohldmann, P.
R:Wohldmann, P.
R:Wohldmann: S51444
A:Reference number: S51414
A:Ression: S51436
A:Ression: S51436
A:Ressidues: 1-386 < WOH>
A:Ressidues: 1-386 < WOH>
C:Ressidues: C.Species: EMBL:U17246; NID:g577192; PID:g577193; MIPS:YLR191w
    Gaps
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    Indels
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C; Keywords: transmembrane protein
F; 264-280/Domain: transmembrane #status predicted <TMM>
F; 313-367/Domain: SH3 homology <SH3>
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100.0%; Pred. No. 11;
ive 0; Mismatches
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0; Mismatches
  Mismatches
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A;Cross-references: SGD:SO004181; MIPS:YLR191w
A;Map position: 12R
C;Superfamily: SH3 homology
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Matches 8; Conserv
                                           1025 RALRKEAR 1032
                                                                                     327 RALRKEAR 334
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272 VFGFPYLL 279
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A.Reference number: 220314
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A.Reference number: 220314
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Rolecule type: DNA
A.Residues: 1-1564 <WIL>
A.Residues: 1-1564 <ARIL
A.Residues: 1-1
                  A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete gench A;Reference number: A70500; MUID: 98295987; PMID: 9634230
A;Accession: G70500; MUID: 98295987; PMID: 9634230
A;Accession: G70500; MUID: 98295987; PMID: 9634230
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Resiones: 1-1101 <CCL>
A;Resiones: 1-1101 <CCL>
A;Cross-references: GB:AL021646; GB:AL123456; NID: G3242278; PIDN: CAA16666.1; PID: e124
A;Genetics: strain H37Rv
A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: 
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156k protein - Plantago asiatica mosaic virus
156k proteis: Plantago asiatica mosaic virus
C;Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 24-Nov-1999
C;Accession: S34230
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C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C.Accession: T27121
S.White, S.
Submitted to the EMBL Data Library, November 1998
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A; Accession: S34230
A; Status: preliminary
A; Molecule type: genomic RNA
A; Cross-references: EMBL: Z21647; NID: 9311644; FIDN: CAA79761.1; FID: 9311645
C; Superfamily: eggplant mosaic virus RNA-directed RNA polymerase
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254 LITLLSTL 261
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C; Accession: T04848; T05369
R: Bevan, M.; Massenet, O.; Clabault, G.; Quigley, F.; Mache, R.; Bancroft, I.; Mewes, H. submitted to the Protein Sequence Database, August 1998
A; Meference number: 215386
A; Accession: T04848
A; Moclecule type: DNA
A; Residues: 1-830 CBEV>
A; Cross-references: EMBL:ALO22347
A; Residues: 1-830 CBEV>
A; Residues: 1-830 CBEV>
A; Residues: 1-830 CBEV>
A; Residues: 1-830 CBEV>
A; Residues: 1-930 CBEV>
A; Recession: T0530
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A; Recession: T0530
A; Residues: EMBL:AL031326
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C;Species: Bornella Burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 15-Oct-1999
C;Accession: D70116
R;Fraser, C.M.; Casjans, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Son, D.; Bowman, C.; Garland, S.; Fujil, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: D70116
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-901 <KRED
A;Cross-references: GB:AE001124; GB:AE000783; NID:92688003; PIDN:AAC66506.1; PID:9268806
A;Experimental source: strain B31
C;Keywords: transcription factor
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C;Species: Mycobacterium tuberculosis
C;Dacies: Mycobacterium tuberculosis
C;Daces: Mycobacterium tuberculosis
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Cole, S.T.; Bartes, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Majandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
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A;Cross-references: GB:BA000019; PIDN:BAB76221.1; PID:g17133658; GSPDB:GN00179 A;Experimental source: strain PCC 7120 C;Genetics:
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                                                                                                                                                                       A; Gene: asr4522
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                                                                                                                                 Dypothetical protein STY1874a [imported] - Salmonella enterica subsp. enterica serovar Typhi
Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: AB0717
R:Parkhill, J: Dougan, G: James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th. T.; Connerton, P.; Crolin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-652, 2001
A;Reference number: AB0502; PMID:11677608
A;Reference number: AB0502; PMID:11677608
A;Accession: AB0717
A;Status: Preliminary
A;Molecule type: DNA
A;Reference number: GB:AL513382; PIDN:CAD02107.1; PID:916502942; GSPDB:GN00176
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C;Species: Mytilus edulis (blue mussel)
C;Species: Mytilus edulis (blue mussel)
C;Species: Mytilus edulis (blue mussel)
C;Accession: A57125
R;Papov, V.V.: Diamond, T.V.; Biemann, K.; Walte, J.H.
J. Biol. Chem. 270, 20183-20192, 1995
A;Title: Hydroxyarginine-containing polyphenolic proteins in the adhesive plaques of the A;Reference number: A57125
A;Title: Hydroxyarginine-containing polyphenolic proteins in the adhesive plaques of the A;Reference number: A57125
A;Accession: A57125
A;Accession: A5725
A;Accession: A5
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C;Species: Nostoc sp.
A:Note: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AB2371
R;Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T.; Sasamoto, S; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AB2371
A;Accession: AB2371
A;Accession: AB2371
A;Reference number: AB2371
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100.0%; Pred. No. 23;
Live 0; Mismatches
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100.0%; Pred. No. 15;
tive 0; Mismatches
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Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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polyphenolic adhesive protein 3A precursor - Mediterranean mussel
N.Alternate names: foot protein 3A
(Species: Mytlius galloprovincialis (Mediterranean mussel)
U.Alternate names: foot protein 3A
(Spates: Mytlius galloprovincialis (Mediterranean mussel)
C.Bate: 23-Uul-1997 #sequence_revision 29-Aug-1997 #text_change 04-Feb-2000
C.Accession: S68954
R.Inoue, K.; Takeuchi, Y.; Milt, D.; Odo, S.; Harayama, S.; Waite, J.H.
R.Inoue, K.; Takeuchi, Y.; Mult, D.; Odo, S.; Harayama, S.; Waite, J.H.
R.Inoue, K.; Takeuchi, Y.; Mult, D.; Odo, S.; Harayama, S.; Waite, J.H.
A.Title: Cloning, sequencing and sites of expression of genes for the hydroxyarginine
A.Reference number: S68954; MulD:96305382; PMID:8706704
A.Molecule type: mRNA
A.Residues: 1-70 < INO>
F.1-24.Domahin: signal sequence #status predicted <SIG>
F.1-24.Domahin: signal sequence #status predicted <AMT>
F.25-70/Product: polyphenolic adhesive protein 3A #status predicted <AMT>
F.27.28,32,38,43,46,50,53,69,70/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #st
F.36,37,45,48,49,62,64,67/Modified site: 4-hydroxyarginine (Arg) #status predicted
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G;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision text_change 09-Nov-2001
C;Accession: AD1030
C;Accession: ACCESSION: ACC
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A;Cross-references: GB:AL513382; PIDN:CAD09341.1; PID:g16505341; GSPDB:GN00176
C;Genetics:
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.36;
0.6%; Score 7; DB 2
100.0%; Pred. No. 31;
rative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches
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C; Species: Nostoc sp.
A; Note to Sp.
C; Date: 14-Dec-2001 #text_change 30-Jun-2002
C; Accession: AG2329
F; Kanacko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabati DNA Res. 8, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A; Reference number: AB1807; MUID:21595285; PMID:11759840
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C.Species: Rickettsia conorii
and Rickettsia Conorii and Rickettsia prowazekii.
S.Cience 293, 2093-2098, 2001
S.Cience 293, 2093-2098, 2001
S.Cience 293
A.Pitle: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A.Reference number: A97700; MUID:21442074; PMID:11557893
A.Status: preliminary
A.Status: preliminary
A.Status: Preliminary
A.Status: Conorii and Rickettsia prowazekii.
A.Status: Preliminary
A.Status: Conorii and Rickettsia prowazekii.
A.Status: Preliminary
A.Status: Conorii and Rickettsia prowazekii.
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C;Species: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AC2172
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A; Cross-references: GB:BA000019; PIDN:BAB75889.1; PID:g17133325; GSPDB:GN00179
A; Cross-references: GB:BA000019; PIDN:BAB75889.1; PID:g17133325; GSPDB:GN00179
A; Experimental source: strain PCC 7120
C; Genetics:
A; Genetics: rp117
C; Superfamily: Escherichia coli ribosomal protein L17
                                      Gaps
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AG2329
50S ribosomal protein L17 [imported] - Nostoc sp. (strain PCC 7120)
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100.0%; Pred. No. 53;
iive 0; Mismatches
red. No. 49;
Mismatches
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Best Local Similarity 100.
Matches 7; Conservative
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nes 7; Conserv
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79 KDKARNR 85
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49 DKIITLA 55
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                                                  hypothetical protein DKFZp434P2119.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Accession: T46384
R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000
A;Accession: T46384
A;Accession: T46384
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-89 <AAA>
A;Cross-references: EMBL:AL137543
A;Residues: 1-89 <AAA>
A;Cross-references: EMBL:AL137543
A;Reperimental source: adult testis; clone DKFZp434P2119
C;Superfamily: tropomodulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        m.
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C; Species: Rattus norvegicus (Norway rat)
C; Species: 12.**Ov-1993 #sequence_revision 08-Nov-1996 #text_change 08-Nov-1996
C; Accession: S14355
R; Meyer, D.J.; Glimore, K.S.; Coles, B.; Dalton, K.; Hulbert, P.B.; Ketterer, Biochem J. 274, 619, 1991
A; Tricken D.J.; Glimore, R.S.; Coles, B.; Dalton, K.; Hulbert, P.B.; Ketterer, Biochem J. 274, 619, 1991
A; Tricken Siderial distinction of rat GSH transferase subunit 10.
A; Reference number: S14355
A; MulD:91174781; PMID:2006926
A; Residues: 1-29; 30-51; 52-60; 61-66; 67-94; 95-112 <MEY>
C; Superfamily: glutathione transferase
C; Keywords: dimer; transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein 91 - Chlorella vulgaris chloroplast
C;Species: chloroplast Chlorella vulgaris
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
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100.0%; Pred. No.
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S14355
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A; Reference number: I40743; MUID:95247702; PMID:7730299
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Best Local Similarity 100.0
Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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98 RVIGKLF 104
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A81663
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Bacteriophage protein homolog lin2580 [imported] - Listeria innocua (strain Clip11262)
C; Special Lasteria innocua
C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C; Accession: AG1754
R; Glaser, P.; Frangeul, L.; Buchald, B.; Baquero, F.; Berche, P.; Bloecker
C; Accession: AG4955
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
C; Accession: AG49682. 2001
D.; Jones, L.M.; Karst, U.
Science 294, 8494882. 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Tiele. Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AG1754
A; Molecule type: DNA
A; Residues: 1-124 GGLA
A; Experimental source: strain Clip11262
C; Genetics:
A; 
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001

A.Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A.R. Accession: AC217

A.Accession: AC217

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-122 <KURN

A.Residues: 1-125 <KURN

A.Residues: 1-
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100.0%; Pred. No. 54;
iive 0; Mismatches
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H71504
ribosomal protein L17 - Chlamydia trachomatis
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Best Local Similarity 100.
Matches 7; Conservative
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A;Gene: all2930
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outer membrane protein XF2345 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Species: Sylella fastidiosa
C;Accession: BB2567
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature: for a complete list of unitors see reference number AS9128 below
A;Note: for a complete list of authors see reference number A59128 below
A;Accession: B82567
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1145 <SIM>A
A;Residues: 1145 <SIM>A
A;Residues: 1145 <SIM>A
A;Residues: 1.145 <SIM
A;Residues: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cispecies: Chlamydia muridarum, Chlamydia muridarum (strain Nigg)
Cispecies: Chlamydia muridarum, Chlamydia trachomatis Morn
Cispecies: Chlamydia muridarum, Chlamydia trachomatis Morn
Cispecies: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Sep-2000
Cispeciesion: A81663
R.Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe Nucleic Acids Res. 28, 1397-1406, 2000
A.Title: Genome sequences of Chlamydia trachomatis Morn and Chlamydia pneumoniae AR35
A.Accession: A81663
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A;Molecule type: DNA
A;Residues: 1-142 <TET>
A;Residues: 1-142 <TET>
A;Coss-references: GB:AE002347; GB:AE002160; NID:g7190815; PIDN:AAF39596.1; PID:g719
A;Experimental source: strain Nigg (MOPn)
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A;Accession: 140747
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: Dnw
A;Residues: 20-115, R',117-141 <GUL>
A;Cross-references: GB:L33834; NID:g620026; PIDN:AAA74990.1; PID:g620030
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                                                                                                                                                                                                                          C)Genetics:
A;Gene: r117
C;Superfamily: Escherichia coli ribosomal protein
C;Keywords: protein biosynthesis; ribosome
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llarity 100.0%; Pred. No. 61;
Conservative 0; Mismatches
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100.0%; Pred. No. 61;
tive 0; Mismatches
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413 ASTGSGV 419
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A60943
Ig heavy chain precursor V region (clone HN.14) - human
C: Species: Homo sapiens (man)
C: Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
A; Desai, R: Spatz, L: Matsuda, T: Ilyas, A.A.; Berman, J.E.; Alt, F.W.; Kabat, E.A.;
A; Status: not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-151 AcDES>
B; Desai, R: Spatz, L: Matsuda, T: Ilyas, A.A.; Berman, J.E.; Alt, F.W.; Kabat, E.A.;
J: Neuroimmunol. 26, 35-41, 1990
A; Tille: Molecular cloning of a human immunoglobulin heavy chain variable (V-H) region was Molecule type: mRNA
A; Residues: 1-36, MX, 38-62, AR, 67-151 AcDE2>
A; Note: this sequence has been corrected in reference A60943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein SA1329 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Accession: B89929
R;Xuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
M; A; Mizutanl-Ui, Y; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C; Sahiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Accession: B89929
A;Accession: B89929
A;Accession: B89929
A;Accus preliminary
A;Residues: 1-149 <KUR>
A;Residues: 1-149 <KUR>
A;Residues: 1-149 <KUR>
C;Genetics: C;Genetics: Strain N315
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, M.A.; da Silvai, A.M.; Silva Jr., W.A.; da Silvai, A.K.; Contents: annotation
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0.6%; Score 7; DB 2;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches
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100.0%; Pred. No. 64;
tive 0; Mismatches
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C;Superfamily: ferric uptake regulator
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Best Local Similarity 100.0
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                                                                                                                                                                                                                                                                            A; Gene: XF2345
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Inspecialistic Bacherichia coli
C; Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C; Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C; Accession: H64930
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUD:97426617; PMID:9278503
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-157 < ELATD
A; Residues
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A, Accession: S75019
A, Status: preliminary
A, Roceaule type: DNA
A, Molecule type: DNA
A, Residues: 1-154
A, Roladues: Lutanione peroxidase
C, Superfamily: glutathione peroxidase
C, Reywords: oxidoreductase; selenocysteine
F;34/Modified site: selenocysteine #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glutathione peroxidase (EC 1.11.1.9) - Synechocystis sp. (strain PCC 6803)
N.Alternate names: hypothetical protein s1r1992
C.Species: Synechocystis sp.
C.Species: Synechocystis sp.
C.Species: Synechocystis sp.
C.Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C.Accession: S75019
R.Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, C.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;34-117/Domain: immunoglobulin homology <IMM>
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llarity 100.0%; Pred. No. 67;
Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                            Query Match 0.6%; Score 7; DB 2; Best Local Similarity 100.0%; Pred. No. 64; Matches 7; Conservative 0; Mismatches
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Best Local Similarity
Matches 7; Conserv
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Quecus vitamin B12 transport periplasmic protein btuE - Escherichia coli (strain K-12) C; Species: Escherichia coli C; Species: Escherichia coli C; Species: Escherichia coli C; Species: Escherichia coli C; Species: Bscherichia coli C; Species: Bscherichia coli C; Species: Bscherichia coli C; Species: 30-Jun 1988 # sequence_revision 31-Oct-1997 #text_change Ol-Mar-2002 C; Accession: F64929; B24498 B; Shao, Y. A; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1957 A; Thite: The complete genome sequence of Escherichia coli K-12. A; Thite: The complete genome sequence of Escherichia coli K-12. A; Reference number: A64720; MUID:97426617; PMID:9278503 A; Accession: F64929 A; Residues: 1-183 cald sequence not shown; translation not shown A; Residues: 1-183 cald Sequence not shown; translation not shown A; Residues: 1-183 cald Sequence of the btucED genes involved in vitamin B12 transport in A; Experimental source: strain K-12, substrain MG1655 A; Cross-reference number: A24498; MUID:86304184; PMID:3528129 A; Accession: B24498 A; MUID:86304184; PMID:3528129 A; Cross-references: GB:M14031; NID:9145441; PIDN:AAA23527.1; PID:9145444 A; Cromment: This sequence is homologous with that of bovine glutathione peroxidase (41 C; Comment: This sequence is homologous with that of bovine glutathione peroxidase (41 C; Comment: Diuge: btuE
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H.
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A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID:20083487; PMID:10617197
A; Accession: B84722
A; Accession: B84722
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Construction: 1-169 <STO>A; Construction: 1-169 <STO>A; Construction: 1-169 <STO>A; Construction: 1-169 <STO>A; Construction: 2
C; Genetics: Atg311570
A; Map position: 2
C; Superfamily: glutathione peroxidase
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. 76;
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Best Local Similarity 100.0%; Pred. No. 71;
Matches 7; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches
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C; Superfamily: glutathione peroxidase
C; Keywords: vitamin Bl2 transport
F; 37/Active site: Cys *status predicted
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glutthione peroxidase (EC 1.11.1.9) - common sunflower
(5) Species: Belianthus annuus (common sunflower)
(5) Species: Helianthus annuus (common sunflower)
(5) Date: 20-Sep-1999 sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
(5) Accession: T14262
(5) Recekel-brevet, P.; Gagne, G.; Tourvielle de Labrouhe, D.; Dufaure, J.P.; Nicolas, P.; Physiol. Plantarum 103, 385-394, 1998
(6) Reference number: 217562
(7) Accession: T14262
                                                                                                                                                    Probable glutathione peroxidase PA0838 [imported] - Pseudomonas aeruginosa (strain PAO1) C; Species: Pseudomonas aeruginosa C; Jater 15-Sep-2000 #text_change 31-Dec-2000 C; Accession: F83541 R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. L.; Lomplete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathon A; Reference number: A82950; MUID: 20437337; PMID: 10984043 A; Accession: F83541 A; Status: preliminary A; Residues: 1-160 ASTO> A; Cross-references: GB: AE004518; GB: AE004091; NID: 99946725; PIDN: AAG04227.1; GSPDB: GN001 A; Experimental source: strain PA01 C; Genetics: A; Ge
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94722

probable glutathione peroxidase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 0.2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: D84722
R;Lin, X.; Kaulf S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujil, C.Y.;
R;Lin, X.; Kaulf S.; Rounsley, S.D.; Shea, M.; Won, W. C.D.; Fujil, C.Y.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
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Pred. No. 68;
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Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches
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hypothetical protein EEED8.12 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Accession: T15923
R; Chissoe, S.
Spublitch to the EMBL Data Library, July 1995
A; Description: The sequence of C. elegans cosmid EEED8.
A; Reference number: 218428
A; Accession: T15923
A; Residuas: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residuas: 1-197 < CHI>A; Residuas: 1-197 < CHI>A; Cross-references: EMBL:U23484; NID:9733597; PID:9733609; PIDN:AAC46772.1; CESP:EEEC
A; Experimental source: strain Bristol N2
C; Genetics:
A; EEED8.12
A; Introns: 103/2
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C. Species: Arabidopsis thaliana (mouse-ear cress)
C. Species: Arabidopsis thaliana (mouse-ear cress)
C. Species: Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C. Accession: A84865
R. Hin, X. Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.E.; Umayam, L.; Tallon, A. Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A. Recession: A84420; MUID:20083487; PMID:10617197
A. Accession: A84865
A. Status: preliminary
A. Molecule type: DNA
A. Mesidues: 1-206 ASIO>
A. CESTO>
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E75310
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 0.3-Dec:1999 #sequence_revision 0.3-Dec-1999 #text_change 28-Jul-2000
C;Accession: E75310
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100.0%; Pred. No. 85;
Live 0; Mismatches
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         Mismatches
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A)Map position: 2
C)Superfamily: glutathione peroxidase
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Best Local Similarity 100.0
Matches 7; Conservative
         Conservative
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                                                                ILFKISS 278
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73 TIEEVEE 79
                                                                                                           9 ILFKISS 15
            7;
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                                                                    272
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T15923
            Matches
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Nighternate names: tetradecancyl phorbol acetate-induced protein 11
C;Species: Wis musculus (house mouse)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 19-Apr-2002
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 19-Apr-2002
C;Accession: 504743
R;Varnum, B.C.; Lim, R.W.; Sukhatme, V.P.; Herschman, H.R.
Oncogene 4, 119-120, 1989
A;Title: Nucleotide sequence of a cDNA encoding TIS11, a message induced in Swiss 3T3 ce
A;Reference number: 504743; MUID:89128189; PMID:2915901
A;Accession: 504743
A;Accession: 504743
A;Accession: S04743
A;Accession: S04743
A;Cross-references: EMBL:X14678; NID:954803; PIDN:CAA32807.1; PID:954804
A;Cross-references: EMBL:X14678; NID:954803; PIDN:CAA32807.1; PID:954804
C;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: Caenorhabditis elegans hypothetical protein Y116A8C.20
C;Keywords: DNA binding; phosphoprotein; zinc finger
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gh.Reference number: A98629; MUID:21156231; PMID:11258796
A;Accession: A98629; MUID:21156231; PMID:11258796
A;Actuas: preliminary
A;Molecule type: DNA
A;Residues: 1-183 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB35840.1; PID:g13361884; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics: Cs22417
C;Superfamily: glutathione peroxidase
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Pred. No. 76;
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100.0%; Pred. No. 76;
iive 0; Mismatches
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nes 7; Conservative
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Matches
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ribosomal protein L13, cytosolic - human N.Alternate names: BBC1 protein C;Species: Homo saplens (man) C;Species: Homo saplens (man) C;Date: 27-May-1994 #sequence_revision 10-Nov-1995 #text_change 13-Aug-1999 C;Accession: S23753 Sharp, M.G.F.; Brammar, W.J.; Walker, R.A.; Varley, J.M. Hum. Mol. Genet. 1, 91-96, 1992 A;Title: Isolation and characterization of a novel gene with differential expression A;Reference number: S23753; MUID:93244791; PMID:1301162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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C)Species: Caenorhabditis elegans
C)Accession: T22984
R:Matthews, P.
Submitted to the EMBL Data Library, January 1996
A)Reference number: 219647
A)Accession: T22984
A)Accession: T233 AMIL>
A)Accession: T234 AMIL>
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A,Residues: 1-211 <ADA>
A,Residues: 1-211 <ADA>
Cross-references: EMBL:X64707; NID:929382; PIDN:CAA45963.1; PID:929383
C,Superfamily: rat ribosomal protein Li3
C,Keywords: cytosol; protein blosynthesis; ribosome
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                                               A;Note: the protein is designated as ribosomal protein L13 C;Superfamily: rat ribosomal protein L13 C;Keywords: protein blosynthesis; ribosome F;2-211/Product: ribosomal protein L13 #status predicted <MAT>
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o. 86;
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100.0%; Pred. No. 87;
.ve 0; Mismatches
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100.0%; Pred. No. 86;
ative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches
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A; Introns: 31/2; 65/3; 94/2; 138/1; 170/3
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Best Local Similarity 100.0
Matches 7; Conservative
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Job time: 91 secs
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Matches 7; Conserv
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F83815
hypothetical protein BH1326 [imported] - Bacillus halodurans (strain C-125)
C; Species: Bacillus halodurans
C; Species: Cipate: Species: F83815
R; Takami, H; Nakasone, K; Takaki, Y; Maeno, G; Sasaki, R; Masui, N; Fuji, F; Hira
Nucleic Acids Res. 28, 4317-7431, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A; Reference number: A83650; MUID: 20512582; PMID: 11058132
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-207 <270>
A; Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BAB05045.1; GSPDB:GNOC
A; Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BAB05045.1; GSPDB:GNOC
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Superfamily: Bacillus subtilis conserved hypothetical protein yqeJ
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; A. Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Veneer, J.C.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma Science 286, 1571-1577, 1999

**Accession Edition of the radioresistant bacterium Deinococcus radiodurans R1. A; Reference number. A 75250; MuID: 20036896; PMID: 10567266

**Accession: E75310

**Accession: E7531
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C; Species: Rattus norvegicus (Norway rat)
C; Date: 21-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C; Accession: JC2368; PC2232; JC2235; PC2157
R; Olvera, J.; Wool, I.G.
Biochem. Biophys. Res. Commun. 201, 102-107, 1994
A; Title: The primary structure of rat ribosomal protein L13.
A; Reference number: JC2235; MUID:94256964; PMID:8198561
A; Accession: JC2368
A; Mollocule type: mRNA
A; Residues: 1-211 < CLVI)
A; Cross-references: EMBL:X78327; NID:9510551; PIDN:CAA55130.1; PID:9510552
A; Molecule type: protein
A; Residues: 2-14; 26-60; 100-180 < CLV2>
A; Experimental source: clone pL13-2, 3
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A;Map position: 1
C;Superfamily: Deinococcus radiodurans hypothetical protein DR2136
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100.0%; Pred. No. 85;
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November 6, 2002, 03:26:03 ; Search time 87 Seconds (without alignments) 531.088 Million cell updates/sec
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1 MGKTIQVFGFPYLLSAEVVK.....RPVLNLSSLRAQLSHRLVLK 1114
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Gapop 60.0 , Gapext 60.0
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ns	Q10245 schizosacch	Q97es6 clostridium	P80667 saccharomyc				рошо	plant						arabidopsi		caenorhab	bacillus h		crice		1cta	_			Q962ul spodoptera				fv5	02170	2648 enta	Q9wu84 mus musculu
SUMMARIES	CI	FA5 PIG	YD1F_SCHPO	HIS8_CLOAB	PEXD_YEAST	MKK2_YEAST	DXS_RHOCA		PEX1_HUMAN	RRPO_P1AMV	REV_HV1Z8	RL17_CHLTR	RL17_CHLMU	CYNS_SULTO	GSHZ_HELAN	GSHX_ARATH	BTUE_ECOLI	YOOC_CAEEL	NADD_BACHD	୍ଲା	RL13_CRIGR	RL13_HUMAN	RL13_ICTPU	RL13_MOUSE	RL13_RAT	YDH1_HSVS7	- 1	GTC1_RAT	- 1	KPYK_THELI	EUTO_SALTY	- 1	31 ENT	CCS_MOUSE
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	Result No.		7	m	4	S	9	7	ω	σ			12			15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

P94507 bacillus su Q58037 methanococc P28037 streptomyce P57755 streptomyce P26877 pseudomonas Q9k873 bacillus ha P11334 spiroplasma Q9z826 chlamydia p Q8rgf (psobacteri O5276) pseudomonas P4184 caenorhabdi Q9z187 rickettsia Q9z187 rickettsia Q9z187 rickettsia P29920 paracoccus P47175 saccharomyc P73538 synechocyst Q11181 caenorhabdi	TIS	8 AA.	update) on update) lvated protein C cofactor).	; Vertebrata; Euteleostomi; uina; Suidae; Sus.	-STRUCTURE MODELING OF F5/8 TYPE A AND C	M., Alexander L.J., Neame P.J.,	mapping, three-dimensional ites and comparative anatomy of	a cofactor that participates ombin to thrombin. a heavy chain and a light nteraction between the two chains	eats. Domains C	proteolytically to the active a heavy chain at the N-C-terminus).			
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		PIG	16-0CT-2001 (Re 16-0CT-2001 (Re 15-JUN-2002 (Re Coagulation fac	scrofa ryota; alia; E	ENCE FF	TISSUE=Liver; MEDLINE=21121490; IGrimm D.R., Colter	H.K.W.; cine fa ein mod	ins."; [. Mol. Li FUNCTION: with fact SUBUNIT: chaln, no	is calc	PTM: Tr cofacto terminu	2 PLAST SIMILAR SIMILAR	This SWISS-PRC between the St the European E use by non-p modified and t entities requi or send an ema	AF P1 P1 PF PF
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DT 15-JUN-2002 (Rel. 41, Last annotation update)
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            Pfam; PF00394; Cu-oxidase; 3.
Pfam; PF00754; F5_R8_type_C; 2.
SMART; SM00731; F85E0; 2.
PROSITE; PS00079; MULTICPER_OXIDASE1; 2.
PROSITE; PS01285; FA5EC_1; 2.
PROSITE; PS01286; FA5EC_2; 2.
Blood coagulation; Glycoprotein; Sulfation; Calcium; Signal; Zymogen; Repeat.
SIGNAL 1 22 POTENTIAL.
CHAIN 23 2258 COAGULATION PACTOR V.
CHAIN 23 737 HEAVY CHAIN (BY SIMILARITY).
PEPTIDE 738 1611 ACTIVATION PEPTIDE (CONNECTING REGION)
                                                                                                                                                                                                           COAGULATION FACTOR V.
HEAVY CHAIN (BY SIMILARITY).
HEAVY CHAIN (BY SIMILARITY).
(BY SIMILARITY).
LIGHT CHAIN (BY SIMILARITY).
F5/8 TYPE A 1.
PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
F5/8 TYPE A 2.
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PLASTOCYANIN-LIKE 6.
F5/8 TYPE C 1.
F5/8 TYPE C 2.
CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
SIMILARITY).
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RA MEDLINE=21848401; PubMed=11859360;

RA WOOd V. GALillam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Squuros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

Squuros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Squuros J., Peat N., Hayles J., Chillingworth T., Churcher C.M.,

RA Gentles S., Gonnor R., Cronin A., Davis P., Heldlago J., Hodgson G.,

RA Gentles S., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Jones K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,

RA Mooney P., Woule S., Randers R., Squares R.,

Rutherford K., Rutter S., Saunders R., Squares S., Stevens K.,

RA Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Weltjens I., Vanstreels E., Reger M., Schaefer M., Mueller-Auer S.,

RA Weltjens I., Vanstreels E., Reger M., Schaefer M., Mueller-Auer S.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Gablel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

RA Gabel C., Fuchs M., Wedder H., Wambutt R., Purnelle B.,

Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

RA Borzym K., Cuzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Galibert F., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,

RA Cerrutti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,

RA Spakovski G.V., Ussery D., Barrell B.G., Nurse P.;

RA The genome sequence of Schizosaccharomyces pombe.";

RY The genome sequence of Schizosaccharomyces pombe.";

RY SMRN FAMILY. STRONG, TO YEBST TRRISON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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15-UN-2002 (Rel. 41, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
115-Unison2 (Rel. 41, Last annotation update)
phosphate transaminase).
HISC OR CAC3031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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BY SIMILARITY.
; F49CAAB79486F71D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.7%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002198; Abh_short.
Pfam; PF00106; adh_short; 1.
PROSITE; PS00061; ADH_SHORT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 216 B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1111111
327 RALRKEAR 334
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Q97ES6;
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SEQUENCE
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STRAIN-AICC 824 / DSM 792 / VKM B-1787;

M MEDLINE-21359325; Pubmed-11466286;

Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubbis J., Qiu D., Hitti J., Wolf Y.I.,
A Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
Genome sequence and comparative analysis of the solvent-producing
T "Genome sequence and comparative analysis of the solvent-producing
T Dacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001)
C -- CATALYTIC ACTIVITY: L-histidinol-phosphate + 2-oxoglutarate = 3-
C (imidazol-4-yl)-2-oxopropyl phosphate + L-glutamate.
C -- COFACTOR: Pyridoxal phosphate (By sainlarity).
C -- COFACTOR: Pyridoxal phosphate (By sainlarity).
C -- SIMILARITY: BELONGS TO CLASS-II OF PYRIDOXAL PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps,
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MEDLINE-97011156; PubMed-8858166;
Elgersma Y., Kwast L., Klein A., Voorn-Brouwer T., van den Berg M.,
Tabak H.F., Distel B.;
"The SH3 domain of the Saccharomyces cerevisiae peroxisomal membrane
protein Pexign functions as a docking site for Pex5p, a mobile
receptor for the import PTS1-containing proteins.";
J. Cell Biol. 135:97-109(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SIRAIN-S288c / AB972;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
Jehnston A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGRFAMS; TIGRO1141; hisC; 1.

PROSITE; PS00599; AA_TRANSFER_CLASS_2; 1.

Histidine biosynthesis; Transferase; Aminotransferase;

Pyridoxal phosphate; Complete proteome.

Pyridoxal phosphate; Complete proteome.

210 210 210 210 SERMINAL PHOSPHATE (BY SIMILARITY).

SEQUENCE 352 AA; 40220 MW; 3375021EBECGBC2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 352;
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01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Peroxisomal membrane protein PAS20 (Peroxin-13).
PEXI3 OR PAS20 OR YLR191W OR L9470.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.7%; Score 8; DB 1;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches
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InterPro; IPR001917; NHtransf_2.
Pfam; PF00155; aminotran_1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBFAMILY.
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P80667;
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                                                                                                                                                                                                                                                                                                                                                           Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L., Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                              PTS1 recognition factor.";
J. Cell Biol. 135:111-121(1996).
-:- FUNCTION: COMPONENT OF THE PERCXISONAL TRANSLOCATION MACHINERY
WITH PEX14 AND PEX17. INTERACTS WITH THE PTS1 RECEPTOR
                                                                                                                 Erdmann R., Blobel G.;
"Identification of Pex13p a peroxisomal membrane receptor for the
                                                                                                                                                                                                 (PASIO/PEX5).
-1- SUBCELLULAR LOCATION: Integral membrane protein. Peroxisomal.
-1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŠEČUENCE FROM N.A.
MEDLINE-93233668; PubMed=8386320;
Izie K., Takase M., Lee K.S., Levin D.E., Araki H., Matsumoto K.,
Oshlina Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-001-1993 (Rel. 27, Created)
01-001-1996 (Rel. 34, Last sequence update)
115-UNU-2002 (Rel. 41, Last anottation update)
MAP kinase kinase MKKZ/SSP33 (EC 2.7.1.-).
MKKZ OR SSP33 OR YPL140C OR LPI6C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales; Saccharomycetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 386;
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                                      Wilson R., Waterston R.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DBEA9A2372185860 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
5. 4.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O.7%; Score 8; DB 1
Similarity 100.0%; Pred. No. 4.5
8; Conservative 0; Mismatches
                                                                               PARTIAL SEQUENCE, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                        MEDLINE=97011157; PubMed=8858167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42706 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264
281
306
386 AA;
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Best Local Similarity
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                                                                                           STRAIN-S288C
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MKK2_YEAST
ID MKK2_YEAST
AC P32491;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

REDINE-9731371; PubMed-9169875;

REDINE-9731371; PubMed-9169875;

RESEARCH-9731371; PubMed-9169875;

RESEARCH-9731371; PubMed A., Albermann K., Allen E., Ansorge W., Araujo, R., Aparicio A., Barrell B.G., Badcock K., Benes V., Araujo, R., Aparicio A., Burcher M., Coster F., Davis R.W., Churcher C.M., Coster F., Davis R.W., Davis R.W., Dipaolo T., Duboois E., Dubetry J.M., Allenting U., Heumann K., Hilbert H., Hillier L., Goffeau A., All J., Hebling U., Heumann K., Hilbert H., Hillier L., Goffeau A., Allen C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J., Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D., Marathe R., Nometh C., Schafer M., Scharfe M., Walsh W., Zollner A., Wo D.H., Hani J., Han
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submitted (JAN-1997) to the EMBL/Genbank/DDBJ databases.
Submitted (JAN-1997) to the EMBL/Genbank/DDBJ databases.
FUNCTION: SERIND/THREOHIE PROTEIN KIRASE INVOLVED IN A SIGNAL
TRANSDUCTION PATHWAY THAT PLAY A ROLE IN YEAST CELL MORPHOGENESIS
AND CELL GROWTH. THIS PATHWAY SERBMS TO STARTS BY SMR9; THEN
INVOLVES THE KIRASE PKI THAY MAY ACT ON THE BCK1 KINASE THAT THEN
PHOSPHORYLATES MKK1 AND MKK2 WHICH THEMSELVES PHOSPHORYLATE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Problem; PF00069; pkinase; 1.
Probom; PD000001; Euk_pkinase; 1.
SMART; SM00200; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_AIP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;
"MKK1 and MKK2, which encode Saccharomyces cerevisiae mitogenactivated protein kinase-kinase homologs, function in the pathway mediated by protein kinase C."; Mol. Cell. Biol. 13:3076-3083(1993).
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-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
MAP KINASE KINASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

PHOSPHORYLATION (BY SIMILARITY).

PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> S (IN REF. 1).
8EACED6C742E148B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D13785; BAA02933.1; -.
EMBL; 013703; AAB68220.1; -.
EMBL; 010280; AAB48038.1; -.
PIR; BA8069; BA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Δ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-88 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 387:103-105(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              374
252
506 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding;
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BINDING
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GREA_BORBU O51157;
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              GREA_BORBU
    RESULT 7
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                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                 MEDLINE-84259352; PubMed-6744416; W. V. Begusch H., Hearst J.E.; Buvan D.C., Bylina E.J., Alberti M., Begusch H., Hearst J.E.; Nucleotide and deduced polypeptide sequences of the photosynthetic reaction-center, B870 antenna, and flanking polypeptides from R.
                                                                                                                                                                                                                                                                                                                                                                                                                  step.
-!- SUBUNT: Homodimer (By similarity).
-!- SIMILARITY: BELONGS TO THE TRANSKETCLASE FAMILY. DXS SUBFAMILY.
                       ;
0
                                                                                                                                                                                                   Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                    01-MAY-1992 (Rel. 22, Created)
15-UMY-2092 (Rel. 22, Last sequence update)
15-UWN-2002 (Rel. 41, Last annotation update)
1-GONY-2002 (Rel. 41, Last annotation update)
1-GONY-D-xylulose 5-phosphate synthase (EC 4.1.3.37) (1-GONYXYlulose-5-phosphate synthase) (DXP synthase) (DXPS).
  Length 506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 641;
                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02779; transket_pr; 1.
Pfam; PF02780; transketolase_c: 1.
TIGRFAMS; TIGRO0204; dransketolase_c: 1.
PROSITE; PS00801; TRANSKETOLASE_1; 1.
PROSITE; PS00802; TRANSKETOLASE_2; 1.
Lyase; Flavoprotein; Thiamine pyrophosphate;
Lsoprene biosynthesis; Thiamine biosynthesis;
SEQUENCE 641 AA; 67943 MW; CBCCOBF23C012201 CRC64;
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  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
Score 8; DB 1;
; Pred. No. 5.8;
0; Mismatches
                                                                                                                  641 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.7%; Score 8; DB 1
100.0%; Pred. No. 7.2
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 211165; CAA77557.1; -. PIR; G28771; G28771. InterPro; IPR000360; Transketolase.
                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; K01183; -; NOT_ANNOTATED_CDS.
EMBL; Z11165; CAA77557.1; -.
0.7%;
                      8; Conservative
                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                         923 ISERVIGK 930
                                                       314 ISERVIGK 321
                                                                                                                                                                                                                                   NCBI_TaxID=1061;
                                                                                                                                                                                                                                                                                                            capsulata.
Cell 37:94
                                                                                                                  DXS_RHOCA
                                                                                             RESULT 6
DXS_RHOCA
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465 GLTANDIR 472 |||||||| 615 GLTANDIR 622

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          burgdorferi.";

IL Nature 390:580-386(1997).

LI Nature 390:580-386(1997).

-1- FUNCTION: NECESSARY FOR EFFICIENT RNA POLYMERASE TRANSCRIPTION

ELONGATION PAST TEMPLATE-ENCODED ARRESTING SITES. THE BARRESTING

SITES IN DNA HAVE THE PROPERTY OF TRAPPING A CERTAIN FRACTION

OF ELONGATION FORD THE PROPERTY OF TRAPPING A CERTAIN FRACTION

OF ELONGATION FROM THE NEW 3'TERMINGS. GREB ALLOWS THE RESUMPTION OF

ELONGATION FROM THE NEW 3'TERMINGS. GREB ALLOWS THE RESUMPTION OF

ELONGATION FROM THE NEW 3'TERMINGS. GREB ALLOWS THE RESUMPTION OF

ELONGATION FROM THE NEW 3'TERMINGS. GREB RELEASES SEQUENCES OF

2 TO 3 NUCLEDIIDES (BY SIMILARITY).

2 TO 3 NUCLEDIIDES (BY SIMILARITY).

--- SIMILARITY: CONTAINS 1 GREB ASSOCIATED DOMAIN 1 (GRAD1).

--- SIMILARITY: BELONGS TO THE GREB/GREB FAMILY.

--- SIMILARITY: BELONGS TO THE GREB/GREB FAMILY.
                                                                                                                                                                                                                                                                                                                                                             STRAIN-ATCC 35210 / B31;
STRAIN-ATCC 35210 / B31;
STRAIN-ATCC 35210 / B31;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
Viterback T., Watthey L., McDonald L., Artiach P., Bowman J.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.;
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probom; PD004918; GreA_GreB; 1.
PROSITE; PS00839; GREAB_1; 1.
PROSITE; PS00830; GREAB_2; 1.
Transcription regulation; DNA-binding; Coiled coil; Complete proteome.
DOMAIN 20 170 GRAD2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Transcription elongation factor greA (Transcript cleavage factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
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                                                                                                                                                                                                                      borrella burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrella.
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COILED COIL (POTENTIAL)
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. 9.8;
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Mismatches
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GRAD1.
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Pfam: PF01272; GreA_GreB: 1.
Pfam; PF03449; GreA_GreB_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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HSSP; P21346; 1GRJ.
TIGR; BE0132; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.08;
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    681
901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                  GREA OR BB0132
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Matches
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us-09-782-874-2.oli.rsp

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.

-! FUNCTION: REQUIRED FOR STABILITY OF PEX5 AND PROTEIN IMPORT INTO THE PEROXISOME MATRIX.

-! SUBCELLULAR LOCATION: Cytoplasmic (Probable).

-! SUBCELLULAR LOCATION: Cytoplasmic (Probable).

-! DISEASE: DEFECTS IN PEX1 ARE THE CAUSE OF PEROXISOME BIOGENESIS DISEASE: GRADE OF PEROXISOME BY DEFECTS IN PEX1 ARE THE CAUSE OF INFOXISOME ASSEMBLY. NEONATAL ADRENOLEUKODYSTROPHY (NALD) IS ONE OF THE PBD LINKED TO DEFECTS IN PEX1.

-! DISEASE: DEFECTS IN PEX1 ARE THE CAUSE OF INFAMILE REFSUM DISEASE.

-! SIMILARITY: BELONGS TO THE AAA FAMILX OF ATPASES.
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND VARIANT NALD ASP-843.
MEDLINE-98061094; Pubmed-9398847;
Reuber B.E. Germain-Lee E., Collins C.S., Morrell J.C.,
Ameritunga R., Moser H.W., Valle D., Gould S.J.;
"Mutations in PEX1 are the most common cause of peroxisome biogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHO cell mutant
                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND VARIANT NALD ASP-843.
MEDLINE-98061095; PubMed-9398848;
Portsteffen H., Beyer A., Becker E., Epplen C., Pawlak A.,
Kunau W.-H., Dodt G.;
"Hunan PEX1 is mutated in complementation group 1 of the peroxisome biogenesis disorders.";
                 PEXI_HUMAN STANDARD, PRT, 1283 AA.

PEXI_HUMAN STANDARD, PRT, 1283 AA.

30-9393; 099994;

30-MAY-2000 (Rel. 39, Created)

30-MAY-2000 (Rel. 39, Last sequence update)

16-0CT-2001 (Rel. 40, Last annotation update)

Peroxisome biogenesis factor 1 (Peroxin-1) (Peroxisome biogenesis
                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND VARIANTS NALD PRO-664 AND ASP-843.
SEQUENCE FROM N.A., AND VARIANTS NALD PRO-664 AND ASP-843.

MEDLIND-98208543; PubMed-9539740;

Tamura S., Okumoto K., Toyama R., Shimozawa N., Tsukamoto T.,
Suzuki Y., Osumi T., Kondo N., Fujiki Y.;

"Human PEXI cloned by functional complementation on a CHO cell
"Fuman PEXI cloned by functional complementation on a CHO cell
"Fuman Sexpossible for peroxisome-deficient Zellweger syndrome of complementation group I.";

Proc. Natl. Acad. Sci. U.S.A. 95:4350-4355(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA_ATPase_centr.
AAA_sub.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB008112; BA&85162.1; -.
EMBL; AC000064; AAB46346.1; ALT_SEQ.
Genew; HGNC: 8850; PEX1.
MIM; 602136; -.
MIM; 202370; -.
MIM; 265510; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003959; AAA_ATPase_
InterPro; IPR003960; AAA_sub.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF030356; AAB99758.1; -. EMBL; AF026086; AAB87880.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 635-1283 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                             disorders.";
Nat. Genet. 17:445-448(1997).
                                                                                                                                                                                                                                                                                                         Nat. Genet. 17:449-452(1997).
                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pauley A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Primary structure of the triple block RNA genes of the Plantago asiatica mosaic virus.";
Dok!, Akad. wauk SSR 328:625-628(1993).
-!- FUNCTION: RNA-replication. The central part of this protein possibly functions as an APP-binding helicase.
-!- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Solovyev A.G., Novikov V.K., Merits A., Savenkov E.I., Zelenina D.A., Tyulkina L.G., Morozov S.Y.; "Genome characterization and taxonomy of Plantago aslatica mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01.NOV-1995 (Rel. 32, Created)
01.NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
RNA replication protein (156 kDa protein) (ORF 1) [Contains: RNA-directed RNA polymerase (EC 2.7.7.48); Probable helicase).
Plantago asiatica mosaic potexvirus (PlAWV).
Viruses; SSRNA positive-strand viruses, no DNA stage; Potexvirus.
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MEDILINE-93237851; Pubmed-6477237;
SOLOVYEV A.G., NOVÍKOV V.K., MOROZOV S.I., Kagramanov V.N.,
Atabekov I.G.;
| Pfam; PF00004; AAA; 1. | SMART, SM00382; AAA; 1. | PROSITE; PS00674; AAA; 1. | W PEOXISOME; ATP-binding; Repeat; Disease mutation. | Proxisome; ATP-binding; Repeat; Disease mutation. | Proxisome; ATP-binding; Repeat; Disease mutation. | Proxisome; ATP (POTENTIAL). | FT NP_BIND 881 888 ATP (POTENTIAL). | FT VARIANT 664 664 L.>P (IN NALD). | FT VARIANT 843 843 G.>D (IN IRD AND NALD). | FT VARIANT 843 843 G.>D (IN IRD AND NALD). | FT VARIANT 843 843 G.>D (IN IRD AND NALD). | PROXISOME AND NALD). | PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1283;
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155616 MW; 66C177E44678A94F CRC64;
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100.0%; Pred. No. 13;
tive 0; Mismatches
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MEDLINE-94157481; Pubmed-8113746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gen. Virol. 75:259-267(1994).
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Best Local Similarity
'-has 8; Conserva
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1385 AA;
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SEQUENCE
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DB 1;

Score 8;

0.7%;

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926 RVIGKLF 932
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            NCBI_TaxID=813;
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Q9PJN5;
                                                                                                                                                                                           Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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RL17_CHLMU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                  AIDS Res. Hum. Retroviruses 4:165-173(1988).
-!- FUNCTION: REV APPEARS TO ACT POST-TANNSCRIPTIONALLY TO RELIEVE NEGATIVE REPRESSION OF GAG AND ENV PRODUCTION.
-!- SUBCELLULAR LOCATION: Nuclear; accumulates in the nucleoli.
-!- PTM: PHOSPHOPROTEIN WHOSE STATE OF PHOSPHOPRATATION IS MEDIATED BY A SPECIFIC SERIEME KINASE ACTIVITY PRESENT IN THE NUCLEUS.
-!- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD
                                                                                                                                                                                                                                                                                                     Yourno J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ranscription regulation; AIDS; Phosphorylation; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                       ö
                                                                                                                                                     01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
REV protein (Anti-repression transactivator protein) (ART/TRS)
                                                                                                                                                                                                                                                                                                                             Nucleotide sequence analysis of the env gene of a new Zairian
                                                                                                                                                                                                                         Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11681;
                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%; Score 7; DB 1; Length 90; 100.0%; Pred. No. 15; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 AA; 10031 MW; B1940D344B0580B7 CRC64;
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0
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RL17_CHLTR STANDARD; PRT; 141 AA. P47760; 084514; 01-FEB-1996 (Rel. 33, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 16-CT-2001 (Rel. 40, Last annotation update) 50S ribosomal protein L17.
                                                                                                                                90 AA.
           Pred. No. 14;
Mismatches
                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000625; REV_protein. Pfam; PF00424; REV; 1
                                                                                                                                                                                                                                                                                         MEDLINE=88281278; PubMed=3395517;
100.08; Fit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J03653; AAA44686.1; -.
HIV; J03653; REV$JY1.
                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Conservative
                                                                                                                               STANDARD;
          Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                             ERILSTLR 432
                                                                  597 ERILSTLR 604
                                                                                                                                                                                                                                                                                                                                                                                                                                         ZAIREAN MALE
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                                                                                                                                                                                                                                                                                                                                         isolate of HIV
                                                                                                                                                                                                                                                                                                                  Gallo R.C.;
                                                                                                                                                                                                      (Fragment).
                                                                                                                               REV_HV1Z8
P05869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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RL17_CHLTR
1D RL17_CI
AC P477_CI
DT 01-FEB
DT 30-MAY
DD 16-OCTY
DE 50S r11
GN RPLQ OI
GN CRPLQ OI
CC BACTER
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STRAIN-MOPA, Nigg;
MEDLINE-20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
                                                                                                                                                                                                                                                                                                                                          ;
:
STRAIN=L2/434/Bu;
MEDLINE=55247702; PubMed=7730299;
Gu L.J., Wenman W.M., Remacha M., Meuser R.U., Coffin J.M., Kaul R.;
"Chlamydia trachomatis RNA polymerase alpha subunit: sequence and structural analysis.";
J. Bacteriol. 177:2594-2601(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                          STRAIN=D/UW-3/Cx;
MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydia trachomatis.";
Science 228:754-759(1994).
-!- SIMILARITY: BELONGS TO THE 117P FAMILY OF RIBOSOMAL PROTEINS.
-!- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
FRAMESHIFT WAS CORRECTED IN POSITION 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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EMBL, AE001323; AAC68107.1; -.
EMBL, AE001323; AAC68107.1; -.
InterPro; IPR000456; Ribosomal_L17. 1.
Pram; PPO1136; Rabosomal_L17; 1.
R ProDom; PD004277; Ribosomal_L17; 1.
R PROSITE; PS01167; RIBOSOMAL_L17; 1.
)R Ribosomal protein; Complete proteome.
Ribosomal protein; Complete Proteome.
116 116 G -> R (IN SEROVAR L2).
16152 MW; DAD293A8FBE86D79 CRC64;
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-00T-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
RPLQ OR TC0793.
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100.0%; Pred. No. 22;
ative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 7; Conserv
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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RESULT 15
       SETTES
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                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-JCM 10545 / 7;

RAPITABLE-1456156; PubMed-11572479;

RAPATABASH I., Alkal A., Kosugi H., Jin-no K., Takahashi M.,

Sekine M., Baba S.-I., Ankal A., Kosugi H., Hosoyama A., Fukui S.,

RA Sekine M., Baba S.-I., Ankal A., Kosugi H., Hosoyama A., Fukui S.,

RA Magai Y., Nishijima K., Otsuka R., Nakazawa H., Takahiya M., Kato Y.,

RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,

RA Aoki K.-I., Masuchi H.;

R. Complete genome sequence of an aerobic thermoacidophilic

Tenarchaeon, Sulfolobus tokodaii strain?";

L. DNA Res. S. 13-140(2001).

C.-I- FUNCTION: Catalyzes the reaction of cyanate with bicarbonate to

produce ammonia and carbon dioxide (By similarity).

C. -I- CATALTIC ACTIVITY: Cyanate (NCO(-)) + H(2)O = carbamate (H(2)N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0972W5;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cyanate hydratase (EC 4.2.1.104) (Cyanase) (Cyanate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                   Nucleic Acids Res. 28:1397-1406(2000).
-!- SIMILARITY: BELONGS TO THE L17P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.6%; Score 7; DB 1; Length 142;
100.0%; Pred. No. 23;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam: PF01196; Ribosomal_L17.
Pfam: PF01196; Ribosomal_L17; 1.
ProDom: PF004077; Ribosomal_L17; 1.
PROSTITE; PF01167; RIBOSOMAL_L17; 1.
PROSTITE; PF01167; RIBOSOMAL_L17; 1.
SROSTITE; PF01167; RIBOSOMAL_L17; 1.
SROUGNOR 142 AA; 16223 MW; B17AD1A1760A0767 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE002347; AAF39596.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP000984; BAB66048.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sulfolobus tokodaii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 7; Conserv
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SEQUENCE FROM N.A.
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Matches
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Washaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudiootyledons; core eudioots; Asteridae, euasterida II; Asterales; Asteraceae, Asteroideae;
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-!- FUNCTION: MAY CONSTITUTE A GLUTATHIONINE PEROXIDASE-LIKE PROFECTIVE SYSTEM AGAINST OXIDATIVE STRESSES.
-!- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized glutathione + 2 H(2)O.
-!- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 167;
                                                                                                                                                                                                             Length 148;
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CF5AC7ACC76558C9 CRC64;
                                                                                                                                                                  33CB637A45B3BB85 CRC64;
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. 26;
                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                             Score 7; DB 1; Pred. No. 23; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update Glutathione peroxidase 1 (EC 1.11.1.9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P00435; 1GP1.
InterPro: IPR000889; Glut_peroxidase.
Pfam; PF00255; GSHPx; 1.
PRINTS; PR01011; GLUTPROXDASE.
PROSTIE; PS00460; GLUTPROXDASE.
PROSTIE; PS00763; GLUTATHIONE_PEROXID_1; 1.
PROSITE; PS00763; GLUTATHIONE_PEROXID_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%; Score 7; DB 1
100.0%; Pred. No. 26;
live 0; Mismatches
                                                                                                SIMILARITY
                                                                                                                    SIMILARITY
SIMILARITY
InterPro; IPR003712; Cyanate_lyase.
Pfam; PF02560; Cyanate_lyase; 1.
TIGRPAMS; TIGR00673; cynS; 1.
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BY
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15-DEC-1998 (Rel. 37, Last sequ
30-MAY-2000 (Rel. 39, Last anno
                                                                                                                                        115 E
                                                                                                                                                                                                               0.6%; 2
100.0%;
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Best Local Similarity 100.0%
Matches 7; Conservative
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Best Local Similarity luv...
7, Conservative
                                                                    Lyase; Complete proteome.
ACT_SITE 89 89
ACT_SITE 92 92
ACT_SITE 115 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heliantheae; Helianthus.
                                                                                                                                                                  148 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           539 VASKCGL 545
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                                                                                                                                                                                                                                                                                                             58 ADKIITL 64
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                                                                                                                    ACT_SITE
ACT_SITE
SEQUENCE
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SEQUENCE
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GSHZ_HELAN
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18944 MW; 23930B83A0AE3251 CRC64;

169 AA;

SEQUENCE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CV. Columbia;
Cheuk R., Chen H., Kim C.J., Koesema B., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=20083487; PubMed=10617197;
MEDLINE=20083487; PubMed=10617197;
MEDLINE X. Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnatead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Omayam L., Tallon L.J., Gill J.E., Ashan M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: MAY CONSTITUTE A GLUTARHIONINE PEROXIDASE-LIKE
PROTECTIVE SYSTEM AGAINST OXIDATIVE STRESSES.
-!-CATALYTIC ACTIVITY: 2 glutathione + H(2)0(2) = oxidized
glutathione + 2 H(2)0.
-!-SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
Turano F.J., Caldwell. C.R., McMahon M.;
"Glutathione peroxidase CDNA from Arabidopsis.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable glutathione peroxidase At2g31570 (EC 1.11.1.9).
AT2G31570 OR T9H9.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AC007071; AAD24836.1; --
EMBL; AX058187; AAL25600.1; --
EMBL; AX048130; AAC3270.1; --
HSSP; P00435; 1GP1.
InterPro: IPR000889; Glut_peroxidase.
PRINTS; PR01011; GLUTPROXDASE.
PROSITE; PS007460; GLUTATHIONE_PEROXID_1; 1.
PROSITE; PS00763; GLUTATHIONE_PEROXID_1; 1.
PROSITE; PS00763; GLUTATHIONE_PEROXID_2; 1.
Oxidoreductase; Peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U94495; AAB52725.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis cDNA clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 402:761-768(1999).
      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
                                                                                                                                                                                                                                        NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. R.
    GSHX_ARATH
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A Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
Itoh T., Kasai H., Kashimoto K., Minura S., Kitakawa M.,
A Kitagawa M., Makino K., Mit. T., Mizobuchi K., Mori H., Mori T.,
A Motomura K., Nakada S., Nakamura Y., Nashimoto H., Nishio Y.,
A Takeda J., Takemoto K., Takeuchi Y., Bada C.,
A Yamamoto Y., Horiuchi T.,
Takeda J., Takemoto K., Takeuchi Y., Wada C.,
Takamoto Y., Horiuchi T.,
Takeda J., Takemoto K., Takeuchi Y., Wada C.,
Toriuchi T., Balenone of the Escherichia coli K-12 genome
Torresponding to the 28.0-40.1 min region on the linkage map.";
DNA Res. 3:363-377(1996)
C --- FUNCTION: NOT ESSENTIAL FOR B12 TRANSPORT; HOWEVER, IT IS AN AUXILIARY COMPONENT OF THE TRANSPORT SYSTEM.
C --- SUBCELLULAR LOCATION: Periplasmic (Probable).
C --- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-HIZ / MGIGES;
MEDIINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-86304184; PubMed-3528129;
Friedrich M.J., Deveaux L.C., Kadner R.J.;
"Nucleotide sequence of the btuCED genes involved in vitamin B
transport in Escherichia coli and homology with components of
periplasmic-binding-protein-dependent transport systems.";
J. Bacteriol. 167:928-934(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997),
  Length 169,
                                                                                                                                                                                                                                                    01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
BTUE OR B1710.
  DB 1;
              100.0%; Prec. ...
0.6%; Score 7; 1
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=12;
MEDLINE-97251357; PubMed-9097039;
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                                         Conservative
                                                                                                                                                                                                                 STANDARD;
                  Local Similarity
ses 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       Escherichia coli
                                                                            539 VASKCGL 545
                                                                                                                 37 VASKCGL 43
                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=562;
                                                                                                                                                                                                               BTUE_ECOLI
P06610;
                                                                                                                                                                                                                                                                                                                                                                                            Escherichia
Query Match
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                                       Matches
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NADD OR BH1326.
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P41125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical RNA-binding protein EEED8.12 in chromosome II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%; Score 7; DB 1; Length 197;
100.0%; Pred. No. 30;
ive 0; Mismatches 0; Indels
                                                                                                              DB 1; Length 183; 0. 28;
                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                         Chissoe S.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WormPep; EEED8.12; CE01885.
InterPro; IPR00504; RNA_rec_mot.
Pfam, PF00076; rrm; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS00136; RRM; 1.
PROSITE; PS00136; RRM, 1.
PROSITE; PS00136; RRM_RNP_1; FALSE_NEG.
Hypothetical protein; RNA-binding.
EQUENCE 197 AA; 21649 MW; AB5C4F7247DD9729 CRC64;
                                                                               2; Cobalt transport; Complete proteome.
183 AA; 20469 MW; C8DB671963A7F235 CRC64;
       HSSP; P00435; 1GP1.

EcoGene; Ed10129; btuE.

InterPro; IPR00089; Glut_peroxidase.

Pfam; PF00255; GSHPx; 1.

PRINTS; PR01011; GLUTPROXDASE.

PROSITE; PS00460; GLUTATHIONE_PEROXID_1; 1.

PROSITE; PS00763; GLUTATHIONE_PEROXID_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 AA.
                                                                                                                                                                                                                             197 AA
                                                                                                                                  Mismatches
                                                                                                             Score 7; E
Pred. No.
                                                                                                                                                                                                                             PRT;
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                                                                                                                       100.0%; Pr
cive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U23484; AAC46772.1; -.
                                                                                                              0.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.

ses 7; Conservative
                                                                                                                                   Conservative
                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
                                                                                                                     Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   839 TIEEVEE 845
                                                                                                                                                     539 VASKCGL 545
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6239;
                                                                                                                                                                   33 VASKCGL 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 TIEEVEE 79
                                                                                 Periplasmic;
SEQUENCE 1
                                                                                                                                                                                                                          YQOC_CAEEL
Q09301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NADD_BACHD
Q9KD91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 18
NADD_BACHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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01-FEB-1995 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
RPL13 OR BBC1.
(Gallus gallus (Chicken).
ENLATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis.";
Nucleic Acids Res. 28:4317-4331(2000).
-!- FUNCTION: CATALYZES THE REVERSIBLE ADENYLATION OF NICOTINATE MONONUCLEOTIDE (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + nicotinate ribonucleotide = diphosphate + deamldo_NAD(+).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable nicotinate-nucleotide adenylyltransferase (EC 2.7.7.18)
(Deamido-NAD(+) pyrophosphorylase) (Deamido-NAD(+) diphosphorylase)
(Nicotinate mononucleotide adenylyltransferase) (NAMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Masui N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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InterPro; IPR004820; Cytidylyltransf.
InterPro; IPR005248; NAMN_addrnsfrase.
Pfam; PF01467; Cytidylyltransf; I.
TIGRPAMS; TIGR00482; TIGR004862; TIGR004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
MEDLINE-20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Me Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=86665;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- PATHWAY: NAD biosynthesis.
-!- SIMILARITY: BELONGS TO THE NADD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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MEDLINE=96437509; PubMed=8840185;
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                          adenylyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus halodurans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371 GPEVNVS 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 GPEVNVS 158
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Gaps

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Indels

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ed. No. 32
Mismatches
      Pred.
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EMBL; BC004954; AAH04954.1; -
EMBL; BC007363; AAH07345.1; -
EMBL; BC007563; AAH07363.1; -
EMBL; BC007805; AAH07967.1; -
EMBL; BC010994; AAH13078.1; -
EMBL; BC010994; AAH13078.1; -
EMBL; BC014167; AAH13078.1; -
EMBL; BC020804; AAH20804.1; -
EMBL; BC020804; AAH20804.1; -
EMBL; BC021863; AAH20804.1; -
PIR; S23753; S23753; CANDANA CONDANA C
      Best Local Similarity 100.0%; P
Matches 7; Conservative 0;
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24130 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 1
210 AA;
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INIT_MET 0
CONFLICT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                              298 VDPRRRN 304
                                                                                                                                                     97 VDPRRRN 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                RESULT 21
RL13_HUMAN
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                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
Cricetulus.
Sawada K., Agata K., Eguchi G.; "Characterization of terminally differentiated cell state by categorizing clones derived from chicken lens fibers."; Int. J. Dev. Biol. 40.1531-535(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Sasaki Y., Itch F., Suzuki H., Hinoda Y., Imai K.;
Sasaki Y., Itch F., Suzuki H., Hinoda Y., Imai K.;
Indentification of genes highly expressed in association with G2 arrest induced by DNA damage of Chinese hamster overy cells by differential display.",
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: BELONGS TO THE L13E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.6%; Score 7; DB 1; Length 210; 100.0%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
DBD005B96A8BA9B4 CRC64;
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484429F34C565720 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 210 AA. 092313; 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update)
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InterPro; IPR001380; Ribosomal_L13E.
Pfam, PF01294; Ribosomal_L13e; 1.
Prochom: PD004443; Ribosomal_L13E; 1.
PROSITE; PS01104; RIBOSOMAL_L13E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D26318; BAA05377.1; -.
InterPro: IPR001380; Ribosomal_L13E.
Pfam, PF01294; Ribosomal_L138; 1.
ProDom; PD004443; Ribosomal_L13E; 1.
PROSITE; PS01104; RIBOSOMAL_L13E; 1.
Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cricetulus griseus (Chinese hamster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INIT_MET 0 0 B
SEQUENCE 210 AA; 24264 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 AA; 24261 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60S ribosomal protein L13.
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INIT_MET 0
SEQUENCE 210 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10029;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 VDPRRRN 103
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RL13_CRIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Length 210;

DB 1;

Score 7;

0.68;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-Brain, Cervix, Lung, Lymph, Pancreas, Placenta, and Uterus;
                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                          "Isolation and characterization of a novel gene with differential expression in benign and malignant human breast tumours."; Hum. Mol. Genet. 1:91-96(1992).
                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93244791; PubMed-1301162;
Adams S.M., Helps N.R., Sharp M.G.F., Brammar W.J., Walker R.A.,
Varley J.M.;
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RL13_HUMAN STANDARD; PRT; 210 AA. P26373; QBPRX0; 01-AUG-1992 (Rel. 23, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 60S ribosomal protein Ll3 (Breast basic conserved protein 1). RPL13 OR BBC1.
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A -> T (IN REF. 1).
; CBBB26F143FAF058 CRC64;
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v 100.0%; Pred. No. --.
... 0; Mismatches
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Best Local Similarity 100...
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NEDLINE-21085660; PubMed=11217851;

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A lazawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A lazawa K., Izawa M., Mishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H.A., Sabburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Sabburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Sabburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Sisi C., King B., Kochiwa H.,

Radota K., Matsudo T., Nikaido I., Pesole G., Quackenbush J.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Rasaki K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Roonstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Radisincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Roonse P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,

Rosaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Radisharaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Radisharaki Y.,

R
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Q -> L (IN REF. 1).
RLFGIRA -> PTLWQSEQ (IN REF. 1).
ARDDYBEKK -> SEGRÜWKRK (IN REF. 1).
3795373F518655F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 409:685-690(2001).
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100.0%; Pred. No. 32;
ive 0; Mismatches 0; Indels
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01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
8 ribosomal protein L13.
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MEDLINE=94256964; PubMed=8198561;
Olvera, J., Wool I.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:105922; Rpl13.
InterPro; IPR001380; Ribosomal_L13E.
Pfam; PF01294; Ribosomal_L13e; 1.
ProDom; PD004443; Ribosomal_L13e; 1.
PROSITE; PS01104; RIBOSOMAL_L13E; 1.
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189 195 RLI
202 210 AEG
210 AA; 24174 MW;
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EMBL; AKO02787; BAB22358.1; -.
EMBL; AKO10989; BAB27309.1; -.
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Best Local Similarity luv...
7; Conservative
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195
210
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INIT_MET 0
CONFLICT 39
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97 VDPRRRN 103
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CONFLICT
SEQUENCE
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RL13_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Patterson A.P., Karsi A., Liu Z.J.;

Patterson A.P., Karsi A., Liu Z.J.;

Patterson A.P., Karsi A., Liu Z.J.;

"Tranalational machinery of channel catfish: II. Complementary DNA and expression of the complete set of 47 60s ribosomal proteins.";

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

-I. SIMILARITY: BELONGS TO THE L13E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                              Ictalurus punctatus (Channel catfish).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii: Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
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Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
; 5D97B80DD4E64172 CRC64;
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STRAIN-C57BL/6J; IISSUE-Embryonic liver, and Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RL13_MOUSE STANDARD; PRT; 210 AA. P47963; Q9DQH1; D9CZ9; P47963; Q9DQH1; D9CZ9; D1-FEB-1996 (Rel. 33, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Rels ribosomal protein Ll3 (A52).
                                                                                                                                                                                                              15-UUN-2002 (Rel. 41, Created)
15-UUN-2002 (Rel. 41, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
60S_ribosomal protein L13.
                                                                                                                                                                    210 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF401567; AAK95139.1; -. InterPro; IPR001380; Ribosomal_L13E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam: PF01294; Ribosomal_L13e; 1.
ProDom; PD00443; Ribosomal_L13E; 1.
PROSITE; PS01104; RIBOSOMAL_L13E; 1.
Ribosomal protein.
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wes 7; Conserv
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        298 VDPRRRN 304
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                                                                                                                                                            RL13_ICTPU Q90YV5;
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SEQUENCE
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RL13_ICTPU
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Gaps

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RL13_SPOFR
RL13_SPOFR
AC 13_SPOFR
AC 13_SPOFR
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                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Geck P., Whitaker S.A., Medveczky M.M., Medveczky P.G.;
Expression of collagenlike sequences by a tumor virus, herpesvirus
sainiri, ",
J. Virol. 64:3509-3515(1990).
"The primary structure of rat ribosomal protein L13.";
Biochem. Biophys. Res. Commun. 201:102-107(1994).
-1- SIMILARITY: BELONGS TO THE L13E FAMILY OF RIBOSOMAL PROTEINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%; Score 7; DB 1; Length 210;
100.0%; Pred. No. 32;
tive 0; Mismatches 0; Indels
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01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypotherical 24.1 kDa protein in DHFR 3'region (ORF2).
Herpesvirus saimiri (strain 484-77).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .1 protein.
214 Aa; 24142 MW; 9869BDBDA89FA42A CRC64;
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24178 MW; 379A6737F30C6EE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.
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100.0%; Pred. No. 33;
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 AA
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InterPro; IPR001380; Ribosomal_L13E.
Probom; PP010444; Ribosomal_L13e; 1.
Probom; P0004443; Ribosomal_L13E; 1.
PROSITE; PS01104; RIBOSOMAL_L13E; 1.
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Guery Match
Best Local Similarity 100...
Best Accountable 7; Conservative
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55
210 AA;
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Best Local Similarity
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SEQUENCE 21
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P25049;
                                                                                                                                                                                                                                                                                                                                                                                                                                            INIT_MET
CONFLICT
SEQUENCE
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RESULT 26

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                              Pancrustacea; Hexapoda;
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SEQUENCE FROM N.A.
STRING-Fischer 344; TISSUE-Liver;
MEDLINE-94327654; PubMed-8051171;
Hayes J.D., Nayon T., Judah D.J., Petersson D.G., Neal G.E.;
"Cloning of cDNAs from fetal rat liver encoding glutathione S-
"Transferase Yc polypeptides. The Yc2 subunit is expressed in adult
rat liver resistant to the hepatocarcinogen aflatoxin Bl.";
J. Biol. Chem. 269:20707-20717(1994).
                                                                                                                                                                                                                                     Lepidoptera; Glossata;
                                                                                                                                                                                                                                                                                                                                                          Landals I., Ogliastro M., Mita K., Nohata J., Lopez-Ferber M., Duonor-Cerutti M., Fournier P., Devauchelle G.; Duonor-Cerutti M., Fournier P., Devauchelle G.; Full.length ribosomal protein sequence from an EST library of Spodoptera frugiperda cells (Sf9)."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: BELONGS TO THE L13E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1987 (Rel. 05, Created)
01-NOV-1955 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glutathione S-transferase Yc-1 (EC 2.5.1.18) (Chain 2) (GST Ycl)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                             Spodoptera frugiperda (Fall armyworm).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;
Insecta; Pteryqota; Mooptera; Endopterygota; Lepidoptera.
Ditrysia; Noctuoidea; Noctuoidea; Amphipyrinae; Spodoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 219;
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100.0%; Pred. No. 33;
1ve 0; Mismatches
                                                  15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
60S_ribosomal protein L13.
  219 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF400183; AAX92155.1; -
InterPro; IPR001380; Ribosomal_Ll3E.
Pfam; PF01294; Ribosomal_Ll3e; 1.
ProDom; PD004443; Ribosomal_Ll3E; 1.
PROSITE; PS01104; RIBOSOMAL_Ll3E; 1.
PRT;
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MEDLINE-85182743; Pubmed-2985614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.0%; Pratches 7; Conservative 0;
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  STANDARD;
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                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                          NCBI_TaxID=7108;
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P04904;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neal G.E.;
Neal G.E.;
Neal G.E.;
Neal G.E.;
Neal G.E.;
Neal G.E.;
Neal G.E.;
Neal G.E.;
Neal G.E.;
Secondated with the expression of a novel alpha-class glutathione
S-transferase subunit, Yc2, which possesses high catalytic activity
for aflatoxin B1-8,9-epoxide.";
Biochem. J. 279:385-398(1991).
C.-I. FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER
OF EXGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES. HAS
SUBSTANTIAL ACTIVITY: TOWARD FALAYOXIN B1-8,9-EPOXIDE.
C.-I. CATALYTIC ACTIVITY: RX + qlutathione = HX + R-S-glutathione.
C.-I. CATALYTIC ACTIVITY: RX + qlutathione = HX + R-S-glutathione.
C.-I. CATALYTIC ACTIVITY: RX + qlutathione = HX + R-S-glutathione.
C.-I. CHECKLOPHER FOCATION: CYLOPASSHOR.
C.-I. DEVELOPMENTAL STRAGE: LIVER FROM ADULT FEMALE RATS CONTAINS ABOUT
C.-I. DEVELOPMENTAL STRAGE: LIVER FROM ADULT
C.-I. DEVELOPMENTAL STRAGE: LIVER FROM ADULT
                                                  "Rat liver glutathione S-transferases. Construction of a cDNA clone complementary to a Yc mRNA and prediction of the complete amino acid sequence of a Yc subunit.";
J. Biol. Chem. 260:5820-5825(1985).
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                                                                                                                                                                                                            SEQUENCE OF 74-220 FROM N.A.
MEDLINE-84264589; PubMed=6204982;
Tu C.-P.D., Lai H.-C.J., Li N.-Q., Weiss M.J., Reddy C.C.;
The YC and Ya subunits of rat liver glutathione S-transferases are the products of separate genes.;
the products of separate genes.;
J. Biol. Chem. 259:9434-9439(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                   PARTIAL SEQUENCE.
STRAIN=FISCHER 344: TISSUE-Liver;
MEDLINE-92061940; Pubmed-1953636;
Hayes J.D., Judah D.J., McLellan L.I., Kerr L.A., Peacock S.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
Telakowski-Hopkins C.A., Rodkey K.A., Bennett C.D., Lu A.Y.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MALE RATS.
SIMILARITY: BELONGS TO THE GST SUPERFAMILY. ALPHA FAMILY
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L -> K (IN REF. 2).
F40F5FC0757EE93F CRC64;
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PIR; A26753; A26753.
PIR; A26754; A26754.
HSSP; P08263: 1077
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100.0%; Pre
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InterPro; IPR004045; GST_Nterm.
Pfam; PF00043; GST_C; 1.
Pfam; PF02798; GST_N; 1.
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P46418;
01-NOV-1995 (Rel. 32, Created)
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183 183 L
220 AA; 25188 MW;
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ses 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MALE RATS.
-!- INDUCTION: BY ETHOXYQUIN, OLTIPRAZ, BUTYLATED HYDROXYANISOLE, AND
                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                        Hayes J.D., Nguyen T., Judah D.J., Petersson D.G., Neal G.E.; "Cloning of cDNAs from fetal rat liver encoding glutathione S-transferase Y polypeptides. The YC2 subunit is expressed in adult rat liver resistant to the hepatocarcinogen aflatoxin Bl."; J. Biol. Chem. 269:20707-20717(1994).
                                                                                                                                                                                                                                                                                                           Pulford D.J., Hayes J.D.; "Characterization of the rat glutathione S-transferase Yc2 subunit gene, GSFA5: identification of a putative antioxidant-responsive element in the 5'. flanking region of rat GSTA5 that may mediate chemoprotection against aflatoxin Bl."; Blochem. J. 318:75-84(1996).
01-NOV-1995 (Rel. 32, Last sequence update)
16-027-2001 (Rel. 40, Last annotation update)
Glutathione S-transferase Yc-2 (EC 2.5.1.18) (Chain 2) (GST Yc2)
(GST class-alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Fischer 344; IISSUB-Liver;
MEDLINE-92061940; PubMed-1953636;
Hayes J.D., Judah D.J., McLellan L.I., Kerr L.A., Peacock S.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! - SIMILARITY: BELONGS TO THE GST SUPERFAMILY. ALPHA FAMILY
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DE8D9D43365664F5 CRC64;
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EMBL; S72206; -; NOT_ANNOTATED_CDS.
EMBL; 832820; AAB46796.1; -.
HSSP; P08263; IGSD.
                                                                                                                                                               STRAIN-Fischer 344; TISSUE-Liver; MEDLINE-94327654; PubMed-8051171;
                                                                                                                                                                                                                                                                                              MEDLINE-96358489; PubMed-8761455;
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InterPro; IPR004045; GST_Nterm.
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Pfam; PF02798; GST_N; 1
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                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                     NCBI_TaxID=10116;
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                                                            GSTYC2 OR GSTA5.
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Salmonella typhimurium
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ID RADC_BACSU
AC Q02170;
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                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                            "Molecular characterization of the genes encoding the tungsten-
containing aldehyde ferredoxin oxidoreductase from Pyrococcus
furiosus and formaldehyde ferredoxin oxidoreductase from Thermococcus
                                                                                                                                                                                             Thermococcus litoralis.
Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
Thermococcus.
              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                               litoralis.";
J. Bacteriol. 177:4817-4819(1995).
J. Bacteriol. 177:4817-4819(1995).
I. CATALYITIC ACTIVITY: ATP + pyruvate = ADP + phosphoenolpyruvate.
I- PACHWAY: Glycolysis; final step.
I- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
I- SIMILARITY: BELONGS TO THE PYRUVATE KINASE FAMILY.
I- SIMILARITY: PELONGS TO THE PYRUVATE MINASE FAMILY.
                                                                                                                                                                                                                                                                STRAIN=DSM 5473;
MEDILINE=55370164; PubMed=7642512;
Kletzin A., Mukund S., Kelley-Crouse T.L., Chan M.K., Rees D.C.,
Adams M.W.W.;
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ilarity 100.0%; Pred. No. 33;
Conservative 0; Mismatches 0; Indels
             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 AA; 24338 MW; A60B906BC742FCAA CRC64;
            ó
                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pyruvate kinase (EC 2.7.1.40) (FX) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
EUTQ OR STM2468.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD001009; Pyruvate_kinase; 1.
PROSITE; PS00110; PYRUVATE_KINASE; PARTIAL.
Transferase; Kinase; Glycolysis; Magnesium.
220 220 220
             Mismatches
 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR001697; Pyruvate_kinase.
            ;
0
100.08;
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Local Similarity 100
nes 7; Conservative
                                                                                                                STANDARD;
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wes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001697
Pfam; PF00224; PK;
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                  1089 KDKARNR 1095
                                                       124 KDKARNR 130
                                                                                                                                                                                                                                NCBI_TaxID=2265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209 VKSFLEK 215
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                                                                                                   KPYK_THELI
ID KPYK_THELI
AC Q56301;
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Q9ZFV5;
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Matches
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           Matches
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                                                                                          RESULT 29
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                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=LT2 / SGSC1412 / ATCC 700720;
MIDDLINE=21534948; UbbMcd=11677609;
MEDLINE=21534948; UbbMcd=11677609;
MCCLelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                      Kofoid E.C., Rappleye C.A., Stojlljkovic I., Roth J.R.; "The 17-gene ethanolamine (eut) operon of Salmonella typhimurium encodes five homologues of carboxysome shell proteins."; J. Bacteriol. 181:5317-5329(1999).
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID-1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 AA; 24992 MW; 75ADAC10E5F88279 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=168;
MEDLINE-93259962; PubMed-8387996;
Butler Y.X., Abhayawardhane Y., Stewart G.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 7; DB 1;
Pred. No. 35;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- PATHWAY: Ethanolamine utilization.
                                                                                                                                                                STRAIN=LT2;
MEDLINE=99395039; PubMed=10464203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%; Sco.
100.0%; Pre
0;
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J. Bacteriol. 174:6717-6728(1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF093749; AAC78113.1; -. EMBL; AE008811; AAL21362.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 413:852-856(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stydene; SG10633; eutQ.
Complete proteome.
SEQUENCE 229 AA; 249
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Best Local Similarity
Matches 7; Conserv
                                                                                                                              SEQUENCE FROM N.A.
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                                                                NCBI_TaxID=602;
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STANDARD;

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1431_ENTHI P42648;
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CCS_MOUSE
                                                         1431_ENTHI
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                                                                                                                                  RESTAINLES FROM N.A.

REACUENCE FROM N.A.

REALINE-98044033: Pubbhed=938437;

REALINE-98044033: Pubbhed=938437;

REDINGS F., Ogasawara N., Moszer I., Bolotin A., Borchert S.,

RA Azevedo V., Bestero M.G., Besslees P., Bolotin A., Borchert S.,

RA Azevedo V., Bestero M.G., Besslees P., Bolotin A., Borchert S.,

RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

RA Borriss R., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.

RA Choi S.K., Codani J.J., Pabret C., Ferrari E., Cammerson P.T.,

RA Enttan K.D., Errigidon J., Fabret C., Ferrari E., Grandi G.,

RA FILE C., Fullta M., Pullta Y., Fulle M.F., Itaya M., Jones L.,

RA Guiseppi G., Guy B.J., Haga K., Hallo M.F., Itaya M., Jones L.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Joris B., Karamata D., Kasahara Y., Klaerr Blanchard M., Klein C.,

RA Joris B., Karamata D., Kasahara Y., Klaerr Blanchard M., Klein C.,

RA Medina N., Mellado R.P., Lardinols S., Lauber J., Lazarevic V.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., None S.,

RA Presecan E., Pujic P., Purnelle B., Roche B., Rose M., Sadale Y.,

RA Presecan E., Pujic P., Purnelle B., Ropoport G., Rey M., Reynolds S.,

RA Sekiquchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

RA Tosato V., Uchiyama S., Vandenbol M., Vanne F., Yasamoto K., Yata K.,

Winters P., Wipat A., Yamanoto H., Yanane K., Yasamoto K., Yata K.,

Winters P., Wipat A., Yamanoto H., Yanane K., Yasumoto K., Yata K.,

RA Viari A., Wanbuut R., Wedler E., Wedler 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Amplification of the Bacillus subtilis maf gene results in arrested septum formation.";
J. Bacteriol. 175:3139-3145(1993).
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SEQUENCE 231 AA; 26146 MW; B93FC0528C5B49F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- FUNCTION: INVOLVED IN DNA REPAIR (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE RADC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ,
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100.0%; Pred. No. 35;
:ive 0; Mismatches
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EMBL; L08793; AAA2283.1; --
EMBL; 299118; CAB14764.1; --
FIR; B45239; B45239.
Subtilist; BG10325; radc.
InterPro; IPR001583; HHL.1.
InterPro; IPR001445; HhH.1.
InterPro; IPR001405; Radc.
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TIGREAMS; TIGRO0608; radc; 1.
PROSITE; PS01302; RADC; 1.
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ProDom; PD007415; RadC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 390:249-256(1997).
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Matches 7; Conservative
                                                                                                                     SEQUENCE FROM N.A.
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CCS_MOUSE (STANDARD); PRT; 274 AA.
09WUB4; 09CRJ9;
115-JUN-2002 (Rel. 41, Last sequence update)
115-JUN-2002 (Rel. 41, Last annotation 
MANS musculus (Mouse).
115-JUN-2002 (Mouse)
115-JUN-2002 (Mouse)
115-JUN-2003 (Mous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Samuelson J., Shen P., Meckler G., Descoteaux S., Fu H., Lohia A.; Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
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Bartnikas T.B., Waggoner D.J., Gitlin J.D.;
The mouse copper chaperone for superoxide dismutase (CCS).";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 0.6%; Score 7; DB 1; Length 239; Similarity 100.0%; Pred. No. 36; 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 AA; 27338 MW; 6BDE1496C8428FFC CRC64;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
14-3-3 protein 1 (14-3-3-1).
Eukanoeba histolytica.
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STRAIN=NOD; TISSUE=Brain;
MEDLINE-20237523; Pubmed-10773661;
MOOFE S.D., Chen M.M., Cox D.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000308; 14-3-3.
Pfam; PF00244; 14-3-3; 1.
PRINTS; PR00305; 1433ETA.
PRODM; P0000600; 14-3-3; 1.
PROSTTE; PS00796; 1433-1; 1.
PROSTTE; PS00796; 1433-1; 1.
Multigene family.
SEQUENCE 239 AA; 27338 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U13418; AAA80185.1; -. HSSP; P29312; 1A38.
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-HM-1: IMSS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         409 LLPKAST 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 LLPKAST 114
                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=5759;
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Pred. No. 41;

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                                                                                                                                                              Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alizawa M., Nishi K., Kiyoswa H., Kodo S., Yamanaka I., Ashior T., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ashuel P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G., Brenstein M.J., Boilunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Boilunga N., Carninci P., de Bonaldo M.F., Ashiors P., Marchlonni L., Mashima J., Mazzarelli J., Monbaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Schoenbach C., Schoen
"Cloning and mapping of murine superoxide dismutase copper chaperone (Ccsd) and mapping of the human ortholog.";
Cytogenet. Cell Genet. 88:35-37(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- FUNCTION: Delivers copper to copper zinc superoxide dismutase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-1- TISSUE SPECIFICITY: Ubiquitous.
-1- SIMILARITY: CONTAINS 1 HMA DOMAIN.
-1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE CU-ZN SUPEROXIDE DISMUTASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COPPER (POTENTIAL).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER AND ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HMA.
SUPEROXIDE DISMUTASE-LIKE.
COPPER (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19DCE48376C9D5A2 CRC64;
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                                                                                                                         STRAIN-C57BL/6J; TISSUE-Embryonic stem cells;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam: PF00080; sodcu; 1.
Pfam: PF00403; HMA; 1.
PRINTS; PR000406; CORDISMTASE.
PROSITE; PS01047; HMA_1; FALSE_NEG.
PROSITE; PS50846; HMA_2; 1.
PROSITE; PS00087; SOD_CU_ZN_1; FALSE_NEG.
PROSITE; PS00087; SOD_CU_ZN_1; CAPECITE; PS00332; SOD_CU_ZN_2; 1.
Chaperone; Copper; Zinc; Metal.binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001934; HeavyMe_transpt.
InterPro; IPR001424; SOD_CU_ZN.
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                                                                                                 SEQUENCE OF 103-274 FROM N.A.
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MGD; MGI:1333783; Cc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Length 274;

DB 1;

Score 7;

0.68;

Query Match

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RA KUNSTE F., Oggsawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., R. Brouliet S., Eruschi C.V., Caldwell B., Capuano V., Carter N.M., Brouliet S., Dovine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., R. Entian K.D., Errington J., Fabret C., Ferral E., Foulger D., Fritz C., Fujita M., Fujita Y., Fabret C., Ferral E., Foulger D., R. Achim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A., Gliseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A., Jonis B., Karamata D., Kasahara Y., Klarr-Blanchard M., Klein C., R. Autia K., Lapidus A., Lardinois S., Mauel C., Medigue C., Moone D., O'Reilly M., Ogawa K., Laudber J., Lazarevic V., Medigue C., Medigue C., Moone D., O'Reilly M., Portetelle D., Porwollik S., Resper M., Ravolta C., Rocha E., Roche B., Rose M., Sadie Y., Rarrout M., Ravolta C., Schleich S., Schroeter R., Scoffone F., Schleich S., Schroeter R., Scoffone F., Serrot E., Vochiama S., Vandenboll M., Vannier R., Vassarotti A., Tacconi E., Takagi T., Takahsshi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Tarkahsshi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Tarkahsshi H., Washia K., Yasarotti A., Tanaka H., Yamane K., Yasarotti A., Tanaka H., Yamane K., Yasarotti A., Tanaka H., Yamane K., Yasarotti A., Wanniete Genome Leeguence of the Gram Positive bacterium Bacillus R. Hatter P., Walter S., Schleice G., Perlander G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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-- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
--- SUBCELLULAR Bacitracin is thought to be involved in inhibition of peptidoglycan synthesis by sequestering undecaprenyl diphosphate reducing the pool of lipid carrier available.
--- SIMILARITY: BELONGS TO THE UPR FAMILY.
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Probably phosphorylates undecaperent to phosphate. Confers: resistance to bacitracin (By similarity).
-!- CATALKTIC ACTIVITY: ATP + undecaprent = ADP + undecaprent)
                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative undecaprenol kinase (EC 2.7.1.66) (Bacitracin resistance
                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
                                        ;
0
                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
100.08; Fit
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                                        7; Conservative
                                                                                                                                                                                                                                                        STANDARD;
                    Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                       30 GTVCALE 36
                                                                                                                                     9 GTVCALE 15
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P94507;
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TIGREAMS; TIGR00768; rink_fam; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 291 AA; 33277 WW; 286A3438290A3BOE CRC64;
               Hypothetical
SEQUENCE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLSA_STRCO
P57755;
                                                                                                                                                                                                    UL07_HSVEB
P28945;
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                                                                                                                                                                                       UL07_HSVEB
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- SIMILARITY: TO M.JANNACHII MJ1001 AND TO E.COLI RIBOSOWAL PROTEIN S6 MODIFICATION PROTEIN (RIMK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

STRAIN=96337999; PubMed=868087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Scrtton G.G., Rikhness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.K., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                        Subtilist; BG13951; upk.
InterPro; IPR003824; BacA.
InterPro; IPR003824; BacA.
TIGRRAMS; TIGROF53; undec_kin_bacA; 1.
Transferase; Kinase; Antiblotic resistance; Transmembrane;
                                                                                                                                                                                                                                                                                              Length 276;
                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                    2ED137A85F5833BD CRC64;
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                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJ0620,
                                                                                                                                                                                                                                                                                              0.6%; Score 7; DB 1
100.0%; Pred. No. 41;
tive 0; Mismatches
                                                                                                                                                                                                      POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                               EMBL; 299119; CAB15093.1; -.
EMBL; U87792; AAB47703.1; ALT_INIT.
                                                                                                                                                                                                                                                                      30345 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U67510; AAB98615.1; -. TIGR; MJ0620; -
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Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                            Local Similarity 100. les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                         49
89
117
117
194
226
256
255
276 AA;
                                                                                                                                                                            Complete proteome.
TRANSMEM 49
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                                                                                                                                                                                                                                                                                                                                                                            111 FEDXIDE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2190;
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058037;
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TRANSMEM
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TRANSMEM
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                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-92295566, PubMed-1318606;
Telford E.A.R., Watson M.S., McBride K., Davison A.J.;
The DNA sequence of equine herpesvirus-1.";
Virology 189:304-316(1992).
-: SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL7,
EHV-1 55, V2VV 53, EBV BBRF2, HCMV UL103 AND HVS-1 42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                       Length 291;
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                                                                       0; Indels
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Interpro: IPRO2000: PETPOS_UL7.
Pfam: PF01677; Herpes_UL7; 1.
SEQUENCE 303 AA; 33854 MW; 4449A86C70ACAOED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Equine herpesvirus type 1 (strain Ab4p) (EHV-1).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
NCBI_TaxID=31520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable glutaminase SCO7049 (EC 3.5.1.2).
SCO7049 OR SC4G1.15.
Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                      01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%; Score 7; DB 1;
100.0%; Pred. No. 45;
ive 0; Mismatches
                       Score 7; DB 1;
          0.6%; Scor.
100.0%; Pred. No. %-,
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                                                                                                                                                                                                                                                                                          303 AA
                                                Pred. No. 43;
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                                                                          Conservative
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Query Match
Best Local Similarity
7; Conserve
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SEQUENCE FROM N.A.
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                                                                                                                                                  111111
264 PSWIGLS 270
                                                                                                                      204 PSWIGLS 210
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                                                                                                                                                                                                                                                                                                                                                                                                              Gene 55 protein
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RARENE RAPARE RA

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InterPro; IPR000073; Abhydrolase.
InterPro; IPR000734; Lipase.
InterPro; IPR000379; Ser_estrs_site.
Pfam, PF00561; abhydrolase; 1.
PROSITE; PS00120; LIPASE.SER; 1.
Hydrolase; Lipid degradation; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AP001511; BAB05101.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   32737 MW;
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Pfam; PF02401; LYTB; 1.
TIGRFAMS; TIGR00216; lytB; 1.
ISOprene biosynthesis; Complet SEQUENCE 314 AA; 34841 MW;
                                   EMBL; D10166; BAA01035.1; -
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Best Local Similarity 100.9
Matches 7; Conservative
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ISPH OR LYTB OR BH1382.
                                                                      A40943.
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                                                                                                                                                                                                                                                                                                                                                             108
235
277
311 AA;
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nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 FLSSGSA 139
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                                                                PIR; A40943; A
HSSP; P22088;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISPH_BACHD
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ACT_SITE
ACT_SITE
SEQUENCE
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      STATE TENTE SECTION OF THE SECTION O
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MEDLINE-92011544; PubMed-1917947;

Ihara F., Kageyama Y., Hirata M., Nihira T., Yamada Y.;

Ihara F., Characterization, and molecular cloning of lactonizing
lipase from Pseudomonas species.";

J. Biol. Chem. 266:18135-18140(1991).

-!- FUNCTION: CATALYZES THE SYNTHESIS OF MACROCYCLIC LACTONES IN
ANNINDROUS ORGANIC SOLVENTS.

-!- CATALYZIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY
                                                   Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Seeger K., Saunders D., Sharp S., Squares K., Rutter S.,
Hopwood D.A.;
Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE AB HYDROLASE SUPERFAMILY. PSEUDOMONAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1992 (Rel. 23, Created)
1-AUG-1992 (Rel. 23, Last sequence update)
15-UNW-2002 (Rel. 41, Last annotation update)
Lactonizing lipase precursor (BC 3.1.1.3) (Triacylglycerol lipase).
                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; Score 7; DB 1; Length 307; ilarity 100.0%; Pred. No. 45; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase; Complete proteome.
SEQUENCE 307 AA; 32555 MW; CCF51DFAE88D2079 CRC64;
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STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AL391039; CAC01547.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas sp. (strain 109).
Bacteria; Proteobacteria.
NCBL_TaxID=306;
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wes 7; Conserv
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P26877:
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Matches
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LIP_PSESP
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-!- FUNCTION: Converts 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate into isopentenyl diphosphate (IPP) and dimethylallyl diphosphate (DMAPP) (By similarity).
-!- PATHWAX: Nonmevalonate terpenoid biosynthesis pathway; seventh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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LACTONIZING LIPASE.
CHARGE RELAY SYGTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
27ACZF3DD3B334D1 CRC64;
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STRAIN=C-125 / JCM 9153;
STRAIN=C-125 / JCM 9153;
STRAIN=C-125 / JCM 9153;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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                                                                                                                                                                                              Length 311;
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                                                                                                                                                                                                                                                               0; Indels
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NCBI_TaxID=86665;
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314 AA; 34841 MW; BCOC12493B22698F CRC64;
                                                                                                                                                                                       0.6%; Score 7; DB 1;
llarity 100.0%; Pred. No. 46;
Conservative 0; Mismatches
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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100.0%; Pred. No. 46;
tive 0; Mismatches
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Complete proteome.
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SEQUENCE
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olidger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Renaudin J., Pascarel M.-C., Bove J.-M.;
"Spiroplasma virus 4: nucleotide sequence of the viral DNA,
regulatory signals, and proposed genome organization.";
J. Bacteriol. 169:4950-4961(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.6%; Score 7; DB 1; Length 320;
100.0%; Pred. No. 47;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Spiroplasma virus 4 (SpV4).
Viruses; ssDNA viruses; Mcroviridae; Spiromicrovirus.
NCBI_TaxID=10855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320 AA; 38090 MW; B4C1B2BCAC1A2058 CRC64;
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01-JUL-1989 (Rel. 11, Last sequence update)
01-JUL-1989 (Rel. 11, Last annotation update)
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MEDLINE=99206606; PubMed=10192388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-88032809; PubMed=2822658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.6
Best Local Similarity 100.
Matches 7; Conservative
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                                                     ||||||||
|159 ISADKII 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 NYIVNDS 42
                         ISADKII 62
                                                                                                                                                                                                                                                                                                                                                                              Gene 2 protein.
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                                                                                                                                                                                                                                 VG2_SPV4
P11334;
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Y526_CHLPN
ID Y526_C
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Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.; "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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MEDLINE=21886394; PubMed=11889109;
Rapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
Bhattacharryya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
                                                                                                                                                                                                                                                                                                                           Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; Comparison of Whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).

-! SIMILARITY: CONTAINS 2 CBS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
4-hydroxythreonine-4-phosphate dehydrogenase (EC 1.11.1.262) (4-fhosphohydroxy)-L-threonine dehydrogenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
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EMBL, AE002183; AAF38092.1; --
EMBL, AP002247; BAA98732.1; --
EMBL, AP002547; BAA98732.1; --
EMBL, AP002547; BAA98732.1; --
EMBL, AP002547; EMSUGA, CBS_domain.
InterPro; IPR00484; CBS_domain.
InterPro; IPR001347; SIS.
Pfam; PF01380; SIS.
Pfam; PF01380; SIS; 1.
SWART; SW00116; CBS; 1.
FIGREAMS; TIGREAMS; TIGREAMS; TIGREAMS; APPOTHATION ATP-binding; Repeat; CBS domain;
Hypothetical protein; ATP-binding; Repeat; CBS domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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CBS 1.
CBS 2.
; 27A3023B6ABE6D2F CRC64;
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Bacteria; Fusobacteria; Fusobacterium.
NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
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100.0%; Pred. No. 48;
tive 0; Mismatches
                                                                                                                                           pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                            STRAIN=J138;
MEDLINE-20330349; PubMed=10871362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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204 258 CB
272 327 CB
329 AA; 35650 MW;
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Best Local Similarity luv...
7; Conservative
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YO94_CAEEL
P41844;
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Matches
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SETRAIN-GE FROM N.A.
STRAIN-GE STAIN-GE STAIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPOA_POSEAE STANDARD, PRT; 333 AA.
052760;
30-MAY-2000 (Rel. 39, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
116-OCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase alpha chain (EC 2.7.7.6) (Transcriptase alpha chain) (RNA polymerase alpha subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ma J.-F., Ochsner U.A., Klotz M.G., Nanayakkara V.K., Howell M.L., Johnson Z., Posey J.E., Vasil M.L., Monaco J.J., Hassett D.J.; Bacterioferrittin A modulates catalase A (KatA) activity and resistance to hydrogen peroxide in Pseudomonas aeruginosa."; J. Bacteriol. 181:3730-3742(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                        Pyridoxine biosynthesis; Oxidoreductase; NAD; Complete proteome.
SEQUENCE 332 AA; 36547 MW; A9032E3F6E7081FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.6%; Score 7; DB 1; Length 332; Best Local Similarity 100.0%; Pred. No. 49; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=FRD1;
MEDLINE=99296583; PubMed=10368148;
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE010535; AAL94432.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 TLEYGQV 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKDDKATA -> TERRQGHCLIVVTTERKVWKGIEPCAIVK
                                                                                                                                                                                     -:- SUBBUIL: CONSISTS OF A SIGMA FACTOR AND THE RNAP CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, 1 BETA' CHAIN AND 1 OMEGA CHAIN (BY SIMILARITY).

-:- DOMAIN: THE AMINO-TERMINAL PORTION IS INVOLVED IN THE ASSEMBLY OF CORE RNAP, WHEREAS THE C-TERMINAL IS INVOLVED IN INTERACTION WITH TRANSCRIPTIONAL REGULATORS (BY SIMILARITY).

-:- SIMILARITY: BELONGS TO THE RNA POLYMERASE ALPHA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                 -!- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
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STRAIN-Bristol N2;
Waterston R.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: STRONG, TO C.ELEGANS K06H7.2.
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llarity 100.0%; Pred. No. 49;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF047025; AAC03116.1; -.
EMBL; AE004841; AAG07626.1; -.
HSSP; P00574; LCOO.
InterPro; IPR01700; RNA_POl_A_bac.
Pfam; PF011000; RNA_POl_A_bac; 1.
Pfam; PF03118; RNA_POl_A_CTD; 1.
ProDom; PD001179; RNA_POl_A_CTD; 1.
ProDom; P101179; RNA_POl_A_CD; 1.
Profom; P101179; RNA_POl_A_CD; 1.
Transferase; Transcription; DNA-directed RNA polymerase;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Hypothetical 40.1 kba protein T20B12.4 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVVT (IN REF. 1). SEQUENCE 333 AA; 36649 MW; 50706D2926207CA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             335 AA.
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Les 7; Conserv
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PRT;

STANDARD;

us-09-782-874-2.oli.rsp

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RUVB_RICPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 47
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EMBL; AE008615; AAL03071.1; ALT_INIT.

InterPro; IPR003059; AAA_ATPARSE.

R InterPro; IPR00046; AAA, 1.

SHART; SM00081; AAA, 1.

TGROBAST; SM00882; AAA, 1.

TGREAMS; TGROBO65; LUVB; I.

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                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                     Gaps
                                                                                                                                                                                                                                                                                                            STRAIN=Malish 7;
MEDINE=21442074; PubMed=11557893;
MEDINE=21442074; PubMed=11557893;
MEDINE=21442074; PubMed=11557893;
Sqata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
Raoult D.;
                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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100.0%; Pred. No. 50;
.ive 0; Mismatches 0; Indels
WormPep; T20B12.4; CE01410.
Hypothetical protein.
SEQUENCE 335 AA; 40139 MW; 9DE51B219062E8E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP (POTENTIAL).
83891BDB0C829C28 CRC64;
                                           Query Match 0.6%; Score 7; DB 1; Best Local Similarity 100.0%; Pred. No. 49; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-3002 (Rel. 41, Last annotation update)
RUVB OR RC0533.
                                                                                                                                                                  PRT; 342 AA.
                                                                                                                                                                                                                                                                Rickettsiaceae; Rickettsieae;
NCBI_TaxID=781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38309 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         342 AA;
                                                                                                                                                                                                                                            Rickettsia conorii.
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome.
                                                                                       477 DFSQIKN 483
                                                                                                           183 DFSQIKN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          681 RASKLLD 687
                                                                                                                                                       RUVB_RICCN
ID RUVB_RICCN
AC Q92187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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Matches
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190 RASKLLD 196

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 396:133-140(1998).

-I-PUNCTION: THE RVA-RUYB COMPLEX IN THE PRESENCE OF AIP RENATURES. CRUCIFORM STRUCTURE IN SUPERCOLLED DNA WITH PALINDROMIC SEQUENCE, INDICATING THAT IT MAY PROMOTE STRAND EXCHANGE REACTIONS IN HODICATING THAT IT MAY PROMOTE STRAND EXCHANGE REACTIONS IN HODICATING THAT IT MAY PROMOTE STRAND EXCHANGE REACTIONS IN HOLIDAY UNCTION MIGRATION BY LOCALIZED DENATURATION AND REANNELING (BY SIMILARITY).

-I-PUNCTION: PARTIOLIPATES TO UV-TOLERANCE OF SYNECHOCYSTIS PCC 6803.

-I-SUBGUNT: FORMS A COMPLEX MITH RUYA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR004605; RuvB.
Parm; PR00004; AAA; 1.
SMART; SM00182; AAA; 1.
TIGRPAMS; TIGR00635; ruvB; 1.
DNA repair; SOS response; ATP-binding; DNA recombination; Helicase;
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99039499; PubMed=9823893;
Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
Eriksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and the origin of
mitochondria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                      Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NADH-ubiquinone oxidoreductase chain 8 (EC 1.6.5.3) (NADH abhydrogenase 1, chain 8) (NDH-1, chain 8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.6%; Score 7; DB 1; Length 342; Best Local Similarity 100.0%; Pred. No. 50; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP (POTENTIAL).
D2F9290E84079BA5 CRC64;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
RUVB OR RP386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR003593; AAA_Arpase.
Interpro; IPR003959; AAA_Arpase_centr.
Interpro; IPR004605; RuvB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NP_BIND 57 64 A
SEQUENCE 342 AA; 38435 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ235271; CAA14843.1;
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                                                                                                                                                               Rickettsia prowazekii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                            NCBI_TaxID=782;
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P29920;
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ID NGO8_PV
AC P29920
DT 01-APR
DT 15-JUL
DE NADH-U
DE Gebydr
GN NGO8.
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EMBL outstation

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                                                                                                                                                                                                                   Gaps
                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypotherical 41.2 KDa protein in RPS4A-BAT2 intergenic region.
YJR147W OR J2204.
                                                                                                                                                                                                                                                                                                                                                                           Length 345;
                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: BELONGS TO THE HSF FAMILY.
                                                                                                                                                                                                                                                                                                                                                        E33B667E569506B4 CRC64;
                                                                                                                                                                                                                                                                            NAD; Ubiquinone; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                          DB 1;
. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 AA.
                                                                                                                                                                                                                                                                                                                                                                         Score 7; DB 1.
Pred. No. 50;
0; Mismatches
                                                                                                                                                                                                                                                                                                              POTENTIAL. POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                 Pfam; PF00146; NADHdh; 1.
PROSITE; PS00667; COMPLEXI_NDI_1; 1.
PROSITE; PS00668; COMPLEXI_NDI_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                  PIR; C45456; C45456.
InterPro; IPR001694; Resp_NADH_dhl.
                                 SEQUENCE FROM N.A.
STRAIN-ATCC 13543;
MEDLINE=93136200; PubMed=8422400;
                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                         0.6%; 3
                                                                                                                                                                                                                                                                                                                                                        38751 MW;
                                                                                                                                                                                                                          EMBL; L02354; AAA25592.1; -.
                                                                                                                                                                                                                                                                                                                                                                                           7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                              102
135
181
210
273
298
329
                                                                                                                                                                                                                                                                                                                               253
278
309
345 AA;
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            671 PFLSMML 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                              Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                             88 PFLSMML 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scarcez T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YJ9L_YEAST
P47175;
                                                                                                                                                                                                                                                                                                       TRANSMEM
TRANSMEM
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TRANSMEM
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YJ9L_YEAST
                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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InterPro; IPR002684; Biotin_synth.
Pfam; PF01792; Biotin_synth; 1.
TIGRFAMS; TIGR00433; bioB; 1.
Biotin blosynthesis; Iron-sulfur; Transferase; Complete proteome.
METAL 88 88 IRON-SULFUR (POTENTIAL).
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the Swiss Institute of Bioinformatics and the
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Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBL_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Dasted)
15-JUL-1998 (Rel. 36, Dast sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Biotin synthase (EC 2.8.1.6) (Biotin synthetase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.6%; Score 7; DB 1
100.0%; Pred. No. 52;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z49646; CAA89680.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
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P73538;
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BIOB_SYNY3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                 0;
                                                                                                                                  Query Match

O.6%; Score 7; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels
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01-NOV-1997 (Rel. 35, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical 41.9 KDa protein C05D10.4 in chromosome III.
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Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 SAM DOMAIN.
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   IRON-SULFUR (POTENTIAL).
IRON-SULFUR (POTENTIAL).
BF7A16FB1CBC68B4 CRC64;
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SEQUENCE 371 AA; 41906 MW;
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Result No.	Score	Query	Query Match Length DB ID	DB	QI.	Description
-	3731	100.0	3731	22	AAD04370	Tomato RNA-directe
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S	987.8		3737	21	AAC63739	Maize RNA-directed
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## ALIGNMENTS

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New nucleic acid molecules encoding polypeptides with RNA-directed RNA polymerase enzymatic activity, useful in modulating gene expression in plants, humans and animals, as well as in plant cell/tissue cultures or plant breeding
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Q Sequence 3731 BP; 1064 A; 669 C; 849 G; 1149 T; 0 other;
Query Match 100.0%; Score 3731; DB 22; Length 3731;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3731; Conservative 0; Mismatches 0; Indels 0; Gaps

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540 900 099 240 240 300 300 360 360 420 420 480 480 900 99 120 120 180 180 Gaps 9 9 GTTGTGATAATAAATTTGGTTGTGCTTCAGTTTCAGTCACTACTGCTGGGTAGTTTTTAT GGAAGTGGTTAAGTCATTCTTAGAGAAATATACAGGATATGGAACTGTATGTGCATTGGA GGTTAAACACTCCAAAGGAGGATCTACAGCATTTGCCAAAGTTCAATTTGCCGACAACAT GGTTAAACAGTCCAAAGGAGGATCTAGAGCATTTGCCAAAGTTCAATTTGCCGACAACAT GAAGGCTTGGGAAATGAAAACTGATATTGTCCAACTGCGGGCATATGTGGATCAGATGGA TGGCATAACTTTGAATTTCGGATGTCAGATATCAGATGACAAGTTTGCAGTGTTGGGAAG TGGTTCAGCTGACTATAAACTTCAGCTTTCATATGAAAATATATGGCAGGTTGTGCTCCA 121 TITGCATAACTICAGGGGGTATICCAGTIGGTGTTAGCATTIGAAAGTCGAACTGCACTI TITGCATAACTICAGGGGGTATICCAGIIGGTGTIAGCATITGAAAGICGAACIGCACIT GGAATTTGGCTACATGGGAAAGACAATTCAGGTTTTCGGATTCCCTTATCTTCTCTGC AAGTGCTGACAAAATCATCACTTTGGCTAATAACAGGCTGTATTTTGGCTCTTCTTATTT GAAATATTCTTTACTTCACCAGGGATTGACTCATCACTCCCCTCAAGTCTTGTGT 3731; Conservative Best Loca Matches 541 121 361 481 481 541 ч 61 61 181 181 241 241 301 301 361 421 421 601 601 do cy ob oy g Qy Db 0.y 0.y g ò δ g ŏ qq ò a οy

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           GCCGGACAAGACCAGCTATATCTCAGAAAGAGTTATTGGAAAGCTTTTCAGGAAAGTGAA
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This sequence represents a cDNA encoding the tomato RNA-directed RNA polymerase (RdRP) protein of the invention. The invention comprises the nucleic acid and protein sequences of RdRP. The protein of the invention can catalyse in vitro transcription of short single stranded RNAs into can catalyse in vitro transcription of short single stranded RNAs into DNA molecules, this transcription can be either primed by RNA or DNA oligonuclectides or be unprimed. The protein may have cytostatic or virucide activities. The sequences of the invention may be used in gene therapy or as an RNA directed RNA synthesis inhibitor. The RdRP CDNA sequence and a template nucleic acid molecule which causes a disease are useful for treating a disease caused by the undesired expression or overexpression of a nucleic acid molecule which causes a disease are useful for treating a disease caused by the undesired expression or overexpression of a nucleic acid molecule in human fraction molecule farived from a nucleic acid and for inhibiting expression of any desired gene by transferring the system can be used in the preparation of a pharmaceutical composition and for inhibiting express their own RdRP. An antibody or an antagonist or inhibitor to the protein are useful for inhibiting RNA directed RNA control of gene expression, as primers for amplification of nucleic acid molecules and as tools for the detection of expression of nucleic acid molecules and as tools for the detection of expression of undesired gene expression in humans and animals and protein sequences are useful for inhumans and animals and the antibody is useful for inhumans and animals and the antibody is useful for inhumans and animals and the antibody is useful for immunoprecipitation or immunolocalisation of the protein, identification in inhumans and enhanced and the antibody is useful for immunoprecipitation or infancting with it and screening expression libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid molecule encoding a polypeptide having the enzymatic activity of RNA-directed RNA polymerase, for modulating gene expression and treating cancer and virus infection in human and animals
Tomato, RdRP; RNA-directed RNA polymerase; in vitro transcription; eytostatic; virucide; RNA synthesis inhibitor; antibody; immunogen; transgenic plant; transgenic antimal; cancer; viral infection; immunoprecipitation; immunolocalisation; ss; gene therapy.
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This sequence represents a cDNA encoding the tomato RNA-directed RNA colymerase (RdRP/HF) of the invention. The invention comprises the nucleic acid and protein sequences of RdRP. The protein of the invention can catalyse in vitro transcription of short single stranded RNAs into can catalyse in vitro transcription can be either primed by RNA or DNA oligonucleotides or be unprimed. The protein may have cytostatic or virucide activities. The sequences of the invention may be used in gene therapy or as an RNA directed RNA synthesis inhibitor. The RdRP cDNA sequence and a template nucleic acid molecule derived from a nucleic acid molecule which causes a disease are useful for treating a disease caused by the undesired expression or overexpression of a nucleic acid molecule which causes a disease are useful for treating a disease caused by the undesired expression or overexpression of a nucleic acid molecule in a human, rat or mouse, by administering the molecules. This system can be used in the preparation of a pharmaceutical composition and for inhibiting expression of any desired gene by transferring the system to organisms that either lack a comparable mechanism or do not sufficiently express their own RdRP. An antibody or an antagonist or inhibitor to the protein are useful for inhibiting RNA directed RNA synthesis and for ensuring stable heterologues, gene expression in transgenic organisms. The sequence is useful for probes and/or for the control of gene expression, as primers for amplification of nucleic acid molecules and as thorapeutic agent for the control of senera and virus control of gene expression in humans and animals and protein sequences are useful for infection in humans and animals and the animody is useful for infection in humans and animals and the animody is useful for infection in humans and animals and animals and protein sequence shown in the specification but was created by the indexer from the wild type RdRP sequence shown in the specification and the protein sequence is not shown in the
                                                                                                                                                                New nucleic acid molecule encoding a polypeptide having the enzymatic activity of RNA-directed RNA polymerase, for modulating gene expression and treating cancer and virus infection in human and animals \phantom{a}
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99.7%; Score 3721.4;
Best Local Similarity 99.8%; Pred. No. 0;
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QQ	oy Db	oy B	Qy Db	Qy Db	Qy Dp	Oy Dp	QY	oy Op	Qy Dp	Qy Dp	oy Db	QY Db	Qy Dp	Sy Op Op	oy Ob	Qy Dp	Qy Dp	Qy

2460 2460 1860 1860 1920 1980 2100 2100 2160 2160 2400 GGTTCATGGAACCAGCTATGTCTTTTCTGATGGAATTGGTAAAATATCTGGTGACTTTGC TGGTGGATATAAAGGTGTTGTGGGGTGTTGATCCGGATTCATCAATGAAGTTGTCTTTGAG ATATCAGCCTTGTTATCTTAATCGTCAACTGATTACGCTCTTGTCTACACTTGGAGTGAA TAATAACAGCAGATCCACCAACAGTAATTTCATTCTGAAGGGAAATGTGGTTGTTGCAAA AAGTGGTGTCAGGACAAACATCTATGAGGATCTTATCAACTCTGCGGAAAGGCTTTGT AATTGGTGATAAAAATTTGAATTTCTTGCATTTTCATCGAGCCAGTTGCGGGATAATTC AGTGTGGATGTTTGCATCAAGACCTGGCCTTACTGCAAATGATATAAGAGCTTGGATGGG TICCTCCAGAGAGTTTTGAGTGTTCTTAGGCATGAGATTGAAGTTATTCCCGATGTAAA TCATAGAGTTGCCTCAAAATGTGGCCCTTCAATATACCCCCATCTGCTTTCCAGATTCGTTA TGGTGGATATAAAGGTGTTGTGGGTGTTGATCCGGATTCATCAATGAAGTTGTCTTTGAG AGATGAAGTTCTCGAACAGAAGCAAAAGGAAGCTGTAGATCAGCTTGATGCTATCTTGCA GITGCAAACCTTCCGCGCATCCAAGTTGCTCGATTTGCGGACTAGATCAAGAATATTAAT TCCAAATGGAAGAACAATGATGGGATGTTTGGATGAATCCAGAACCTTGGAATATGGTCA GGTGTTTGTTCAGTTTACTGGTGCTGGACATGGAGAGTTTTCTGACGATTTACATCCATT GGTGTTTGTTTCAGTTTACTGGTGCTGGACATGGAGAGTTTTCTGACGATTTACATCATT 2101 1441 1621 1681 1741 1741 1801 1861 1921 1981 1981 2041 2041 2221 2281 2341 1501 1561 1561 1621 1681 1801 1861 1921 2101 2161 2161 2221 2281 2341 2401 2401 2461 2461 1501 07 07 07 08 g q o O δ 원 상 원 Q Db Ω g δŽ 음 δ g ò φ

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GCACCACATGGTAGATTGTGTTTTCCCTCAGAAAGGAAAAGACCTCATCCGAATGA
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                                                                                                                                                                                                                                   Soybean RNA-directed RNA polymerase FIS contig, SEQ ID NO:
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gene marker; plant virus resistance; plant breeding; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sakai
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for controlling gene expression and
plant virus resistance
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۷9 ط	371	AAAATCATCACTTTGGCTAATAACAGGCTGTATTTTGGCTCTTGTTATTTG 421	
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Qy Db	918	TTCGAGGAAAGTTTTTTCCACTATGCAGAACGTGAAACAATATTACTTTACAGACTGGT 928	8 7
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QY	989	10	48 91
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Qy Db	1109	GCATGCATTGAGCATGCCTTAGAGAAACTGTACTATATAAAGGAGTGCTGTTATGATCCC 116	68
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Qy Db	1289	AAAGTTTATTTTGTGGTCCAGAGGTTAATGTTTCCAATCGGGTTCTCCGCAATTATTCT 13 	48
Qy Db	1349	GAAGACATAGADAACTITCITCGIGITTCITITGITGADGAGGAGTGGCAGAAACIGTAT 14(	08 51

1816 2102 2176 2222 2282 2402 ICTACAGACTTATTACCAAAAGCAAGTACTGGAAGTGGTGTCAGGACAAACATCTATGAG 1468 CTTAGGCATGAGATTGAAGTTATTCCCGATGTAAAG------GTTCATGGAACCAGC 1743 CATAGGGATGAAGTTGAAATTATTCCTGATGTGAAGAAGCTTACATATGATGGAAACGAA **ACCAACAGTAATTTCATTCTGAAGGGAAATGTGGTTGTTGCAAAAAATCCATGCTTGCAT** 1586 GGCCTTACTGCAAATGATATAAGAGCTTGGATGGGTGATTTTTCGCAGATCAAGAATGTC AAAAAACAAAGAGAAACTGTTAATCAACTGAACACTATACTAACAGATTCATTAAAGGCT AACTGTGGTTATAAGCCTGATGCTGAGCCCTTTCTTTCAATGATGTTGCAAACCTTCCGC ACTEGTGCTGGACATGGAGAGTTTTCTGACGATTTACATCCATTTAATAACAGCAGATCC GCATTTTCATCGAGCCAGTTGCGGGATAATTCAGTGTGGATGTTG----CATCAAGACCT 1623 GGAIGIACIGCITACAIAAGGAAAIGGAIGGGAAAIITIAGCCAGAITAGGAAIGII 1646 GCAAAATATGCTGCCAGACTTGGTCAATCTTTTGGTTCCTCCAGAGAGACTTTGAGTGTT TATGTCTTTTCTGATGGAATTGGTAAAATATCTGGTGACTTTGCTCATAGAGTTGCCTCA CTTAATCGTCAACTGATTACGCTCTTGTCTACACTTGGAGTGAAAGATGAAGTTCTCGAA CAGAAGCAAAAGGAAGCTGTAGATCAGCTTGATGCTATCTTGCATGATTCTTTGAAGGCA CAGGAGGCTTTGGAATTGATGTCTCCTGGAGAGACACTAATATTCTCAAGGCAATGCTA 1452 TCAACTGATTTATCATCACGTTCACAGA------ACAAGAAAACTGAGATATACACC AAATGTGGCCTTCAATATACCCCATCTGCTTTCCAGATTCGTTATGGTGGATATAAAGGT **AGGATCTTATCAACTCTGCGGAAAGGCTTTGTAATTGGTGATAAAAAATTTGAATTTCTT** 1706 1817 1863 1923 1983 2043 2103 2163 2177 2343 2403 2451 1469 1503 1529 1757 1877 1937 1997 2057 2223 2237 2283 2297 2357 1409 ΩD ά g õ g ŏ g δý 셤 Qγ Q ò g QY Db οy C Q Q Q D οy g Sy 셤 à 유 òγ 셤  $\overset{\circ}{\partial}$ a ò g ò 셤

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for controlling gene expression and providing mechanisms to engineer
plant virus resistance
                                                                                 RNA polymerase; expressed sequence tag; plant virus resistance; plant breeding;
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Matches 1997; Conservative
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                                                                                                                                           New nucleic acid fragments encoding RNA-directed RNA polymerase useful for controlling gene expression and providing mechanisms to engineer plant virus resistance
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The present sequence encodes a plant SGS2 polypeptide. SGS2 is an RNA-dependent RNA polymerase and is involved in transgene silencing. Inactivation of SGS2 is used to increase transgene stability and expression in plants, particularly crop plants, especially maize, corn, barley, sorghum, soya, sugar cane, beet, tobacco or cotton plants. Overexpression of SGS2 can be used to increase resistance to viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A new plant SGS2 gene involved in encoding an RNA-dependent RNA polymerase and in transgene silencing, increases transgene stability and expression in transgenic plants when it is inactivated -
                                                                                                                                                                                                3195 rcgagrecrigecadrecaagrecrcarardaacacaacreaacrecrcrecraa 3254
                                                                                                                              3135 ACATCTAACAATGCGGCTTATGATGGAGAAGTTGGAAGTTGCTGGTGGTGGTGGTGATTTGTC
CCAGACTTCATGGATAAGCCGGACAAGACCAGCTATATCTCAGAAAGAGTTATTGGAAAG
                         corcacineargeaaageageargerarcecraragarcagagaagarcerregaage
                                                      CTTTTCAGGAAAGTGAAGGACAAAGCACCTCAGGCTAGCTCTATCGCGACCTTCACAAGA
                                                                          3044 GATGTTGCAAGGAGATCATATGATGCTGATATGGAAGTTGATGGATTTGAAGATTACATT
                                                                                                                                                                       GACGAAGCTTTTGACTACAAAACTGAATATGACAACAAGCTGGGTAATTTAATGGACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                              SGS2; RNA-dependent RNA polymerase; transgene silencing; transgene stability; crop plant; viral resistance; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of a plant SGS2 polypeptide
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10; 2005 2066 2126 2182 1648 1718 1708 1832 2006 2065 2125 2242 1478 ATACCCCATCTGCTTTCCAGATTCGTTGGTGGATATAAAGGTGTTGTGGGTGTTGATC 1892 CCAATCGGGTTCTCCGCAATTATTCTGAAGACATAGATAAACTTTCTTCGTGTTTTTTG 1382 TAAGAAGGGTCCTAGTAACACCATGCAAAGTTTATTTTTGTGGTCCAGAGGTTAATGTTT 1322 Gaps **ACAACATAAAGTTAGATGTCCTTGGATGGAGCAAATATCAGCCTTGTTATCTTAATCGTC AACTGATTACGCTCTTGTCTACACTTGGAGTGAAAGATGAAGTTCTCGAACAAGAAGAAA** ATAAGCCTGATGCTGAGCCCTTTCTTTCAATGATGTTGCAAACCTTCCGCGCATCCAAGT CCAGACTTGGTCAATCTTTTGGTTCCTCCAGAGAGACTTTGAGTGTTCTTAGGCATGAGA TGGAATTGATGTCTCCTGGAGAGAACACTAATATTCTCAAGGCAATGCTAAACTGTGGTT CAGATATAAAAACATGGGTGGGGAAGTTCAAAGA---CAAGAATGTGGCAAAATGTGCTG GTAAAATATCTGGTGACTTTGCTCATAGAGTTGCCTCAAAA-----TGTGGCCTTCAAT TTGATGAGGAGAGAAACTGTATTC------TACAGACTTATTACCAAAA GCAAGTACTGGAAGTGGTGT-------CAGGACAAACATCTATGAGAGGATCTTAT ATGATATAAGAGCTTGGATGGGTGATTTTTCGCAGATCAAGAATGTCGCAAAATATGCTG 57; Length 3591; Score 305.8; DB 22; Length
Pred. No. 3.2e-73;
0; Mismatches 917; Indels h 8.2%; Similarity 51.0%; 13; Conservative ( Query Match Best Local Simi Matches 1013; 1719 1709 1779 1766 1833 1826 1893 1886 1946 2006 2067 2066 2127 2126 1232 1479 1592 1649 2007 1263 1383 1430 1472 1539 1532 1599 1659 1323 1292 oy Oy g QΫ́ g QΥ g DP OX g οy Dp

2419 2546 2779 2839 2900 2959 2599 CTAGCTCTATCGCGACCTTCACAAGAGATGTTGCAAGGAGATCATATGATGCTGATATGG AAGTIGAIGGATTIGAAGATTACATTGACGAAGCTTTTGACTACAAAACTGAATATGACA ACAAGCTGGGTAATTTAATGGACTACTATGGCATAAAAACAGAGGCTGAAATACTTAGTG TGCTCGATTTGCGGACTAGATCAAGAATATTTATTCCAAATGGAAGAACAATGATGGGAT -GTCTATAGAAAATTGTTTCTCCAAACATGGGTCTCGTTTTAAGGAGACAAAGAAGATG TTCGTGTTTTAAAGGCTGTAAATGTTCGAGCGCTGCACCACATGGTAGATTGTGTAT CGATGGAATATCCTCCAGCACCCAGCATACAGTTGGACCATGATGTCACAATTGAGGAAG TTGAAGAGTACTTCACCAACTATATTGTGAATGACAGTTTGGGAATCATAGCAAATGCCC CTGAGCTCTTTTCAATTGCAGTGGACTTTCCAAAGACTGGTGTTCCCGCTGAAATACCAT GACATGGAGATTTTCTGACGATTTACATCCATTTAATAACAGCAGATCCACCAACAGTA GTGGCAT 3204 2780 2960 3138 3140 2540 2600 2661 2660 2721 2720 2781 2840 2901 2961 3018 3020 3078 3198 2361 2420 2607 2247 2243 2307 2303 2367 2427 2487 2547 g Óγ 90 00 00 00 δŽ QQ δŸ g δ a δ οy οy g qq Q Dp 07 07 08 08 09 95 P οy

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                                                        Rice, plant; RNA-directed RNA polymerase; FIS; gene mapping; gene marker; plant virus resistance; plant breeding; ss.
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                                     Rice RNA-directed RNA polymerase FIS sequence, SEQ ID NO:
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                                                                                                                                                                                   (DUPO ) DU PONT DE NEMOURS & CO (PION-) PIONEER HI-BRED INT INC.
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1054 1351 1411 2327 2387 1294 2447 2507 2567 1471 2627 2147 2207 2267 δŽ g QY Db OY Db οy g δy qq οy g δ ద ò 10; 1440 TITGIAATIGGIGATAAAAAITIGAAITICITGCAITITCAICGAGCCAGTIGCGGGAI 1555 AAITGAGIGGAIGGIIGGAICGACGAGGCCIGGCCITACIGCAAAIGAIGAIAAGAGCIIGG 1615 AATTAITCIGAAGACATAGATAACTITCTTCGIGTITCTTTGTIGATGAGGAGIGGGAG 1399 CCAAAATCTCCGTCCATCACTTTAGATGATGGGTTGGTATGTAAGAAGGGTCCTAGTA 1279 1280 ACACCATGCAAAGTTTATTTTTGTGGTCCAGAGGTTAATGTTTCCAATCGGGTTCTCCGC 1339 Gaps GIGCTGAACAACAATGIGCTCAACICCTTCACIGCACCAATIGICAAAGACIIGAIGICG 1441 AAGTGGTGTCAG-----GACAAACATCTATGAGAGGATCTTATCAACTCTGCGGAAAGGC 1400 AAACTGTA-------TTCTACAGACTTATTACCAAAAGCAAGTACTGG 8.2%; Score 304.2; DB 21; Length 2816; llarity 50.6%; Pred. No. 7.7e-73; Conservative 0; Mismatches 944; Indels 57; BP; 782 A; 572 C; 725 G; 736 T; 1 other; Best Local Similarity Matches 1027; Conserv

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TITGCICATAGAGITGCCICAAAATGIGGCCTICAATATA---CCCCAICTGCTITCCAG 1852 ATGGGTGATTTTTCGCAGATCAAGAATGTCGCAAAATATGCTGCCAGACTTGGTCAATCT 1675 GATCAAGACATGATCCCGCCA-----AGGCAAGTCCAGCCGATGGAATATCCTCCAGCA GTGGTTGCTAAAAAATCCATGCTTGCATCCTGGTGATATTCGTGTTTTAAAGGCTGTA GATGCTATCTTGCATGATTCTTTGAAGGCACAGGAGGCTTTGGAATTGATGTCTCCTGGA TTTCTTTCAATGATGTTGCAAACCTTCCGCGCATCCAAGTTGCTGATTTGCGGACTAGA TTGGAATATGGTCAGGTGTTTGTTCAGTTTACTGGTGCTGGACATGGAGAGTTTTCTGAC GATTTACATCCATTTAATAACAGCAGATCCACCAACAGTAATTTCATTCTGAAGGGAAAT AAGCATGGGTCAAGATTTTCATCAACAGATAAAAACACAGAGGTCATTTT---GGGTACT ATTCGTTATGGTGGATATAAAGGTGTTGTGGGTGT-----TGATCCGGATTCATCAATG **ACACTTGGAGTGAAAGATGAAGTTCTCGAACAGAAGCAAAAGGAAGCTGTAGATCAGCTT** GAGAACACTAATATTCTCAAGGCAATGCTAAACTGTGGTTATAAGCCTGATGCTGAGCCC **TCAAGAATATTTATTCCAAATGGAAGAACAATGATGGGATGTTTGGATGAATCCAGAACC** AAGTCAGCTTGGTTCTTTGCCGAGGACAGAAGACAACGGTGGAAGCAATTAGGAAGTGG TITGGTTCCTCCAGAGAGACTTTGAGTGTTCTTAGGCATGAGATTGAAGTTATTCCCGAT GTAAAGGTTCATGGAACCAGCTATGTCTTTTCTGATGGAATTGGTAAAATATCTGGTGAC CTIGGAIGGAGCAAATAICAGCCTIGITATCITAAICGICAACIGAITACGCICTIGICI ATGGACGGTTCACAAGTAAGAATGTTCG-----AAGATGCTGCTCGAATGGGGGCAGTGC **AAGTTGTCTTTGAGAAAGAGCATGTCGAAATATGAATCAGACAACATAAAGTTAGATGTC** 1531 1616 1676 1736 1796 1853 757 1907 1967 2027 937 466 526 580 640 697 817 877 2087 697

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                                                                                                                                                                                                                Length 1281;
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                             Sequence 1281 BP; 359 A; 282 C; 299 G; 338 T; 3 other;
                                                                                                                                                                                                              Score 282; DB 21;
Pred. No. 6.7e-67;
0; Mismatches 533;
                                                                                                                                                                                                                Query Match 7.6%;
Best Local Similarity 55.1%;
Matches 687; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid fragments encoding RNA-directed RNA polymerase useful for controlling gene expression and providing mechanisms to engineer plant virus resistance
                                                                                                                                       TICITIATIACTIGGGAIGACAAACIGAITCCGGAGAAGGIIGAIGCACCIAIGGACIAC 1015
                                                                                                                                                                                                                                   IACTITGIITGCTGGGATCAAGACATGATCCCGCCAAGGCAAGTCCAGCCGATGGAATAI 2671
                               CAGAAAGGAAAAAGACCTCATCCGAATGAATGTTCTGGGAGTGATTTGGATGGGGGATATC 2611
                                                                                                                                                                       ITCACCAACTATATTGTGAATGACAGTTTGGGAATCATAGCAAATGCCCATGTCGTATTT 2791
                                                                                                                                                                                                                   GCAGACAGAGAACCTGATATGGCCATGAGTGATCCATGCAAAAAACTTGCTGAGCTCTTT 2851
                                              Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA-directed RNA polymerase; expressed sequence tag; gene marker; plant virus resistance; plant breeding;
                                                                                                                           CCTCCAGCACCCAGCATACAGTTGGACCATGATGTCACAATTGAGGAAGTTGAAGAGTAC
                                                                                                                                                                                             1076 TTCGTCAGTTACATGATAAACGATACCCTCGGTGCCATCTCCACCGCCCACTTGATCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           r)
                                                                                                                                                                                                                                                                                                                                                                                                                   Maize RNA-directed RNA polymerase EST contig, SEQ ID NO: 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang
                                                                                                                                                                                                                                                                            1196 TCCATGGGGGTCGACTTCGCCAAGACGGGAGCTCAGCCCCAAGATTCC 1242
                                                                                                                                                                                                                                                                 TCAATTGCAGTGGACTTTCCAAAGACTGGTGTTCCCGCTGAAATACC 2898
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P-PSDB; AAB28534.
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gene mapping;
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                                                                                                                                                                                        GTICAACIGGCCAAGCICITCICIAIAGCIGICGAITTCCCAAAGACIGGAGTGCCGGCT 121
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                                                                                                                                                         2831 AAAAAACTTGCTGAGCTCTTTTCAATTGCAGTGGACTTTCCAAAGACTGGTGTTCCCGCT
                                                                                                                                                                                                                                                                                                          CTGATTCCACATGAGCTACATGTCAAGGAGTATCCTGACTTCATGGAGAAACTCGACAAA
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                                                                                                                                                                                                                                                                                                                                                        CCTCAGGCTAGCTCTATCGCGACCTTCACAAGAGATGTTGCAAGGAGATCATATGATGCT
                              740:
                           Score 276.2; DB 21; Length
Pred. No. 2e-65;
0; Mismatches 231; Indels
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transgene stability; crop plant; viral resistance; ss.
Sequence 740 BP; 217 A; 141 C; 205 G; 166 T; 11 other;
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                                7.48;
64.28;
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                                               Similarity 64.2
11; Conservative
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                                                                Matches 451;
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promoter
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Best Local
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2441 CAGATATAAAAACATGGATGGGGAAGTT---CAAAGACAAGAATGTGGCAAAATGTGCTG
                                                                                                                                       1779 GTAAAATATCTGGTGACTTTGCTCATAGAGTTGCCTCAAA*----TGTGGCCTTCAAT
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                                       CCAGACTTGGTCAATCTTTGGTTCCTCCAGAGAGACTTTGAGTGTTCTTAGGCATGAGA
                                                                           CTAGGATGGGCCTGTGCTTCTCCTCCACATATGCCACTGTAGATGTCATGCCTCACGAGG
                                                                                                                  TIGAAGITATICCCGAIGTAAAGGIICAIGGAACCAGCIAIGICITITCIGAIGGAAIIG
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ABL71773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes a plant SGS2 polypeptide. SGS2 is an RNA-dependent RNA polymerase and is involved in transgene silencing. Inactivation of SGS2 is used to increase transgene stability and expression in plants, particularly crop plants, especially maize, corn, barley, sorghum, soya, sugar cane, beet, tobacco or cotton plants. Overexpression of SGS2 can be used to increase resistance to viral infection in plants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAATCGGGTTCTCCGCAATTATTCTGAAGACATAGATAACTTTCTTCGTGTTTCTTTG 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1383 TTGATGAGGAGTGGGAGAACTGTATTC-----TACAGACTTATTACCAAAA 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAACTCTGCGGAAAGGCTTTGTAATTGGTGATAAAAATTTGAATTTCTTGCATTTTCAT 1538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCATATTAACCGATGGGTTTAAACTATGTGGTAGAAAATACAGTTTTCTAGCATTCTCAG 2380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A new plant SGS2 gene involved in encoding an RNA-dependent RNA polymerase and in transgene silencing, increases transgene stability and expression in transgenic plants when it is inactivated -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1263 TAAGAAGGGTCCTAGTAACACCATGCAAAGTTTATTTTTGTGGTCCAGAGGTTAATGTTT 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2141 CCAACAGGGTACTCAGGAGATACAAAGCTGTTGCTGAAAGATTTTTGCGGGTAACTTTCA 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGGAIGAAAGIAIGCAGACCAIAAAIICGAAIGIICICICIITACIIIGIIGCICCIAIIG 2260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2261 TGAAGGATTTGACATCAAGTTCTTCTCCCAGAAGACCTACGTTTTTAAAAGAGTGAAGA 2320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGAGCCAGTIGCGGGAIAAITCAGIGIGGAIGTITGCAICAAGACCIGGCCTIACIGCAA 1598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 220.4; DB 22; Length
Pred. No. 1.4e-49;
0; Mismatches 641; Indels
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                                                                                                                                                                                                                                                                                                                                                                                             (RHOB-) RHOBIO.
(INRG ) INST NAT RECH AGRONOMIQUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Page 30-32; 46pp; French
                                     /number="1"
3565..3986
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4863..6863
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Best Local Similarity 51.5%;
Matches 733; Conservative (
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                                                                                                                                                                                                                                                                                                                26-JAN-2000;
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The present sequence describes a purified corn tassel-derived polynucleotide sequence (cdps) comprising a nucleic acid sequence colynucleotide sequence (cdps) comprising a nucleic acid sequence selected from those given in ABL/10627 to ABL/6833. The cdps sequences cencede corn tassel-derived polypeptides (CDPs). The cdps sequences (can be used for determining altered gene expression, to recover regulatory elements and to follow inharitance of desirable characteristics through hybrid breeding programs. (I) are also useful characteristics through hybrid breeding programs. (I) are also useful in the evaluation, and alteration of desired characteristics associated with growth and development, disease resistance, environmental adaptability, quality and yield, and as molecular markers for studying inheritance of multigene traits in a plant breeding program. (I) can be used to produce a tassel-specific profile of gene transcription, a can be used to produce a tassel-specific profile of gene transcription, a lemantes, in nucleic acid sequences from DNA increases a polypeptide, to identify, isolate or extend infanties, in nucleic acid hybridisation or amplification technologies, as query sequences to determine hybridisation, and to identify the for use in Southern or Northern hybridisation, and to identify the presence of and/or to determine the degree of similarity between two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid
2560 AAAAAGACCTCATCCGAATGAATGTTCTGGGAGTGATTTGGATGGGGATATCTACTTTGT 2619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polynuclectide; cdps; hybrid breeding; CDPs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inheritance; characteristic; growth; development; disease resistance; environmental adaptability; quality; yield; molecular marker; multigene trait; plant breeding; corn tassel; gene; ss.
                            134 TGAGAGGCCGCACGCGAATGAAGCATCTGGGAGTGATCTTGATGGGGATCTAGATCTTGT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 24; Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel purified corn tassel-derived polynucleotide useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corn tassel-derived polynucleotide (cdps) SEQ ID NO:1096.
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                                                                                                           2620 ITGCTGGGATCAAGACATGATCCCGCCAAGGCAA 2653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 95.4;
                                                                                                                                                           194 AACATGGGATGAAACCTTATACCACCTGGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID 1096; 201pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sherman BK;
                                                                                                                                                                                                                                                                                              ABL71722 standard; cDNA; 274
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                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tassel-derived
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LALG/) LALGUDI R V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SHER/) SHERMAN B K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-163647/21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-DEC-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                               Corn; corn tassel-derived polynucleotide; cdps; hybrid breeding; CDPs; inheritance; characteristic; growth, development; disease resistance; environmental adaptability; quality; yield; molecular marker; multigene trait; plant breeding; corn tassel; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel purified corn tassel-derived polynucleotide useful for
                                                                                                                                                                 Corn tassel-derived polynucleotide (cdps) SEQ ID NO:1147.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67;
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0; Mismatches
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        ABL71773 standard; cDNA; 282 BP
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                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-163647/21
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Matches 147; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          breeding programs
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                                                           ABL71773;
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(SHER/)
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2884 TCCCGCTGAAATACCATCTCAGTTGCGCCCTAAAGAATACCCAGACTTCATGGATAAGCC 2943
                                                                                                                                                                    2944 GGACAAGACCAGCTATATCTCAGAAAGAGTTATTGGAAAGCTTTTCAGGAAAGTG--AAG 3001
                                                                                                                                                                                                 122 TGACAAAACCACATACAAATCGCATAAACGTGATAGGAAAGCTCTTTAGGGAAGTGGAAAG 181
                                                                                                               63 TCCAGCTGTTATACCTCCTGAACTTATGTC-AAAGAATATCCTGACTTCATGGAGAAGNC 121
  3 ICAATGTGTTAAGCTTGCAAGGTTGTTTTCAACAGCAATTGACTTTCCTAAAACTGGNGT 62
                                                                                                                                                                                                                                                                              3002 GACAAAGCACCTCAGGCTAGCTCTATCGCGACCTTCACAAGAGATGTTGCAAGGAGA 3058
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                                                                                                                                                                                                                                                                                                        2620
                                                                            2447 GIGGIIGIIGCAAAAAICCAIGCIIGCATCCIGGIGAIAIICGIGIIIITAAAGGCIGIA 2506
                                                                                                                                                                                      2507 AAIGITCGAGCGCIGCACCACATGG-----TAGAIIGIGITGTAIICCCICAGAAAGGA 2560
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                                                                                                                                                                                                                                          62 TAIGACCCIGGAIIGGAIGCIAGGGGICITAIIGAIIGIGIIGIAIIICCICAGAGAGGG 121
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Best Local Similarity 65.4%; Pred. No. 3.4e-13;
Matches 155; Conservative 0; Mismatches 79; Indels 3; Gaps
                                6; Gaps
                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 ACTIGGGAIGACAAACIGAIICCGGAGAAGGIIGAIGCACCIAIGGACIACACIGCAAC 240
                                                                                                                     2 GTTGCAATCACAAAAAACCCTTGTCTCCATCCTGGTGATGTCAGAGTACTTGAAGCTGTA
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                             Indels
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65.7%; Pred. No. 6.9e-16;
iive 0; Mismatches 76;
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Best Local Similarity
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Soybean; plant; RNA-directed RNA polymerase; expressed sequence tag; EST;
gene mapping; gene marker; plant virus resistance; plant breeding; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weng Z, Sakai H, Cahoon RE, Wang J, Zhong G;
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182 AAATATCAACAAAGTGCCGGGGCAATTACATCCTTCACAAAATTGGTTGCGAGAAGA 238
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(PION-) PIONEER HI-BRED INT INC.
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US-09-740-029-3 53226 1275 11796 11796 11796 2004 2004 3003 397658 397658 11134 1138 3249 1134 1138 3248 3248 3248 3248 32248 32248 32248 32248 32248 32248 304 1537 8188 3831 42999 1867 00000000000000000000000 2002, 19:22:12 ; Search time 158 Seconds (without alignments) 7867.093 Million cell updates/sec US-09-782-874-1 3731 1 GAAATATTCTTTACTTACTT......AGTTTCATCTTCTTGTAAA 3731 5.1.3 Compugen Ltd. hits satisfying chosen parameters: 310279 seqs, 166577418 residues GenCore version Copyright (c) 1993 - 2002 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries nucleic search, using sw model IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Minimum DB seq length: 0 Maximum DB seq length: 200000000 2, November οţ Title: Perfect score: Scoring table: ı Total number OM nucleic Sequence: Searched: .. 0

Sequence 4, Appl Sequence 19, Appl Sequence 19, Appl Sequence 126, Appl Sequence 6, Appli Sequence 6, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 7451, Ap Sequence 7451, Ap Sequence 7451, Ap Sequence 23, Appli Sequence 623, Appli Sequence 623, Appli Sequence 623, Appli Sequence 12414, Ap Sequence 12414, Appli Sequence 12414, Appli Sequence 12414, Appli Sequence 12414, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli

## ALIGNMENTS

RESULT 1 US-09-782-874-1   US-09-782-874-1   Sequence 1, Application US/09782874   Patent No. US20010023067A1   Fatent No. US20010023067A1   GENERAL INFORMATION:   APPLICANT: Wassenegger, Michael   Schadel, Leonhard   Schadel, Winfried	TITLE OF INVENTION: MCCLEIC ACID MOLECULES ENCODING POLYPEPTIDES HAVING THE ENYMATIC ACTIVITY OF NA-DIRECTED RNA POLYMERASE (RdRP) CORRESPONDENCE ADDRESS: ADDRESSE: FISH & NEAVE STREET: 1221 Avenue of the Americas CITY. New York	COUNTRY: USA  ZIP: 10020  COMPUTER FRADABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: IBM PC compatible  OPERATING SYSTEM: PC-DOS/MS-DOS  SOFTWARE: Patentin Release #1.0, Version #1.30  CURRENT APPLICATION DATA:  PILING DATE: U8-FEb-2001  CLASSIFICATION: CIPROMEN: US/09/782,874	PRIOR APPLICATION DATA:  APPLICATION UNMER: US 08/811,583 FILING DATE: 05-MAR-1997 ATTORNEY/AGENT INFORMATION:  NAME: Haley, James F.  REGIESTRATION NUMBER: MG-1 TELECOMMUNICATION INFORMATION:  TELEPHONE: 212-596-900 TELEPAX: 212-596-900 TELEPAX: 212-596-900 INFORMATION EOR SEQ ID NO: 1:  SEQUENCE CHARACTERISTICS:  LENGTH: 3731 base pairs

AN

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Published_Applications_NN:*

1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NNW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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14: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*

Database

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SUMMARIES  Description	US-09-782-874-1 Sequence 1, Appl		10	,			Sequence			Sequence	Sequence 6,	6 Sequence 144	Sequence 412,			ι.		324	
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å Query Match	100.0	5.9	7.6	2.0	1.1	1.1	1.1	1.1	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
Score	3731	106.8	95.4	75	40.4	40.2	39.5	39.5	38	37.8	37.8	37.6	36.4	36.4	36.2	36	35.6	35.6	35.6
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                                                                      Score 3731; I
Pred. No. 0;
; Mismatches
                                                     ID NO: 1:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
CULE TYPE: CDNA
                                         NAME/KEY: CDS
LOCATION: 194..3535
SEQUENCE DESCRIPTION: SEQ
                                                                     Query Match

Best Local Similarity 100.0%;
Matches 3731; Conservative 0;
                      ORIGINAL SOURCE:
ORGANISM: Tomato
                  MOLECULE
                                   FEATURE
                                                          US-09-782-874-1
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GGTTCCCAATGTCCAGCCTCCGGAAGGAATTTCAATTCCCTACAAGATTTTGTTCAAAAT
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Patent No. US2001005133541

GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath, V.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN; FILE REFERENCE: PL-0009 US
CURRENT APPLICATION NUMBER: US/09/294,093B

CURRENT APPLICATION NUMBER: US/09/294,093B

CURRENT APPLICATION NUMBER: G0/082,567

PRIOR FILING DATE: April 21, 1998

NUMBER OF SEQ ID NOS: 6207

SOFTWARE: PERL PROGram

SEQ ID NO 1147

LENGTH: 282
                                                                                                                                                                                                                                                                                                                                                     ATATGATGCTGATATGGAAGTTGATGGATTTGAAGATTACATTGACGAAGCTTTTGACTA
            GGCTGAAATACTTAGTGGTGGCATTATGAAGGCATCAAAAACTTTTGACCGCAGAAAGA
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                                           CAAAACTGAATATGACAACAAGCTGGGTAATTTAATGGACTACTATGGCATAAAAACAGA
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NAME/KEX: misc_feature
OTHER INFORMATION: Incyte ID No. US20010051335A1 700343843H1
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ORGANISM: Zea mays
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TYPE: DNA

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1. OTHER INFORMATION: Clone ID: 700966775H1

US-09-878-574-10527
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SEQ ID NO 10527
LENGTH: 260
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Best Local Similarity
Matches 130; Conserva
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US-09-764-864-1673/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
FILE REFRENCE: PL-0009 US
CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR FILING DATE: April 21, 1998
NUMBER OF SEQ ID NOS: 6207
SOFTWARE: PERL PROGRAM

SEQ ID NO 1096
LENGTH: 274
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                                       DB 10; Length 282;
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; OTHER INFORMATION: Incyte ID No. US20010051335A1 700343770H1
US-09-294-093B-1096
                                          2.9%; Score 106.8; DB 10; Length 68.7%; Pred. No. 2.1e-19; Live 0; Mismatches 67; Indels
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Patent No. US20010051335A1
GENERAL INFORMATION:
APPLICANT:
Lalgudi, Raghunath, V.
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; Sequence 10527, Application US/09878574
; Patent No. US20020110548A1
                                                               Best_Local Similarity 68.79
Matches 147; Conservative
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US-09-294-093B-1147
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GENERAL INFORMATION:
APPLICANT: Bytum, Joseph R.
APPLICANT: Ta Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Plants
FITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
PRIOR RILING DATE: 2001-12-21
PRIOR FILING DATE: 1999-06-14
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Best Local Similarity 50.0%; Pred. No. 3.5;
Matches 101; Conservative 0; Mismatches 101; Indels 0;
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Patent No. US20020132753A1

GENERAL INFORMATION:

APPLICANT: ROSEN et al.

TITLE OF INVENTION:

FILE REFERENCE: PT223

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper;

NUMBER OF SEQ ID NOS: 1792

SOFTWARRE: Patentin Ver. 2.0

SEQ ID NO 1673

LENGTH: 23071
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1166 TAAGTGAGATCAATATTTGTTTGGAAAAAAATCTTGGGAAACAACCAAGGGTTTTCGC 1225
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                                                                                                                                                                                                                                                      220 AITCCCTTATCTTCTCTCTGCGGAAGTGGTTAAGTCAITCTTAGAGAAATATACAGGATA 279
                                                                                                                                                                                                                                                                                                                                                                                                  280 TGGAACTGTATGTGCATTGGAGGTTAAACAGTCCAAAGGAGGATCTAGAGCATTTGCCAA 339
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                                                                                                             160 TITGAAAGTCGAACTGCACTTGGAATTTGGCTACATGGGAAAGACAATTCAGGTTTTTCGG
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APPLICANT: Syskind, Judith W.
APPLICANT: Syskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Carr, Grant J.
APPLICANT: Tanamonto, Robert T.
APPLICANT: Yanamonto, Robert T.
APPLICANT: APPLICANT: Prokaryotes
TITLE OF INVENTION: Prokaryotes
FILE OF INVENTION NUMBER: 60/20/31
PRIOR APPLICATION NUMBER: 60/20,848
PRIOR FILING DATE: 2000-05-23
PRIOR PRILING DATE: 2000-05-23
PRIOR PRILING DATE: 2000-10-23
PRIOR PRILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PLILING DATE: 2001-02-16
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Pred. No. 1.7;
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APPLICANT: Haselbeck, Robert
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Best Local Similarity
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US-09-815-242-8362
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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: Acomica-x-1
CURRENT APPLICATION NUMBER: US 60/20/464,761
CURRENT PILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-04
PRIOR FILING DATE: 2000-09-04
PRIOR FILING DATE: 2000-09-04
PRIOR FILING DATE: 2000-09-04
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
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12651 TAAATTATTTTACAGATTGCAATTTCAAAGATTTACAACTATTTTATGGGAAAAHGCTTT 12592
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CTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.6
US-09-864-761-10600
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PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
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PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PILING DATE: 2001-01-30
PRIOR PLILNG DATE: 2000-09-21
PRIOR PLILNG DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                          Sequence 10600, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                        Db 12591 TTTTAATGATATTGAGGCTT 12570
                                                                        2210 CTTTCAATGATGTTGCAAACCT 2231
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Sequence 124, Application US/09952832
Sequence 124, Application US/09952832
Sequence 124, Application US/09952832
Sequence 124, Application US/09952832
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-74
CURRENT APPLICATION NUMBER: US/09/962,832
CURRENT FILING DATE: 2001-09-25
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Patent No. US200201025661
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL SPYROPOULOS, DEMETRI
APPLICANT: ROUGEULLE, CLAIRE
APPLICANT: AVNER, PHILLIP R.
TITLE OF INVENTION: IDENTIFICATION OF NEURAL DEFECTS ASSOCIATED WITH THE
TITLE OF INVENTION: NUCLEOSOMAL ASSEMBLY PROTEIN 112 GENE
TITLE OF INVENTION: 03495-0203-00000
CURRENT APPLICATION NUMBER: US/09/847,665
CURRENT FILING DATE: 2001-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1880 TACCTGGTATAAATTATAAAAGCAGAATATCTATATTGATCAAACCTTTATATTTCCTAA 1821
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                                                                                                                                                                                                                                                                               317 GGAGGATCTAGAGCATTTGCCAAAGTTCAATTTGCCGACAACATAAGTGCTGACAAAATC 376
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AAAACIGATATIGICCAACIGCGGGCATAIGIGGAICAGAIGGAIGGCATAACITIGA 494
                                                                                          573 TIGIGAGATAGATACACTATACGCAGCATATITCAATCATAATCATATGGTCATAATGC
                                                                                                                                                  3145 GGGTAATTTAATGGACTACTATGGCATAAAAACAGAGGCTGAAATACTTAGTGGTGGTG
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                                                  TGGATTTGAAGATTACATTGACGAAGCTTTTGACTACAAAACTGAATATGACAACAAGCT
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Pred. No. 6.4;
0; Mismatches 125; Indels
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PRIOR APPLICATION NUMBER: US/60/235,077

PRIOR FILING DATE: 2000-09-25

PRIOR FILING DATE: 2000-09-25

PRIOR FILING DATE: 2000-09-25

NUMBER: WS/60/235,280

SEQ ID NO 124

LENGRARE: PatentIn version 3.0

SEQ ID NO 124

LENGRH: 5191
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Best Local Similarity 47.5%;
Matches 113; Conservative
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US-09-962-832-124
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                                               2965 AGAAAGAGTTATTGGAAAGCTTTTCAGGAAAGTGAAGGACAAAGCACCTCAGGCTAGCTC 3024
                                                                                                                                                  TATCGCGACCTTCACAAGAGATGTTGCAAGGAGATCATATGATGCTGATATGGAGTTGA 3084
                                                                                                                                                                                                                                                  TGGATTTGAAGATTACATTGACGAAGCTTTTGACTACAAAACTGAATATGACAACAAGGT 3144
                                                                                                                                                                                                                                                                                  GAAAGAGTTAAGAGTAGATATTATTCTTGGTGATAAAAGATCCTATTAGAAT 692
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                                                                                                                                                                                               453 AAAAGAAGCTGTTGACGATTTTAATAGTGAAGTAAAAGAAATTCAATATAAAGAAAAGA 512
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                                                                                             453 AAAAGAAGCIGITGACGATITITAATAGTGAAGTAAAAGAAATTCAATATAAAGAAAAAGA 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Obligation, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Tranick, John D.
APPLICANT: Tranick, John D.
APPLICANT: Tranick, John D.
APPLICANT: Tranimorto, Robert T.
APPLICANT: Animomoto, Robert T.
APPLICANT: Xu, H. Boward
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: PROKARYOTES
FILE REPERENCE: ELITRA.011A
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
0; Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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PRIOR FILLING DATE: 2000-05-23
PRIOR FILLING DATE: 2000-05-23
PRIOR PILLING DATE: 2000-05-26
PRIOR PILLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/24,578
PRIOR FILLING DATE: 2000-10-23
PRIOR FILLING DATE: 2000-11-27
PRIOR FILLING DATE: 2000-11-27
PRIOR FILLING DATE: 2000-12-22
PRIOR FILLING DATE: 2000-12-22
PRIOR FILLING DATE: 2000-12-22
PRIOR FILLING DATE: 2001-20-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 4555
LENGTH: 2109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4555, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATON:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Staphylococcus aureus US-09-815-242-4555
Matches 137; Conservative
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-09-815-242-4555
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3380 AGAGGCCTGCATATAGATAAGAATTTCAGGCAAAACTACATTTATTGTTAATAACAGCTT 3439
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    3200 TAAGTGAGATCAATATTTGTTTGGAAAAAATCTTGGGAAACAACCAAGGGTTTTCGC 3259
                                                                                                                                                                                          1320 TTGTTGTCCTGCTTCATTTTGCAATAACAATGCAGTAGAATTTAAAACTTGGATGCTTA 3379
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                                                                                                3260 TGTTGTTGTTTTTCTTTTTTTTTTTTTTTTAGTCCTTTAGCCTAGTGGATTTAATT
                                                                                                                                             280 TGGAACTGTATGTGCATTGGAGGTTAAACAGTCCAAAGGAGGATCTAGAGCATTTGCCAA
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Sequence 1446, Application US/09974300
Sequence 1446, Application US/09974300
Sequence 1446, Application US/09974300
Sequence No. US20020146721A1
SEPTICANT: Berks, Randy M.
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Morbid For Monitoring Multiple Gene
CURRENT APPLICATION NUMBER: 09/080,598
FRIOR FILING DATE: 2001-10-05
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
SPRIOR PILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FRASEQ for Windows Version 4.0
SEQ ID NO 1446
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US-09-864-761-412/c
US-09-864-761-412/c
; Partent No. US20020048763A1
; GENERAL INFORMATION:
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US-09-974-300-1446
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US-09-974-300-1446
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Patent No. US20020102566A1
GENERAL INFORMATION:
APPLICANT: ROGNER, UTE
APPLICANT: ROGNER, UTE
APPLICANT: ROGNER, UTE
APPLICANT: ROGNER, UTE
APPLICANT: AVENUE, PHILP R.
ITLE OF INVENTION: IDENTIFICATION OF NEURAL DEFECTS ASSOCIATED WITH THE
ITLE OF INVENTION: NUCLESOSOMAL ASSEMBLY PROTEIN 112 GENE
FILE REFERENCE: 03495-0203-00000
CURRENT APPLICATION NUMBER: US/09/847,665
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/202,111
PRIOR APPLICATION NUMBER: 60/202,111
PRIOR APPLICATION NUMBER: 60/202,111
SEQ ID NO 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 TITGAAAGTCGAACTGCACITGGAAITTGGCTACATGGGAAAGACAAITCAGGITTTCGG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 TGGAACTGTATGTGCATTGGAGGTTAAACAGTCCAAAGGAGGATCTAGAGCATTTGCCAA 339
                                                                                                                                                                                                                                                                                                                             100 CTACTGCTGGGTAGTTTTTATTTTGCATAACTTCAGGGGGTATTCCAGTTGGTGTTAGCA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 ATTCCCTTATCTTCTCTCTGCGGAAGTGGTTAAGTCATTCTTAGAGAAATATACAGGATA 279
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Pred. No. 4.9;
0; Mismatches 177; Indels
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PRIOR APPLICATION NUMBER: 60/202,111
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 6
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                                                                                                                                                                                                                                    Query Match
1.0%;
Best Local Similarity 44.9%;
Matches 144; Conservative
                                                                  SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 2720
                                                                                                                                     TYPE: DNA
CRGANISM: Homo sapiens
US-09-847-665-3
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CRGANISM: Homo sapiens
US-09-847-665-6
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US-09-847-665-6
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TITLE OF INVENTION: No. 10S20020082234Alel Prokaryotic Polynucleotides, Polypeptides and Their Uses NUMBER OF SEQUENCES: 534
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601 IGGITCAGCIGACTATAAACTICAGCITICATAIGAAAATATAIGGCAGGIIGIGCTCCA 660
                                      320 GGATCTAGAGCATTTGCCAAAGTTCAATTTGCCGACAACATAAGTGCTGACAAAATCATC 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3191;
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ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESC for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beecham Corporation
Road
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49.0%; Pred. No. 13;
tive 0; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,980
FILING DATE: 27-Aug-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/936,165
FILING DATE: «CURROWN»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-09-939-980-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P5
                                                                                                                                                                                                                                                                                                          Sequence 194, Application US/09939980 Patent No. US20020082234A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pratt, Julie
Reichard, Richard
Rosenberg, Martin
Ward, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
LENGTH: 3191 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lonetto, Michael
Nicholas, Richard
                                                                                                                                                                    121 CTACCCAGAAGCTAGAGAGCT 100
                                                                                                              661 ICGTCCATAIGGTCAAAAIGCT 682
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ADDRESSEE: SmithKline
STREET: 709 Swedeland
                                                                                                                                                                                                                                                                                                                                                                                                                      Burnham, Martin
Hodgson, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Knowles, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Black, Michael
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Best Local Similarity 49.0°
Matches 94; Conservative
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US-09-939-980-194
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                                                           APPLICANT: Chen, Wensheng
TILLE DF INVENTION: Hanze, David K,
APPLICANT: Chen, Wensheng
TILLE DF INVENTION: GENE EXPENSION ANLISIS BY MICHORERAY
TILLE DF INVENTION: GENE EXPENSION ANLISIS BY MICHORERAY
TILLE DF INVENTION: GENE EXPENSION ANLISIS BY MICHORERAY
CHERRY APPLICATION WHORE: ACOIL-05-23
CHRENT APPLICATION WHORE: GOOD-02-04
FRICH APPLICATION WHORE: GOOD-03-04
FRICH APPLICATION WH
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TYPE: DAA

ORGANIEM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO ACOO7543.4

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN HELAO, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN HELAO, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
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76; Conservative
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                                                                                           3286 AAGAGCCTGGTTCAAGAGGCGTAATGATAT--AGATGACATGTTACCAAAGGCTTCGGCT 3343
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                                                              380 ACTITIGGCIAATAACAGGCTGTATTTTGGCTCTTCTTATTTGAAGGCTTGGGAAATGAAA 439
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US-09-764-847-1401/c
; Sequence 1401, Application US/09764847
; Sequence 1401, Application US/09764847
; Settent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.; TITLE OF INVENTION: NUCLEIC Acids, Proteins, and Antibodies
; TITLE OF INVENTION: NUCLEIC Acids, Proteins, and Antibodies
; TITLE OF INVENTION: NUMBER: US/09/764.847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PARENTIN Ver. 2.0
; SEQ ID NO 1401
; LENGTH: 1196
; TYPE: DAM HOMO Sapiens
US-09-764-847-1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1196;
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1.0%; Score 36.2; DB 10; Length 1
Best Local Similarity 50.9%; Pred. No. 8;
Matches 138; Conservative 0; Mismatches 128; Indels
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Search completed: November 5, 2002, 23:26:24 Job time: 283 secs

Title: Perfect score:

Sequence:

OM nucleic

: uo

Run

Scoring table:

Searched:

Minimum DB Maximum DB

Database

us-09-782-874-1.rst

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AW649811 EST328265
BE920043 EST423812
BE433646 EST42812
AW933692 EST358761
AJ807433 AJ484433
BG111608 EST595184
BG111609 EST597184
BG192042 EST431460
AL896465 EST505996
BF102042 EST437289
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BG189665 EST31997
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BG189665 EST31997
BG1733 GG182800
BG256333 SP-10 SP-
BG415065 HVSMEKODO
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BG97153 GHB7F10.
BG966709 GHB2F11.
BG966709 GHB2F11.
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BH558894 BOGXE78TF
BQ916044 QHB16J11.
BH467203 BOGGD34TR
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QHB28A10.
BJ26864
QHB17L01.
QGG16J23.
GG10P80Y
EST617080
saq68c11.
QHB41F18.
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1 (bases 1 to 2199)
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes

2 (bases 1 to 2199)
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Submitted (25-APR-2002) Maize Mapping Project, University
Missouri, Columbia, MO 65211, USA
Lication/Qualifiers
1. 2199
/organism="Zea mays"
/db_xref="MaizedB:637927"
/db_xref="MaizedB:637927"
/clone="PC0135426"
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Zea mays PCO135426 mRNA sequence.
AY103827
AY103827.1 GI:21206905
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   AW649811
BEB220043
BW9329186
AW9329186
BO113692
BO111609
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BH467203
      Zea mays.
Zea mays
    RESULT 1
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LOCUS
DEFINITION
ACCESSION
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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REFERENCE
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BQ507474 EST614889
BG594667 EST493345
BL203182 EST52122
BE43532 EST406610
BG597875 EST496553
                                                                                                                   (without alignments)
13327.164 Million cell updates/sec
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1 GAAAIATTCTTIACTTACTT......AGTTTCATCTTCTAAA 3731
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                                                                                                     ; Search time 4534 Seconds
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                  GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                     2002, 19:15:22
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Maximum Match 100%
Listing first 45 summaries
                                                                           nucleic search, using sw model
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720.4 661.8 625.4 603.2

Score

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                     Jobbs assembles resulting from the application of public assembles resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project 530 g 584 t
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                                                                                                                                                          Gaps
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clone_lib="Maize Mapping Project/DuPont Cornsensus"
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                                                                                                                                 Length 2199;
                                                                                                                                 Score 720.4; DB 11; Length Pred. No. 2.3e-173; 0; Mismatches 601; Indels
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ilarity 64.1%;
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AATCAGGGGTIGAAAAGAGCTCATTTCATTAGTTTCCCTGGTQTGTTATGACCAGCTA 3445 3157 2977 3037 2617 2677 1034 2797 1154 1214 2917 854 GITICTIGGGATCCACATCTIATTCCAAGTCGTTTGGTGGATCCTATGGACTAACTCCA GGAAAGCTTTTCAGGAAAGTGAAGGACAAAGCACCTCAGGCTAGCTCTATCGCGACCTTC TACATTGACGAAGCTTTTGACTACAAAACTGAATATGACAACAAGCTGGGTAATTTAATG GACTACTATGGCATAAAAACAGAGGCTGAAATACTTAGTGGTGGCATTATGAAGGCATCA AAAACTTTTGACCGCAGAAAAGATGCTGAGGCCATTAGTGTTGCTGTGAGGGCCTTGAGG AAGGAGGCAAGAGCCTGGTTCAAGAGGCGTA------ATGATATAGATGACATG 1626 AAAGAAGCTAGGTCGTGGTTCAATGAGATGAGCACAGGAGAGGAGGATGGCCAAGATGCCATG 3326 TTACCAAAGGCTTCGGCTTGGTACCACGTTACATATCATCCTACATATTGGGGGTTGCTAC ACTEGAAAAGTAGTTGTCGCCAAAAATCCTTGTCTCCACCCTGGTGACATACGGGTTCTC GTTTGCTGGGATCAAGACATGATCCCGCCAAGGCAAGTCCAGCCGATGGAATATCCTCCA AACTATATTGTGAATGACAGTTTGGGAATCATAGCAAATGCCCATGTCGTATTTGCAGAC AGAGAACCTGATATGGCCATGAGTGATCCATGCAAAAAACTTGCTGAGCTCTTTTCAATT GGAAAAAGACCTCATCCGAATGAATGTTCTGGGAGTGATTTGGATGGGGATATCTACTTT 2918 GAATACCCAGACTTCATGGATAAGCCGGACAAGACCAGCTATATCTCAGAAAGAGTTATT ATCCAGATTAAGAAGG 3461 3278 1386 3386 1746 1806 3038 3158 3218 3446 1155 1215 2978 3098 2498 2558 915 2618 975 2678 1035 2738 2798 2858 855 Q o do δλ 셤 δ g οy g δ q δŏ g ŏ g δ g δ g à g ò ď δ q à g QY Db Q δ DÞ Qy QΥ

RESULT 2 BQ507474

612

544 671 604 731 664 791

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Solanum tuberosum
Solanum tuberosum
Solanum tuberosum
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
E 1 (bases 1 to 725)
S van der Heeven R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A.,
Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.
Generations of ESTs from sprouting potato eyes
U published (2000)
Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1.800-711-6195, email cdna@resgen.com
Seq primer: Misser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG594667 T25 bp mRNA linear EST 12-APR-2001 EST493345 cSTS Solanum tuberosum cDNA clone cSTS8119 5' sequence, mRNA sequence.
BG594667.1 GI:13612807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              672 GICAAAAIGCICAGITICICCICAIACAGIIATIIGGIGCICCICGGAICIAIAAGAGAC
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Pred. No. 1.5e-158;
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/organism="Solanum tuberosum"
/organism="Solanum tuberosum"
/outlivar="Kennebec or Binjte"
/db.xref="taxon:4113"
/clone="STMG059"
/clone="STMG059"
/clone="Lb="Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues"
/issue_type="mixed tissues"

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BQ507474 1773 bp mRNA linear EST 22-JUL-2002 EST614889 Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues Solanum tuberosum cDNA clone SIMGQ59
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Pred. No. 1.4e-158;
0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                           5' end, mRNA sequence.
BQ507474
BQ507474.2 GI:21923304
BST.
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17.7%;
Best Local Similarity 94.7%;
Matches 729; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cdna@resgen.com
Seq primer: T3.
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AL Unpublished (2001)

Contact: CUGI

Contact: CUGI

Clemson University

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

100 Jordan Hall, Clemson.edu/orders/index.html.

Location/Qualifiers

1. 659

/ Cultivar="TA496, E6203"
/ Clone="CTOSIC7"
/ Clone="CTOSIC7"
/ Clone="CTOSIC7"
/ Liseu-type="Suspension cultures"
/ Liseu-type="suspension cultures"
/ Lab_host="SOLR"
/ Ab_host="SOLR"

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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons; core eudicots;
Asteridae, euasterids I; Solanales, Solanaceae, Solanum;
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                                      CGIGITITAAAGGCIGIAAAIGIICGAGCGCIGCACCACAIGGIAGAIIGIGIAIIC 2548
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van der Boeven,R., Sun,H., Bezzerides,J., Cho,J., Utterback,R.
Ronning,C. and Tanksley,S.
Generation of ESTs from Tomato Suspension Cultures
        Gaps
                                                                   61
                                                                                                                 GAAAGAGTTATTGGAAAGCTTTTCAGGAAAGTGAAGGACAAAGCACCTCAGGCTAGCTCT
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      Mismatches
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      Conservative
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                                 BE435332 618 bp mRNA linear EST 18-MAY-2001 EST406410 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA clone cLEG26C9, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBluescriptsKmcUadapt; Site_1: EcoR1; Site_2: Xho1; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp." 115 c 149 g 157 t 1 others
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                                                                                                                                                                                                                                             1 (bases 1 to 618)
Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Glovannoni,J.J. and Tanksley
                                                                                                                                                          Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2801 GAACCTGATATGGCCATGAGTGATCCATG-CAAAAACTTGCTGAGCTCTTTTCAATTGC 2859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2860 AGTGGACTTTCCAAAGACTGGTGTTCCCGCTGAAATACCATCTCAGTTGCGCCCTAAAGA 2919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2920 ATACCCAGACTTCATGGATAAGCCGGACAAGACCAGCTATATCTCAGAAAGAGTTATTGG 2979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3100 CATTGACGAAGCTTTTGACTACAAAACTGAATATGACAACAAGGTGGGTAATTTAATGGA 3159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1040 AAGAGATGTTGCAAGGAGATCATATGATGCTGATATGGAAGTTGATGGATTTGAAGATTA 3099
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                                                                                                                                                                                                                                                                                                                                     Generation of ESTs from tomato fruit tissue, breaker stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                      Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib-"tomato breaker fruit, TIGR"
/tissue_type="Pericarp"
/tissue_type="Pericarp"
/lab_nost="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .618
/organism="Lycopersicon esculentum"
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 605; DB 10;
Pred. No. 5.4e-144;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:4081"
/clone="clEG26C9"
                                                                                                       BE435332.1 GI:9433175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.2%;
ilarity 99.7%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                          (2000)
                                                                                                                                                                                                                                 Lycopersicon.
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                                                                                                                                                                                                                                                                                                                                                          Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196
                                                                                                                                         tomato.
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Matches 616)
                                                DEFINITION
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AUTHORS
RESULT 5
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/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI: Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG597875 682 bp mRNA linear EST 12-APR-2001 EST496553 cSTS Solanum tuberosum cDNA clone cSTS19C12 5' sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a; Tracheophyta;
eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids; euasterids; core eudicots; Losaes 1 to 682)

van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B. Generations of ESTs from sprouting potato eyes Unpublished (2000)

Contact: Cathy Ronning

The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries Division tell 1.800-711-6195, email cdna@resgen.com
                                                                                                                                     3220 AACTITIGACCGCAGAAAAGATGCTGAGGCCATTAGTGTTGCTGTGAGGGCCTTGAGGAA 3279
                                                                                                                                                                                                                                                                                                                        3340 GGCTTGGTACCACGTTACATATCATCCTACATATTGGGGTTGCTACAATCAGGGGTTGAA 3399
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  CATTGACGAAGCTTTTGACTACAAAACTGAATATGACAACAAGCTGGGTAATTTAATGGA 360
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                                                                                                                                                                                                                                                                                                                                                  3160 CTACTATGGCATAAAAACAGAGGCTGAAATACTTAGTGGTGGCATTATGAAGGCATCAAA
                                                                      361 CTACTATGGCATAAAAACAGAGGCTGAAATACTTAGTGGTGGCATTATGAAGGCATCAAA
                                                                                                                                                                                421 AACTITIGACCGCAGAAAAGAIGCIGAGGCCAITAGIGIIGCIGIGAGGGCCIIGAGGAA
                                                                                                                                                                                                                              3280 GGAGGCAAGAGCCTGGTTCAAGAGGCGTAATGATATAGATGACATGTTACCAAAGGCTTC
                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="grouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xxef="Laxon:4113"
/clone="GSTS19012"
/clone="GSTS19012"
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Solanum tuberosum
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BG597875
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BG597875
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Match 15.5%;
Local Similarity 98.3%;
Les 585; Conservative (
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   source
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Jaclata, V. Vrebalov, J., White, R., van der Hoeven, R.S., Holt, I.E.,
Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M.,
Nierman, W., Fraser, C.M., Glovannoni, J.J., Martin, G.B. and Tanksley
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                                    62 AGGAGGIATTCCAGTIGGIGATTAGCATTIGAACGICGAACTGCACTIGGAATTIGGCTG
                                                                                       313 CAAAGGAGGATCTAGAGCATTTGCCAAAGTTCAATTTGCCGACAACATAAGTGCTGACAA
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                                                                                                                                                                                                 AW649811 597 bp mRNA linear EST 16 EST328265 tomato germinating seedlings, TAMU Lycopersicon esculantum cDNA clone cLE1913 5', mRNA sequence. AW649811 GI:7411049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          germinating tomato seed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: CUGI
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Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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BE920043. GI:10446119
EST.
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                                                                                       183 GATATCTACTTTGTTGCTGGGATCAAGACATGATCCCGCCAAGGCAAGTCCAGCCGATG
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 Length 597
                                     Indels
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Score 579; DB 10;
Pred. No. 2.5e-137;
0; Mismatches 10;
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Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

I (bases 1 to 610)
S van der Hoven, R.S.), Bezzerides, J., Holt, I.E., Liang, F., Cho, J.,
Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning
C.M., Fry W.E., Tanksley, S.D. and Baker, B.
Generation of ESTs from potato leaves and petioles
Unpublished (2000)
Contact: Cathy Ronning
Contact: Cathy Ronning
For clone request: plasse contact Research Genetics, Libraries
Division tell 1-800-711-6195, email cdna@resgen.com.
                                         Holt,I.E., Liang,F., Cho,J.,
Bougri,O., Buell,C.R., Ronning
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.1%; Score 565.2; DB 12; Length 610;
.larity 96.6%; Pred. No. 8.7e-134;
Conservative 0; Mismatches 18; Indels 3;
                                                                                                                                                                                                                                                                                                    /clone_lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_nost="SOLR"
                                                                                                                                                                                                                              /organism="Solanum tuberosum"
/cultivaz="Kennebec"
/db xref="taxon:4113"
/clone="GSTB3D19"
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BE433646 EST 18-WAY-2001 EST400175 tomato breaker fruit, TIGR Lycopersicon esculentum CDNA clone cLEG16J9, mRNA sequence.
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Abdala, Vrebblov, J., White, R., van der Hoeven, R.S., Holt, I.E.,
Liang, F., Hansen, T. S., Craven, M.B., Bowman, C.L., Ronning, C.M.,
Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley
                                                                                                                                                                                                                                                                                                         Lycopersicon esculentum
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBluescriptSKmcUadapt; Site_1: EcoR1; Site_2: Xhol; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Generation of ESTs from tomato fruit tissue, breaker stage Unpublished (2000)
Contact: CUGI
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clemson University
clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
Location/Qualifiers
1..570
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/cultivar="ma496"
/db_xref="taxon:4081"
/clone="cEGG1659"
/clone="lb="tcmato breaker fruit, TIG
/tissue_type="Pericarp"
/dev_stage="Pericarp"
/lab_host="SOLR"
                                                                                                                                                                                                                                       BE433646.1 GI:9431489
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  GAAGTTGATG 3086
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Best Local (
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/organism="Lycopersicon esculentum"
/cultivar="TA496"
/cul
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Alcala, J. Vrebalov, J., White, R., Matern, A. L., Holt, I. E., Liang, F., Upton, J., Hansen, T., Craven, M. B., Bowman, C. L., Ahn, S., Ronning, C. M., Farser, C. M., Martin, G. B., Tanksley, S. D. and Glovannoni, J. Generation of Errs from tomato fruit tissue (1999)
Confract: CGGI
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                   TGAAGGGAAATGTGGTTGCTAGAAAAATCCATGCTTGCATCCTGGTGATATTCGTGTTT
                                                                             2496 TAAAGGCTGTAAATGTTCGAGCGCTGCACCACATGGTAGATTGTGTTGTATTCCCTCAGA
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Pred. No. 1.6e-124;
0; Mismatches 5;
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Best Local Similarity 99.1%;
Matches 532; Conservative
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525 bp mRNA linear EST 18-MAY-2001 mature green, TAMU Lycopersicon esculentum ', mRNA sequence.
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1 (bases 1 to 525)

Alcala, J., Vrebalov, J., White, R., Matern, A.L., Holt, I.E., Liang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Glovannoni, J. Generation of Ests from tomato fruit tissue Unpublished (1999)
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/organism="Lycopersicon esculentum"

/orlantar="Taxon:408"

/clone="cleF56cH8"

/clone=lib="tomato fruit mature green, TAMU"

/tissue_type="fruit pericarp"

/dev_stage="mature green (3-5 days pre-ripening)"

/lab_host="805R"

/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
                                                                                                                                                                                                                                                                 2934
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                       61 GGACCATGATGTCACAATTGAGGAAGTTGAAGAGTACTTCACCAACTATATTGTGAAGGA
                                                                                                               CATGAGTGATCCATGCAAAAACTTGCTGAGCTCTTTTCAATTGCAGTGGACTTTCCAAA
                                                                                                                                                                                                 2875 GACTGGTGTTCCCGCTGAAATACCATCTCAGTTGCGCCCTAAAGAATACCCAGACTTCAT
                                                                                                                                                                                                                                                                                         241 GACTGGTGTTCCCGCTGAAATACCATCTCAGTTGCGCCCTAAAGAATACCCAGACTTCAT
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                                                                                       2755 CAGTTTGGGAATCATAGCAAATGCCCATGTCGTATTTGCAGACAGGAACCTGATATGGC
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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cDNA clone cLEF56C18 5'
AW933692
AW933692.1 GI:8109093
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AW933692
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BQ111608 521 bp mRNA linear EST 22-JUL-2002
EST597184 mixed potato tissues Solanum tuberosum cDNA clone STMCB87
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(Cases 1 to 521)

Buell, C.R., Hart, A., Baker, B., Tankaley, S., Fry, W., Smart, C., Restrepo, S., Giffiths, H., van der Hoeven, R., Tsai, J. and Karamycheva, S.A.

Generation of a set of potato cDNA clones for microarray analyses Unpublished (2002)

On Apr 17, 2002 this sequence version replaced gi:20163570.
Nhol; CLEF - Fruit were tagged at the lcm stage and harvested 3-5 days prior to ripening. Fruit were cut in half to verify the seeds were indeed 'immature' and the seeds and locules were discarded prior to freezing the
                                                                                                                                                                                                                                                                                                                                                                                                               2643
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9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato@tigr.org
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BQ111608
BQ111608.2 GI:21915035
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Solanum tuberosum
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AUTHORS
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1. .521
/organism="Solanum tuberosum"
/origins="Rennebec or Binjte"
/db_xref="taxon:4113"
/clone="STMCB67"
/clone="STMCB67"
/clone="TSMCB67"
/clone="Wector: pBluescript SK(-); Site_1: EcoRI; Site_2: Anot: supplier: Combination of untreated and Phytophthora infestans-treated libraries of stolons, leaves, leaflets, axiliary buds of stem explants, petioles, germinating eyes tubers, or roots:"
/ tubers, or roots:"
/ tubers, close in 139 t
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AJ487433 Solanum tuberosum cv. Provita Solanum tuberosum cDNA clone
AJ487433
                                                                                                                                                                                                                                                                                                                                                                       1;
This clone is available through the Research Genetics, contact the Research Genetics for further information 1-800-711-6195 or cdna@resgen.com
Seq primer: T3.
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Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                       12.9%; Score 482.6; DB 14; Length 521; llarity 96.7%; Pred. No. 1.3e-112; Conservative 0; Mismatches 14; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATATCTCAGAAGAGTTATTGGAAAACTTTTCAGGAAAGT
                                                                  Location/Qualifiers
1. .521
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5' sequence,
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum. I (bases I to 550)
Gebhardt.C., Walkemeler,B., Henselewski,H., Barakat,A., Delseny,M. and Stueber,K.
                                                         Comparative mapping between potato (Solanum tuberosum) and Arabidopsis thaliana reveals structurally conserved domains and ancient duplications in the potato genome (Unpublished (2002) Contact: Gebhardt C Plant breeding and yield physiology MPI for Breeding Research Carl-von-Linne Weg 10, Cologne, D-50829, Germany.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                      3180 AGGCTGAAATACTTAGTGGTGGCATTATGAAGGCATCAAAAACTTTTGACCGCAGAAAAG 3239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 14;
                                                                                                                                                                                                                                                                               Length 550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG592782 529 bp mRNA linear EST491460 cSTS Solanum tuberosum cDNA clone cSTS2K4
                                                                                                                                                                                                                                  /clone_lib="Solanum tuberosum cv. Provita" 91 c 125 g 152 t
                                                                                                                                                                                                                                                                              Score 473.6; DB 9;
Pred. No. 2.7e-110;
0; Mismatches 24;
                                                                                                                                                                        /organism="Solanum tuberosum"
/cultivar="Provita"
/db_xref="taxon:4113"
/map="V"
                                                                                                                                                                                                                       /clone="P3f8"
                                                                                                                                                                                                                                                                               tch 12.7%; al Similarity 93.1%; 512; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CIGCAACATA 3655
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                            REFERENCE
AUTHORS
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1. 529
/organism="Solanum tuberosum"
/organism="Solanum tuberosum"
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/clone="Lib="cSTS"
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/tissue_type="sprouting eyes from tubers"
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/de_stage="12-14 weeks post harvest"
/db_host="%colf"
/db_host="SOLR"
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/note="weetor: pBluescript SK(-); Site_1: EcoRI; Site_2:
/note="weetor: pBluescript SK(-); Site_1: EcoRI; Site_2:
/doctor: pBluescript SK(-)
                                                                                                                                                                              SM Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Hagnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

E 1 (bases 1 to 529)

S van der Hoeven, R., Bezzerides, J., Sun, E., Cho, J., Chiemingo, A.,
Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.
Generations of ESTs from sprouting potato eyes

I Unpublished (2000)

Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
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ilarity 95.1%; Pred. No. 1.6e-106;
Conservative 0; Mismatches 22;
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mRNA sequence.
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BG592782.1 GI:13610922
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Matches 485; Conserv
                                                                                                                                                     potato.
Solanum t
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us-09-782-874-1.rst

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/organism="Lycopersicon esculentum"
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/note="vector: pBlueSoript SK(-); Site_1: EcoR1, Site_2:
/note = vector: pBlueSoript SK(-); Site_1:                                                                                                                                                                                                                            A1896465
EST265896 tomato callus, TAMU Lycopersicon esculentum cDNA clone cLEC15G23, mRNA sequence.
A1896465.
A1896465.1 GI:5602355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l (bases 1 to 421)
Alcala J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J. Generation of ESTs from tomato callus tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lycopersicon esculentum
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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Best Local Similarity 100.0%; Pred. No. 7.4e-97;
Matches 421; Conservative 0; Mismatches 0; Indels
Location/Qualifiers
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AI896465
LOCUS
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AUTHORS
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Search completed: November 5, 2002, 23:19:25 Job time: 4565 secs

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                                 GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Gapop 60.0 , Gapext 60.0
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Searched:

Run on:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Tomato RNA-directe Tomato C.protein h Tomato RNA-directe Soybean RNA-directed Tomato RNA-directed Tomato C.protein-s Maize RNA-directed Tomato RNA-directed Tomato RNA-directed Tomato RNA-directed Tomato RNA-directed
SUMMARIES	AAU10006 AAE00897 AAE00898 AAB28533 AAB28533 AAU10009 AAU100097 AAU10007 AAU10008
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% Query Match Length DB 1	11114 11114 11118 11128 11108 1108 1108 1108 1108 1
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INIYERILSTLRKGFVIGDKKFEFLAFSSSQLRDNSVWMFASRPGLTANDIRAWMGDFSQ 480

121

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This sequence represents the tomato RNA-directed RNA polymerase (RdRP) protein of the invention. The invention comprises the nucleic acid and protein sequences of RGRP. The protein of the invention can catalyse in vitro transcription of short single stranded RNAs into DNA molecules, this transcription can be either primed by RNA or DNA oligonucleotides the uprimed. The protein may have cytostatic or vitrucide activities. The sequences of the invention may be used in gene therapy or as an RNA disease are useful for treating disease caused by the undestred adisease are useful for treating a disease caused by the undestred expression or overexpression of a nucleic acid molecule which causes a disease are useful for treating the molecules. This system can be used in the preparation of a pharmaceutical composition and for inhibiting expression of any desired gene by transferring the RdRP system to expression of any desired gene by transferring the RdRP system to cryptism that either lack a comparable mechanism or do not sufficiently expression of any desired gene expression in transgenic organisms.

The sequence is useful for inhibiting RNA directed RNA synthesis and for ensuring stable heterologous, gene expression in transgenic organisms. The sequence is useful for inhibiting RNA directed RNA synthesis and for expression, as primers for amplification of the control of gene expression of undesired gene expression in humans and animals. The RdRP is useful as a therapeutic agent for the control of cancer and virus infection in humans and animals and animals and inmunoprecipitation or immunologalisation of the protein, identification immunoprecipitation or immunologicalisation of the protein sequences are useful as a charapeut or immunological protein sequences are useful for immunological protein
                                                                                                                                                New nucleic acid molecule encoding a polypeptide having the enzymatic activity of RNA-directed RNA polymerase, for modulating gene expression and treating cancer and virus infection in human and animals -
         HL;
         Sanger
      Schiebel W,
                                                                                                                                                                                                                                                                       Claim 1; Page 19-22; 34pp; English.
   Riedel L,
                                                            2001-595798/67.
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                                                                                         N-PSDB; AAS17837
   Wassenegger M,
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Length 1114; ; 0 Indels 22; .; В 100.0%; Score 1114; 100.0%; Pred. No. 0; Conservative 0; Mismatches Similarity Best Local Simmatches 1114;

ö 300 300 360 IITLANNRLYFGSSYLKAWEMKTDIVQLRAYVDQMDGITLNFGCQISDDKFAVLGSTEVS 120 IQFGIGLKKFFFFLSSGSADYKLQLSYENIWQVVLHRPYGQNAQFLLIQLFGAPRIYKRL 180 RRRNVACIEHALEKLYYIKECCYDPVRWLTEQYDGYLKGRQPPKSPSITLDDGLVYVRRV 360 9 1 MGKTIQVFGFPYLLSAEVVKSFLEKYTGYGTVCALEVKQSKGGSRAFAKVQFADNISADK 60 TLQTGFTFFVSQKSALVPNVQPPEGISIPYKILFKISSLVQHGCIPGPALNVYFFRLVDP TLQTGFTFFVSQKSALVPNVQPPEGISIPYKILFKISSLVQHGCIPGPALNVYFFRLVDP ENSCYSFFKETPDDQWVRTTDFPPSWIGLSSSLCLQFRRGVRLPNFEESFFHYAERENNI 61 61 121 121 181 241 241 301 181 301 361 g δy g δ g q Qγ ò g οy qq

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gene therapy; RNA-directed RNA polymerase; RdRP; gene expression; nic plant; tissue culture; plant breeding; therapy; C-protein.
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SKCGLQYIPSAFQIRYGGYKGVYGVDPDSSMKLSLRKSMSKYESDNIKLDVLGWSKYQPC
                                                                                                                                         LNCGYKPDAEPFLSMALQTFRASKLLDLRTRSRIFIPNGRTWMGCLDESRTLEYGQVFVQ
                                                                                                                                                                                                                                    FTGAGHGEFSDDLHPFINSRSTNSNFILKGNVVVAKNPCLHPGDIRVLKAVNVRALHHVV
                                                                                                                                                                                                                                                                                                                  EEVEEYFTNYIVNDSLGIIANAHVVFADREPDMAMSDPCKKLAELFSIAVDFPKTGVPAE
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                                IKNVAKYAARLGQSFGSSRETLSVLRHEIEVIPDVKVHGTSYVFSDGIGKISGDFAHRVA
                                                                                                                           YLNRQLITLLSTLGVKDEVLEQKQKEAVDQLDAILHDSLKAQEALELMSPGENTNILKAM
                                                                                                                                                                        INCGYKPDAEPFLSMMLQTFRASKLLDLRTRSRIFIPNGRTMMGCLDESRTLEYGQVFVQ
                                                                              SKCGLQYTPSAFQIRYGGYKGVVGVDPDSSMKLSLRKSMSKYESDNIKLDVLGWSKYQPC
                                                                                                                                                                                                                      FIGAGHGEFSDDLHPFNNSRSTNSNFILKGNVVVAKNPCLHPGDIRVLKAVNVRALHHMV
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/label= p430
/note= "C-protein-specific antibody for immunisation of rabbits"
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/labbl= P432
/note= "C-protein-specific antibody
immunisation of rabbits"
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                                                                                                                                                                                                                                                                        New nucleic acid molecules encoding polypeptides with RNA-directed RNA polymerase enzymatic activity, useful in modulating gene expression in plants, humans and animals, as well as in plant cell/tissue cultures or plant breeding
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         /label= P433
/note= "C-protein-specific antibody fo immunisation of rabbits"
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/label= P431
/note= "C-protein-specific antibody fo immunisation of rabbits"
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Pred. No. 0;
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(RIED/) RIEDEL L.
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Best Local Similarity
Matches 1114; Conserv
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N-PSDB; AAD04370.
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                                                                                                                                                                      LVTPCKVYFCGPEVNVSNRVLRNYSEDIDNFLRVSFVDEEWEKLYSTDLLPKASTGSGVR
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                        LVTPCKVYFCGPEVNVSNRVLRNYSEDIDNFLRVSFVDEEWEKLYSTDLLPKASTGSGVR
                                                                                               TNIYERILSTLRKGFVIGDKKFEFLAFSSSQLRDNSVWMFASRPGLTANDIRAWMGDFSQ
                                                                                                                                                  IKNVAKYAARLGQSFGSSRETLSVLRHEIEVIPDVKVHGTSYVFSDGIGKISGDFAHRVA
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                                                                         INIYERILSTLRKGFVIGDKKFEFLAFSSSQLRDNSVWMFASRPGLTANDIRAWMGDFSQ
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12-OCT-2000
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                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                 The present sequence is tomato RNA-directed RNA polymerase 800 (RdRPB00) protein which corresponds to position 700-917 of C-protein. C-protein is capable of RNA-directed RNA synthesis, thus using RNA as a template for synthesising complementary RNA molecules. RdRP nucleid as useful for modulating gene expression in plants, humans and animals. This may lead to various physiological, developmental and/or morphological changes. Transgenic plants containing RdRP nucleic acid is especially useful in plant cell or tissue cultures and in plant breeding. RdRP is useful in gene therapy, particularly for treating a disease that
                                                                                              New nucleic acid molecules encoding polypeptides with RNA-directed RNA polymerase enzymatic activity, useful in modulating gene expression in plants, humans and animals, as well as in plant cell/tissue cultures or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Soybean; plant; RNA-directed RNA polymerase; gene mapping; gene marker; plant virus resistance; plant breeding.
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                                                                                                                                                                                                                                                            is caused by the undesirable expression or overexpression of
                                                                                                                                                                                                                                                                                                 Length 218;
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soybean RNA-directed RNA polymerase, SEQ ID NO: 12.
                                                          Sanger HL;
                                                                                                                                                                                                                                                                                                19.6%; Score 218; DB 22; I
100.0%; Pred. No. 4.3e-224;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKLAELFSIAVDFPKTGVPAEIPSQLRPKEYPDFMDKP 917
                                                          3
                                                                                                                                                Example 3; Column 39-42; 31pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA
                                                          Schiebel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB28533 standard; Protein; 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-APR-2000; 2000WO-US09105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0128094
         97US-0811583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                          ij
                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 218; Conservative
                                                          Riedel
                            (WASS/) WASSENEGGER M. (RIED/) RIEDEL L.
                                                                            WPI; 2001-289830/30.
                                                                                                                                                                                                                                                                               218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200060097-A1
                                                          Wassenegger M,
                                                                                                                             plant breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-APR-1999;
         05-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-2000
                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB28533;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid fragments encoding RNA-directed RNA polymerase useful for controlling gene expression and providing mechanisms to engineer plant virus resistance
                                                                                                                                                                                      RNA-directed RNA polymerase useful providing mechanisms to engineer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maize; plant; RNA-directed RNA polymerase; gene mapping; gene marker; plant virus resistance; plant breeding.
                                                                                                                                                                                                                                                                                                                                   The present sequence is part of a plant RNA-directed RNA polymerase protein. Polynucleotides encoding RNA-directed RNA polymerases were isolated from plant CDNA libraries. They are useful as probes for genetically and physically mapping qenes, and as markers for traits linked to those genes. They are useful for controlling gene expression and provide mechanisms to engineer plant virus resistance. They are also useful for plant breeding to develop lines with desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                       Zhong
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                                                                          Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1125;
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                                                                          Cahoon RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cahoon RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21; It
9.9e-14;
thes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 2.0%; Score 22; DB Local Similarity 100.0%; Pred. No. 9.5 ies 22; Conservative 0; Mismatches
                                                                          Sakai H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ή
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                                                                                                                                                                                         New nucleic acid fragments encoding
for controlling gene expression and
plant virus resistance
(DUPO ) DU PONT DE NEMOURS & CO E I. (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB28530 standard; Protein; 1108 AA.
                                                                                                                                                                                                                                                                                          Claim 10; Page 50-54; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maize RNA-directed RNA polymerase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       822
                                                                             Weng Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     801 RPHPNECSGSDLDGDIYFVCWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-2000; 2000WO-US09105.
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                                                                             Orozco EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-679376/66.
N-PSDB; AAC63739.
                                                                                                                      WPI; 2000-679376/66.
N-PSDB; AAC63742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1125 AA;
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Wed Nov

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protein. Polynucleotides encoding RNA-directed RNA polymerases were isolated from plant cDNA libraries. They are useful as probes for genetically and physically mapping genes, and as markers for traits linked to those genes. They are useful for controlling gene expression and provide mechanisms to engineer plant virus resistance. They are also useful for plant breeding to develop lines with desired phenotypes.
                          5555555x8
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1108 AA; Sequence

Gaps : 0 Length 1108; Score 19; DB 21; Length 11 Pred. No. 1.6e-10; Mismatches 0; Indels 1.7%; Scor. 100.0%; Pre 794 RPHPNECSGSDLDGDIYFV 812 RPHPNECSGSDLDGDIYFV 809 Local Similarity 100. les 19; Conservative Query Match 791 Matches qq δy

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AAU10009 standard; Peptide; 17 AA. AAU10009; AAU10009

Tomato, RdRP; RNA-directed RNA polymerase; in vitro transcription; vortostatic; virucide; RNA synthesis inhibitor; antibody; immunogen; transgenic animal; cancer; viral infection; immunoprecipitation; immunolocalisation; P432; gene therapy. Tomato RNA-directed RNA polymerase (RdRP) immunogenic peptide P432.

(first entry)

08-MAY-2002

Lycopersicon esculentum

US2001023067-A1.

20-SEP-2001

08-FEB-2001; 2001US-0782874.

97US-0811583. 05-MAR-1997;

WASS/) WASSENEGGER M.

RIED/) RIEDEL

Wassenegger M, Riedel L,

Sanger HL;

Schiebel W,

WPI; 2001-595798/67

New nucleic acid molecule encoding a polypeptide having the enzymatic activity of RNA-directed RNA polymerase, for modulating gene expression and treating cancer and virus infection in human and animals

Example 7; Page 14; 34pp; English.

This sequence represents the tomato RNA-directed RNA polymerase (RdRP) immunogenic peptide P432 used to immunise rabbits and produce an RdRP-specific antibody. The invention comprises the nucleic acid and protein sequences of RdRP, the protein of the invention can catalyse in vitro transcription of short single stranded RNAs into DNA molecules, this transcription can be either primed by RNA or DNA oligonucleotides or be upprimed. The protein may have eytostatic or virucide activities. The sequences of the invention may be used in gene therapy or as an RNA directed RNA synthesis inhibitor. The RdRP cDNA sequence and a template nucleic acid molecule which causes a disease are useful for treating a disease caused by the undestred expression or overexpression of a nucleic acid molecule in a human, rat or mouse, by administering the molecules. This system can be used in the preparation of a pharmaceutical composition and for inhibiting expression of any desired gene by transferring the RdRP system to organisms that either lack a comparable mechanism or do not sufficiently 

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                                                                                                                                                                                                                                                                                                                                                                                                                                       Tomato; gene therapy; RNA-directed RNA polymerase; RdRP; gene expression; transgenic plant; tissue culture; plant breeding; therapy; C-protein; antibody; immunisation.
express their own RGRP. An antibody or an antagonist or inhibitor to the protein are useful for inhibiting RNA directed RNA synthesis and for ensuring stable heterologous, gene expression in transgenic organisms. The sequence is useful for probes and/or for the control of gene expression, as primers for amplification of nucleic acid molecules and additionally, nucleotide and protein sequences are useful for suppression of undestried gene expression in humans and animals. The RGRP is useful as a therapeutic agent for the control of cancer and virus infection in humans and animals and the antibody is useful for immunoprecipitation or immunolocalisation of the protein identification of polypeptides interacting with it and screening expression libraries.
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      Tomato C-protein-specific antibody, P432 for immunisation of rabbits.
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                                                                                                                                                                                                  Length 17;
                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                  1.5%; Score 17; DB 22; I
100.0%; Pred. No. 4.1e-10;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                AAE00901 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0811583.
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                                                                                                                                                                                                                                                       331 EQYDGYLKGRQPPKSPS 347
                                                                                                                                                                                                                                                                                                                                                                                                  04-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                      1 EQYDGYLKGRQPPKSPS 17
                                                                                                                                                                                                                 Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lycopersicon esculentum.
                                                                                                                                                                            17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS6218142-B1.
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                                                                                                                                                                                                      Query Match
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Matches
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The present sequence is a tomato C-protein-specific antibody, P432 chosen for immunisation of rabbits. C-protein having RNA-directed RNA polymerase (RdRP) activity is capable of RNA-directed RNA synthesis, thus using RNA as a template for synthesising complementary RNA molecules. RdRP nucleic acid is useful for modulating gene expression in plants, humans and animals. This may lead to various physiological, developmental and/or morphological changes. Transgenic plants containing RdRP nucleic acid is especially useful in plant cell or tissue cultures and in plant breading RdRP is useful in gene therapy, particularly for treating a disease that is caused by the undesirable expression or overexpression of a gene. New nucleic acid molecules encoding polypeptides with RNA-directed RNA polymerase enzymatic activity, useful in modulating gene expression in plants, humans and animals, as well as in plant cell/tissue cultures or Example 7; Column 24; 31pp; English. WPI; 2001-289830/30. plant breeding

Sanger HL;

Schiebel W,

Riedel L,

Wassenegger M,

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(WASS/) WASSENEGGER (RIED/) RIEDEL L.

Wed Nov

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Tomato; RdRP; RNA-directed RNA polymerase; in vitro transcription; cytostatic; virucide; RNA synthesis inhibitor; antibody; immunogen; transgenic plant; transgenic animal; cancer; viral infection; immunoprecipitation; immunolocalisation; P430; gene therapy.
                                  RNA-directed RNA polymerase (RdRP) immunogenic peptide P430.
                                                                                                                                                                                                             2001US-0782874.
                                                                                                                                                                                                                                       97US-0811583.
           (first entry)
                                                                                                                                                                                                                                                                                                        Riedel L,
                                                                                                                                 Lycopersicon esculentum.
                                                                                                                                                                                                                                                                  (WASS/) WASSENEGGER M. (RIED/) RIEDEL L.
                                                                                                                                                                                                                                                                                                                                  WPI; 2001-595798/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 AA;
                                                                                                                                                          US2001023067-A1.
                                                                                                                                                                                                                                                                                                          Wassenegger M,
                                                                                                                                                                                                             08-FEB-2001;
                                                                                                                                                                                                                                       05-MAR-1997;
            08-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid fragments encoding RNA-directed RNA polymerase useful for controlling gene expression and providing mechanisms to engineer plant virus resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is part of a plant RNA-directed RNA polymerase protein. Polynucleotides encoding RNA-directed RNA polymerases were isolated from plant cDNA libraries. They are useful as probes for genetically and physically mapping genes, and as markers for traits linked to those genes. They are useful for controlling gene expression and provide mechanisms to engineer plant virus resistance. They are also useful for plant breeding to develop lines with desired
                                                                                                                                                                                                                                                                                Maize; plant; RNA-directed RNA polymerase; gene mapping; gene marker;
plant virus resistance; plant breeding.
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                                                      Gaps
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                           Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.3%; Score 15; DB 21; I 100.0%; Pred. No. 6.8e-07; ive 0; Mismatches 0;
                                       4.1e-10;
nes 0;
                                                                                                                                                                                                                                                      Maize RNA-directed RNA polymerase, SEQ ID NO: 14.
                            DB 22;
                           1.5%; Score 17; DB
100.0%; Pred. No. 4.1
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sakai H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 23; Page 55-56; 62pp; English.
                                                                                                                                                                         AAB28534 standard; Protein; 230 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weng Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0128094.
                                                                                                                                                                                                                                                                                                                                                                                                      06-APR-2000; 2000WO-US09105.
                                                                                                                                                                                                                             (first entry)
                                                                               331 EQYDGYLKGRQPPKSPS 347
                                                                                               1 EQYDGYLKGRQPPKSPS 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.3
Best Local Similarity 100.
Matches 15; Conservative
                         Query Match 1.5
Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-679376/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230 AA;
 17 AA;
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N-PSDB; AAC63743
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                                                                                                                                                                                                                                                                                                                                                                                                                                  07-APR-1999;
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                                                                                                                                                                                                  AAB28534;
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  Sequence
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AAU10007
ID AAU1
XX
AC AAU1
                                                                                                                                                 RESULT 8
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Sanger HL;

Schiebel W,

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This sequence represents the tomato RNA-directed RNA polymerase (RARP) immunogenic peptide P430 used to immunise rabbits and produce an RARP-specific antibody. The invention comprises the nucleic acid and and protein sequences of RARP, the protein of the invention can catalyse in vitro transcription of short single stranded RNAs into DNA molecules, this transcription can be either primed by RNA or DNA coligonicleotides correctly and protein may have cytostatic or virucide activities. The sequences of the invention may be used in gene therapy or as an RNA disease are useful for treating a disease caused by the undesired card molecule derived from a nucleic acid molecule which causes a disease are useful for treating a disease caused by the undesired expression or overexpression of a nucleic acid molecule which causes a disease are useful for treating a disease caused by the undesired expression or overexpression of a nucleic acid molecule which causes or mouse, by administering the molecules. This system can be used in the preparation of any desired gene by transferring the RARP system to corpanisms that either lack a composition and for inhibiting expression of any desired gene by transferring the RARP system to corpanisms that either lack a composition and for inhibition to the corpus system of an unit of sand expression, as primers for antibody or an antagonist or inhibitor to the corpus system of the control of gene expression of the control of gene expression of the control of gene expression of undesired gene expression in humans and animals and protein sequences are useful for subpression of undesired gene expression in humans and animals and the antibody is useful for immunoprecipitation or immunolocalisation of the protein, in humans and animals and the antibody is useful for immunoprecipitation or immunolocalisation of the protein.
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New nucleic acid molecule encoding a polypeptide having the enzymatic activity of RNA-directed RNA polymerase, for modulating gene expression and treating cancer and virus infection in human and animals .
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. 5.6e-07;
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100.0%; Pred. No. 5.6
ive 0; Mismatches
                                                                                                                                                                                           Example 7; Page 14; 34pp; English.
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nes 14; Conserv
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1007 ASKTFDRRKDAEAI 1020

14

1 ASKTFDRRKDAEAI

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AAE00899 standard; peptide; 14 AA.

AAE00899;

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This sequence represents the tomato RNA-directed RNA polymerase (RGRP) immunogenic peptide P431 used to immunise rabbits and produce an RGRP-specific antibody. The invention comprises the nucleic acid and appearances of RGRP, the protein of the invention can catalyse in protein sequences of RGRP, the protein of the invention can catalyse in vitro transcription of short single stranded RNAs into DNA molecules, this transcription of short single stranded RNAs into DNA molecules, this transcription can be either primed by RNA or DNA colgunous confides. Or be unprimed. The protein may have cytostatic or virucide activities. The sequences of the invention may be used in gene therapy or as an RNA directed RNA synthesis inhibitor. The RdRP CDNA sequence and a template conclete acid molecule derived from a nucleic acid molecule which causes a disease are useful for treating a disease caused by the undesired concerns. This system can be used in the preparation of any desired gene by transferring the RGRP system to preparation of any desired gene by transferring the RGRP system to organisms that either lack a comparable mechanism or do not sufficiently expression of any desired gene by transferring the RGRP system to organisms. The sequence is useful for inhibiting RNA directed RNA synthesis and for ensuring stable heterologous, gene expression in transgenic organisms. The sequence is useful for probes and/or for the control of gene expression of undesired gene expression in humans and animals. The RdRP is useful for mamplification of the control of cancer and virus infection in humans and animals and the antibody is useful for immunoprecipitation or immunolocalisation of the protein; denotein denotein denotein defention of immunoprecipitation or immunolocalisation of the protein in purance and entered of the control of cancer and virus infection in humans and animals and the antibody is useful for immunoprecipitation or immunolocalisation of the protein general protein and protein sequences are useful for immunose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid molecule encoding a polypeptide having the enzymatic activity of RNA-directed RNA polymerase, for modulating gene expression and treating cancer and virus infection in human and animals -
                                                                                                                                                                                                                                 Tomato, RdRP; RNA-directed RNA polymerase; in vitro transcription; cytostatic; virucide; RNA synthesis inhibitor; antibody; immunogen; transgenic plant; transgenic animal; cancer; viral infection; immunoprecipitation; immunolocalisation; P431; gene therapy.
                                                                                                                                                                                         Tomato RNA-directed RNA polymerase (RdRP) immunogenic peptide P431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sanger HL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.3%; Score 14; DB 22; I
100.0%; Pred. No. 5.6e-07;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schiebel W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7; Page 14; 34pp; English.
                                             AAU10008 standard; Peptide; 14 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-2001; 2001US-0782874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAR-1997; 97US-0811583.
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                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                           Lycopersicon esculentum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-595798/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      US2001023067-A1.
                                                                                                                                           08-MAY-2002
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                                                                                           AAU10008;
RESULT 10
AAU10008
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                                                                                                            Tomato; gene therapy; RNA-directed RNA polymerase; RdRP; gene expression; transgenic plant; tissue culture; plant breeding; therapy; C-protein; antibody; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid molecules encoding polypeptides with RNA-directed RNA polymerase enzymatic activity, useful in modulating gene expression in plants, humans and animals, as well as in plant cell/tissue cultures or plant breeding
                                                                                   Tomato C-protein-specific antibody, P430 for immunisation of rabbits.
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                                                                                                                                                                                                                                                                                                                                                                                   Sanger HL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.3%; Score 14; DB 22; I 100.0%; Pred. No. 5.6e-07; ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                     Schiebel W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 7; Column 24; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE00900 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                             97US-0811583.
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                                                                                                                                                                                                                                                                                                                                                                                     Wassenegger M, Riedel L,
                                                           04-JUL-2001 (first entry)
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les 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                         RIED/) RIEDEL L.
                                                                                                                                                                                                                                                                             05-MAR-1997;
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                                                                                                                                                                                                                                              17-APR-2001.
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ID AAE0
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AC AAE0
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DT 04-J
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Gaps

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Length 14; Indels

Query Match
Best Local Similarity 100.0
Matches 14; Conservative

Zhong G;

Wang J,

Cahoon RE,

Sakai H,

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& CO E I.
                                                        Weng Z,
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                        (DUPO ) DU PONT DE NEMOURS 6 (PION-) PIONEER HI-BRED INT
   99US-0128094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                            549 PSAFQIRYGGYKGV 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beclin C, Elmayan T,
                                                        Odell JT, Orozco EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
                                                                            WPI; 2000-679376/66.
N-PSDB; AAC63738.
                                                                                                                                                                                                                                                                                                                                                          62 PSAFQIRYGGYKGV
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                                                                                                                                                                                                                                                                             417 AA;
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   07-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-NOV-2001
                                                                                                                                                                                                                                                          phenotypes
                                                                                                                                                                                                                                                                              Seguence
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                      therapy; RNA-directed RNA polymerase; RdRP; gene expression; lant; tissue culture; plant breeding; therapy; C-protein;
                                                                                                                                                                                                                                                   New nucleic acid molecules encoding polypeptides with RNA-directed RNA polymerase enzymatic activity, useful in modulating gene expression in plants, humans and animals, as well as in plant cell/tissue cultures or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maize; plant; RNA-directed RNA polymerase; gene mapping; gene marker; plant virus resistance; plant breeding.
Tomato C-protein-specific antibody, P431 for immunisation of rabbits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.3%; Score 14; DB 22; Length 14; 100.0%; Pred. No. 5.6e-07; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maize partial RNA-directed RNA polymerase, SEQ ID NO: 4.
                                                                                                                                                                                                            Sanger HL;
                                                                                                                                                                                                           Schiebel W,
                                                                                                                                                                                                                                                                                                         Example 7; Column 24; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB28529 standard; Protein; 417 AA.
                                                                                                                                                       97US-0811583
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                                                                                                                                                                                                          Riedel L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100,
hes 14; Conservative
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                      Tomato; gene therapy; Ri
transgenic plant; tissue
antibody; immunisation.
                                                                 Lycopersicon esculentum
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                                                                                                                                                                         (WASS/) WASSENEGGER M. (RIED/) RIEDEL L.
                                                                                                                                                                                                                                WPI; 2001-289830/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 AA;
                                                                                                                                                                                                           Wassenegger M,
                                                                                                                                                                                                                                                                                     plant breeding
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                                                                                                                                05-MAR-1997;
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                                                                                                           17-APR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB28529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maize;
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AAB28529
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New nucleic acid fragments encoding RNA-directed RNA polymerase useful for controlling gene expression and providing mechanisms to engineer plant virus resistance
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                                                                                                                                                                                                                               The present sequence is part of a plant RNA-directed RNA polymerase protein. Polymerases encoding RNA-directed RNA polymerases were isolated from plant cDNA lbraries. They are useful as probes for genetically and physically mapping genes, and as markers for traits linked to those genes. They are useful for controlling gene expression and provide mechanisms to engineer plant virus resistance. They are also useful for plant breeding to develop lines with desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14; DB 21; Length 41
Pred. No. 1.4e-05;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGS2; RNA-dependent RNA polymerase; transgene silencing; transgene stability; crop plant; viral resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of a plant SGS2 polypeptide.
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                                                                                                                                                               Claim 10; Page 34-35; 62pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (RHOB-) RHOBIO.
(INRG ) INST NAT RECH AGRONOMIQUE.
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Best Local Similarity 100.0%; Pi
Matches 14; Conservative 0;
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Pred. No. 0.00072; Mismatches 0;

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llarity 100.0%; Conservative C

Best Local Similarity Matches 11; Conserv

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The present sequence represents a plant SGS2 polypeptide. SGS2 is an RNA-dependent RNA polymerase and is involved in transgene silencing. Inactivation of SGS2 is used to increase transgene stability and expression in plants, particularly crop plants, especially maize, corn, barley, sorghum, soya, sugar cane, beet, tobacco or cotton plants. Overexpression of SGS2 can be used to increase resistance to viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid molecules encoding polypeptides with RNA-directed RNA polymerase enzymatic activity, useful in modulating gene expression in plants, humans and animals, as well as in plant cell/tissue cultures or
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                          Length 1196;
                                                                                                                                                                                                                                                                                                                                1.1%; Score 12; DB 22; Length 11
100.0%; Pred. No. 0.0052;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide #1 obtained by micro-sequencing RdRP protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE00903 standard; peptide; 11
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                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
Les 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KASAWYHVTYHP 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1124 KASAWYHVTYHP 1135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (WASS/) WASSENEGGER M.
                                                                                                                                                                                                 infection in plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-289830/30.
                                                                                                                                                                                                                                                                    1196 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transgenic plant;
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plant breeding
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                                                                                                                                                                                                                                                                       Sequence
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Length 11;

DB 22;

Score 11;

1.08;

Query Match

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This sequence represents the tomato RNA-directed RNA polymerase (RdRP) immunogenic peptide P433 used to immunise rabbits and produce an RdRP-specific antibody. The invention comprises the nucleic acid and protein sequences of RdRP, the protein of the invention can catalyse in vitro transcription of short single stranded RNAs into DNA molecules, this transcription can be either primed by RNA or DNA oligonucleotides or be unprimed. The protein may have cytostatic or virucide activities. The sequences of the invention may be used in gene therapy or as an RNA disease are useful for treating a disease caused by the undesired a disease are useful for treating a disease caused by the undesired a disease are useful for treating a disease caused by the undesired cypression of an overexpression of an uncleic acid molecule which causes a disease are useful for treating the molecules. This system can be used in the preparation of any desired gene by transferring the RdRP system to cyanisms that either lack a composition and for inhibition to the expression of any desired gene by transferring the RdRP system to cyanisms that either lack a comparable mechanism or do not sufficiently expression of any desired gene by transferring the RdRP system to cyanisms. The sequence is useful for inhibiting RNA directed RNA synthesis and for ensuring stable heterologous, gene expression in transgent organisms. The sequence is useful for impulsitionally, nucleotide and protein sequences are useful for sapility, nucleotide and protein sequences are useful for sapility, nucleotide and protein sequences are useful for supplication of sequences are useful for supplication of the control of gene expression in humans and animals and the animals and the multipody is useful for infinitionally, indectide and protein sequences are useful for infinitionally indectide and protein sequences are useful for infinitely and the sequence is useful as a therapeutic agent for the control of cancer and virus infection in humans and animals and animals an enti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid molecule encoding a polypeptide having the enzymatic activity of RNA-directed RNA polymerase, for modulating gene expression and treating cancer and virus infection in human and animals -
                                                                                                                                                                                                                                                                                                                                                      Tomato, RGRP, RNA-directed RNA polymerase; in vitro transcription; vyrostatic, virucide; RNA synthesis inhibitor; antibody; immunogen; transgenic plant; transgenic animal; cancer; viral infection; immunoprecipitation; immunolocalisation; P433; gene therapy.
                                                                                                                                                                                                                                                                                                           Tomato RNA-directed RNA polymerase (RdRP) immunogenic peptide P433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sanger HL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schiebel W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 7; Page 14; 34pp; English.
                                                                                                                                                               AAU10010 standard; Peptide; 13 AA.
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EYPDFMDKPDK 919
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                      1 EYPDFMDKPDK
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RESULT 17

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New nucleic acid fragments encoding RNA-directed RNA polymerase useful for controlling gene expression and providing mechanisms to engineer plant virus resistance
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                                                                                                                                                                                              plant; RNA-directed RNA polymerase; gene mapping; gene marker; virus resistance; plant breeding.
                                                                                                                                                        Rice RNA-directed RNA polymerase, SEQ ID NO: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; Page 46-49; 62pp; English.
                                         AAB28532 standard; Protein; 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DUPO ) DU PONT DE NEMOURS & CO (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Weng Z,
                                                                                                                                                                                                                                                                                                                                                                                                            99US-0128094.
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                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Odell JT, Orozco EM,
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N-PSDB; AAC63741.
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                                                                                                                                                                                                                                                          Oryza sativa.
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                                                                              AAB28532;
    RESULT 18
AAB28532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a tomato C-protein-specific antibody, P433 chosen for Immunisation of rabbles. C-protein having RNA-directed RNA polymerase (RdRP) activity is capable of RNA-directed RNA synthesis, thus using RNA as a template for synthesising complementary RNA molecules. RdRP nucleic acid is useful for modulating gene expression in plants, humans and animals. This may lead to various physiological, developmental and/or morphological changes. Transgenic plants containing RdRP nucleic acid is especially useful in plant cell or tissue cultures and in plant breeding. RdRP is useful in gene therapy, particularly for treating a disease that is caused by the undesirable expression or overexpression of a gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy; RNA-directed RNA polymerase; RdRP; gene expression; it plant; tissue culture; plant breeding; therapy; C-protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid molecules encoding polypeptides with RNA-directed RNA polymerase enzymatic activity, useful in modulating gene expression in plants, humans and animals, as well as in plant cell/tissue cultures or
of polypeptides interacting with it and screening expression libraries
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100.0%; Pred. No. 0.0099;
ive 0; Mismatches 0; Indels
                                                         Score 10; DB 22; Length 13.
Pred. No. 0.0099;
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100.0%; Pred. No. v..
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                                                                                                                                                                                                                                                                                             AAE00902 standard; peptide; 13 AA.
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                                                                                               Local Similarity 100.
ses 10; Conservative
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antibody; immunisation.
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Best Local Similarity
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                                       13 AA;
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                                                                                                                                                                                Gaps
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Query Match 0.9%; Score 10; DB 21; Length 836; Best Local Similarity 100.0%; Pred. No. 0.51; Matches 10; Conservative 0; Mismatches 0; Indels
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, mannomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                          The present sequence is part of a plant RNA-directed RNA polymerase protein. Polymuclectides encoding RNA-directed RNA polymerases were isolated from plant cDNA libraries. They are useful as probes for genetically and physically mapping genes, and as markers for traits linked to those genes. They are useful for controlling gene expression and provide mechanisms to engineer plant virus resistance. They are also useful for plant breeding to develop lines with desired
for controlling gene expression and providing mechanisms to engineer plant virus resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID NO 17425; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                      Length 60;
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. 0.5;
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100.0%; Pred. No. 0.5
tive 0; Mismatches
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                                                          62pp; English.
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18-MAY-2000; 2000US-0577409.
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                                                          Claim 23; Page 60;
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                                                                                                                                                                                                                                                                    60 AA;
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                                                                                                                                                                                                                                  phenotypes.
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                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is part of a plant RNA-directed RNA polymerase protein. Polymucleotides encoding RNA-directed RNA polymerases were isolated from plant cDNA libraries. They are useful as probes for genetically and physically mapping genes, and as markers for trafts linked to those genes. They are useful for controlling expression and provide mechanisms to engineer plant virus resistance. They are also useful for plant breeding to develop lines with desired
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00.0%; Pred. No. 0.7;
ve 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Soybean RNA-directed RNA polymerase, SEQ ID NO: 20.
                                                                                                                                                                                      Sakai H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'n
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                                                                                                                            (DUPO ) DU PONT DE NEMOURS & CO E I.
(PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                          New nucleic acid fragments encoding
for controlling gene expression and
plant virus resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DUPO ) DU PONT DE NEMOURS & CO E I. (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                          Claim 10; Page 41-45; 62pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pr
                                                                                                                                                                                      Weng Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB28537 standard; Protein; 60
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                                                    06-APR-2000; 2000WO-US09105
                                                                                          99US-0128094
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N-PSDB; AAC63746.
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                                                                                                                                                                                                                                            N-PSDB; AAC63740
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                  12-OCT-2000.
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RESULT 23
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                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                       Corn; histidine biosynthetic enzyme; HisA; clone p0085.cscail9r; phosphoribosylformimino-5-aminoimidazole carboxamide.ribotide isomerase; herbicide; fungicide.
treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a phosphoribosylformimino-5-
aminoimidazole carboxamide ribotide isomerase (HisA) which is a
histidine biosynthetic enzyme. The sequence is derived from
p0085.cscailyr clone isolated from a corn shoot culture cDNA library
p0085. The present sequence is useful in altering the
levels of HisA enzyme in transformed plant cells.
It may also be used for discovering compounds that have the ability
to inhibit activity of the isomerase, and therefore act as herbicides
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                                                                                                                                                                                                                                                                                   Corn histidine biosynthetic enzyme HisA from clone p0085.cscai19r.
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                                                                                       0.7%; Score 8; DB 22; Length 93;
100.0%; Pred. No. 8.8;
Live 0; Mismatches 0; Indels
                                                                                                               0; Indels
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Mismatches
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                                                                                                                                                                                                                 AAY70941 standard; Protein; 130 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cahoon RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.7%; Soc
Best Local Similarity 100.0%; Pr
Matches 8; Conservative 0;
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                                                                                 Ouery Match
Best Local Similarity 100.
Watches 8; Conservative
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N-PSDB; AAD00287.
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                                                                                                                                    127 LKKFFFFL 134
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                                                                  93 AA;
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51 LKKFFFFL 58
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AMU18235 standard, Protein; 283 AA.

AMU18235;
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AMU18235;
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AMU18235;
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AMU18235;
XX
El-NOV-2001 (first entry)
XX
El-NOV-2001 (first entry)
XX
Human: Nh-binding protein histone; chrom domain protein;
XX
Human: Man-binding protein; histone; chrom domain protein;
XX
Infections disease; neurological disease; genetic abnormality;
XX
Infections disease; neurological disorder; gene therapy;
XX
Infections disease; neurological disorder; disease; disease;
XX
Infections disease; disease
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2000US-0231242

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2000US-0249244
2000US-0249245
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            08-SEP-2000;
08-SEP-2000;
12-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
13-0CT-2000;
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29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
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The present invention relates to the isolation of novel DNA-binding proteins, and cDNA (AAS29030-AAS29157) and genomic sequences encoding proteins and cDNA (AAS29030-AAS29157) and genomic sequences encoding for these proteins action modifier) domain proteins, and Y-box binding proteins may contribute to diseases resulting from aberrant DNA organisation and/or gene transcription. The sequences of the invention are useful in screening assays to identify antagonists and/or agonists chat may enhance or block activities mediated by DNA-binding proteins. Blockers of DNA-binding proteins may be useful in treating disorders cauch as mailginant diseases (e.g. cancer), autoimmune disorders cauch as mailginant diseases (e.g. cancer), autoimmune disorders city arthitis), genetic abnormalities (e.g. cystic fibrosis), infectious diseases (e.g. HIV) and neurological disorders (e.g. Alzheimer's diseases). The polynucleotide sequences of the invention may also be used in gene therapy. AAU18154-AAU18281 represent novel DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid molecules encoding human secreted chromosomal binding proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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100.0%; Pred. No. 25;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; SEQ ID No 220; 561pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA, Barash SC, Ruben SM;
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17-NOV-2000; 2000US-0249264.

17-NOV-2000; 2000US-0249265.

17-NOV-2000; 2000US-0249297.

17-NOV-2000; 2000US-0249299.

17-NOV-2000; 2000US-0249299.

17-NOV-2000; 2000US-0250160.

01-DEC-2000; 2000US-0250160.

05-DEC-2000; 2000US-0251030.

05-DEC-2000; 2000US-0251888.

05-DEC-2000; 2000US-0251856.

08-DEC-2000; 2000US-0251856.

08-DEC-2000; 2000US-0251869.

08-DEC-2000; 2000US-0251869.

08-DEC-2000; 2000US-0251869.

08-DEC-2000; 2000US-0251869.

08-DEC-2000; 2000US-0251869.

08-DEC-2000; 2000US-0251869.

08-DEC-2000; 2000US-0251989.

08-DEC-2000; 2000US-0251989.
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Best Local Similarity 100.
Matches 8; Conservative
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N-PSDB; AAS29111.
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The present sequence represents human Vpr interacting protein (hVIP). DNA encoding hVIP can be used to transform host cells to express the protein. Sequences complementary to the DNA can be used in methods for inhibiting expression of hVIP, treating an individual who has cancer, and for inhibiting hVIP activity in a cell. The hVIP can also be used to treat hyperproliferative diseases and some autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents human vpr interacting protein (hVIP). DNA encoding hVIP can be used to transform host cells to express the protein. Sequences complementary to the DNA can be used in methods for inhibiting expression of hVIP, treating an individual who has cancer, and for inhibiting hVIP activity in a cell. The hVIP can also be used to treat hyperproliferative diseases and some autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; VIP; hVIP; cellular receptor; HIV-1; cell cycle; cancer; hyperproliferative disease;
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                                                                                                       Human Vpr interacting protein for, e.g. treatment of cancer
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                  Weiner
                                                                                                                                                                                                                                                                                                                                  0.7%; Score 8; DB 2
100.0%; Pred. No. 30;
:ive 0; Mismatches
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                Patel M,
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                                                                                                                                       Claim 1; Page 51-52; 58pp; English
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Best Local Similarity 100.
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                Ayyavoo V, Mahalingam
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N-PSDB; AAX55872.
                                                  WPI: 1999-277596/23.
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autoimmune disease.
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                                                                     N-PSDB; AAX55871
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Wheat; histidine biosynthetic enzyme; HisA; clone wleln.pk0018.bl0; phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; VIP; hVIP; cellular receptor; HIV-1; cell cycle; cancer; hyperproliferative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a phosphoribosylformimino-5-
aminoimidazole carboxamide ribotide isomerase (HisA) which is a
histidine biosynthetic enzyme. The sequence is derived from
wheln.pk0018.bi0 clone isolated from a wheat leaf cDNA library wleln.
The present sequence is useful in altering the
levels of HisA enzyme in transformed plant cells.
It may also be used for discovering compounds that have the ability
to inhibit activity of the isomerase, and therefore act as herbicides
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                                                                                                                                                                                                                                                                                                                                                                      Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase, polypeptide (P), useful for discovering compounds which inhibit isomerase activity and act as herbicides and fungicides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 0.7%; Score 8; DB 21; Length 327; Best Local Similarity 100.0%; Pred. No. 29; Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                               DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 46-47; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY09307 standard; Protein; 341 AA
                                                                                                                                                                                                                                                                                   Cahoon RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Vpr interacting protein.
                                                                                                                                                                             99WO-US24698
                                                                                                                                                                                                               98US-0105409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; Vpr interacting
G2/M phase transition;
                                                                                                                                                                                                                                                                                   Allen SM,
                                   herbicide; fungicide
                                                                                                                                                                                                                                                                                                                     WPI; 2000-350713/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G2/M phase transiti
autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             327 AA;
                                                                     Triticum aestivum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   520 TSYVESDG 527
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                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAD00293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and fungicides.
                                                                                                       WO200024867-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9919359-A1
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                                                                                                                                                                           21-OCT-1999;
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                                                                                                                                         04-MAY-2000
                                                                                                                                                                                                                                                                                   Abell LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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RESULT 25 AAY09307

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2000US-0234233
2000US-02342424
2000US-0234997
2000US-0234998
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2000US-0246610
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01-SEP-2000

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                          Gaps
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                                                                                                                                                                                                                                                                                                                                      Human, DNA-binding protein, histone, chromo domain protein, chromatin organisation modifier, Y-box binding protein, DNA organisation; gene transcription; malignant disease, autoimmune disorder; rheumatic disease; genetic abnormality; infectious disease, neurological disorder; gene therapy; immunomodulatory; anti-HIV; anti rheumatic; anti microbial;
                          0; Indels
  100.0%; Pred. No. 30; ative 0; Mismatches
                                                                                                                                                                                                                                                                                                      Novel human DNA-binding protein #2.
                                                                                                                                                                                            AAU18155 standard; Protein; 477 AA
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2000US-0229344
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                                                                                                                                                                                                                                                                    (first entry)
    Best Local Similarity 100.
Matches 8; Conservative
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26 FFFLSSG 33
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16-MAR-2000; 2

18-APR-2000; 2

19-APR-2000; 2

19-APR-2000; 2

28-JUN-2000; 2

28-JUN-2000; 2

28-JUN-2000; 2

11-JUL-2000; 2

11-JUL-2000; 2

11-JUL-2000; 2

14-AUG-2000; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic.
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17-NOV-2000;

17-NOV-2000;

08-DEC-2000;

05-DEC-2

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isoprenoids. More particularly the invention provides isolated nucleic acids, substantially pure polypeptides, host cells, and methods for the production stoprenoid compounds. The polypeptides are useful for the production of isoprenoids, especially COQ(10). Expressing the pure polypeptides, which has 1-deoxyxylulose-5-phosphate synthase (DKS) activity or decaprenyl diphosphate synthase (DDS) activity, is useful for increasing production of COQ(10) in a cell having endogenous DDS activity. This sequence represents a protein relating to the isoprenoid production of the invention.
                                                                                                                Isoprenoid; CoQ(10); 1-deoxyxylulose-5-phosphate synthase; DXS; DDS;
decaprenyl diphosphate synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to methods and materials for the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                            Isoprenoid related protein sequence SEQ ID No 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Substantially pure polypeptides having e.g., 1-deoxyxylulose-5-phosphate synthase activity, production of isoprenoids, especially CoQ(10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herbicidally active polypeptide SEQ ID NO 2282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.7%; Score 8; DB 2
100.0%; Pred. No. 55;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 6; 246pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   Zidwick MJ;
                                                                                                                                                                                                                                                                                                                                         29-SEP-2000; 2000US-236580P.
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                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity luv...
8; Conservative
                                                                                                                                                                              Rhodobacter capsulatus.
                                                                                                                                                                                                                                                                                                                                                                                                                        Gokarn R, Jessen H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-416480/44.
                                                                                                                                                                                                                                                                                                                                                                               (CRGI ) CARGILL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              641 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 465 GLTANDIR 472
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                                        13-SEP-2002
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AA021854;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid molecules encoding human secreted chromosomal binding proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to the isolation of novel DNA-binding proteins, and cDNA (AAS29030-AAS29157) and genomic sequences encoding for these proteins. DNA-binding proteins such as histones, chromo chromatin organisation modifier) domain proteins, and Y-box binding proteins may contribute to diseases resulting from aberrant DNA organisation and/or gene transcription. The sequences of the invention are useful in screening assays to identify antagonists and/or agonists that may enhance or block activities mediated by DNA-binding proteins. Blockers of DNA-binding proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         such as malignant diseases (e.g. cancer), autoimmune disorders (e.g. diabetes mellitus), rheumatic diseases (e.g. rheumatoid arthritis), genetic abnormalities (e.g. cystic fibrosis), infectious diseases (e.g. HIV) and neurological disorders (e.g. Alzheimer's disease). The polynucleotide sequences of the invention may also be used in gene therapy. AAU18154-AAU18281 represent novel DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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100.0%; Pred. No. 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; SEQ ID No 140; 561pp; English.
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100.0%; Pir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
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N-PSDB; AAS29031.
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nes 8; Conserv
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                                                                                                                17-NOV-2000;
17-NOV-2000;
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08-DEC-2000;
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Sequence Query Match

Best Loc Matches

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RESULT 28
AAO21854
ID AAO218

proteins

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ABG09723;
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                                                                                                                                            The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an B-value sequences are actor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.
                                                                            Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                             Claim 5; SEQ ID NO 2282; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                   0.7%; Score 8; DB 23; Length 830;
100.0%; Pred. No. 70;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #9408.
                                                                                                                                                                                                                                                                                                                                                                                ABG09417 standard; Protein; 1600 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT;
28-AUG-2001; 2001WO-EP09892,
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                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 100.
                                       Tietjen K, Weidler M;
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                                                          WPI; 2002-269010/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                 830 AA;
                                                                                                                                                                                                                                                                                                            606 LITLLSTL 613
                                                                                                                                                                                                                                                                                                                               162 LITLLSTL 169
                    (FARB ) BAYER AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAS73604
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                                                                                                             organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
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The invention relates to isolated polynucleotide (I) and probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The charter is a series of (II). The polymerating expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving constituting a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymenteotide sequences have applications in dispnostics, forensics, gene mapping, identification of mutations in to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human of agenemic data for this patent did not appear in the printed sequence the types of the invention.

Note: The sequence data for this patent did not appear in the printed sequence in the printed sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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Pred. No.
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polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving cartivity of (II) or to treat disease states involving cartivity of (II) or to treat disease states involving a food supplement. (II) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and the produce cate and sequences of the invention.

Note: The sequence data for this patent did not appear in the printed are the print of the pr
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food supplement; medical imaging; diagnostic; genetic disorder.
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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as
      (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abbarrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the very sequences.
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food supplement; medical imaging; diagnostic; genetic disorder.
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100.0%; Pred. No. 1.7e+02;
ative 0; Mismatches 0;
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23-AUG-2000; 2000US-0649167.
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8; Conservative
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                                                                                                                                                                                                                                                                                                      2168 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for identifying expressed genes. (I) is useful in gene therapy techniques

(II) is useful for generating antibodies against it, detecting or

(II) is useful for generating antibodies against it, detecting or

quantitating a polypeptide in tissue, as molecular weight markers and as

a food supplement. (II) and its binding partners are useful in medical

imaging of sites expressing (II). (I) and (II) are useful for treating

disorders involving aberrant protein expression or biological activity.

The polypeptide and polymucleotide sequences have applications in

The polypeptide and polymucleotide sequences have applications in

The polypeptide of genetic disorders or other traits to assess biodiversity

and to produce other types of data and products dependent on DNA and

amino acid sequences. ABG00010-ABG30377 represent novel human

Mote: The sequence data for this patent did not appear in the printed

specification, but was obtained in electronic format directly from WIPO.
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Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human diagnostic protein #9411.
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23-AUG-2000; 2000US-0649167.
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N-PSDB; AAS73607.
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a food supplement. (II) and its binding partners are useful in medical imaging of sites expression (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences.
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23-AUG-2000; 2000US-0649167.
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Matches 8; Conservative
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N-PSDB; AAS76474.
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disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to asses biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human happened as sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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100.0%; Pred. No. 1.80+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #20013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG20022 standard; Protein; 2176 AA.
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diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 repressent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a tomato RNA-directed RNA polymerase (RdRP) peptide sequence used to create a degenerate nucleotide sequence and degenerate PCR primers used to amplify the RdRP cDNA sequence of the invention. The invention comprises the nucleic acid and protein sequences of RdRP, the protein of the invention can catalyse in vitro transcription of short single stranded RNA into DNA molecules, this transcription can be either primed by RNA or DNA oligonucleotides or be unprimed. The protein may have cytostatic or virucide activities. The sequences of the invention may be used in gene therapy or as an RNA directed RNA synthesis inhibitor. The RdRP cDNA sequence and a template
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid molecule encoding a polypeptide having the enzymatic activity of RNA-directed RNA polymerase, for modulating gene expression and treating cancer and virus infection in human and animals -
                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                         Tomato RNA-directed RNA polymerase (RdRP) 130 kDa-15 AS sequence.
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a disease are useful for treating a disease caused by the undestred expression or overexpression of a nucleic acid molecule in a human, rat or prouse, by administering the molecules. This system can be used in the preparation of a pharmaceutical composition and for inhibiting capression of any desired gene by transferring the RGRP system to cryanisms that either lack a comparable mechanism or do not sufficiently expression of any desired gene by transferring the RGRP system to protein are useful for inhibiting RNA directed RNA synthesis and for protein are useful for inhibiting RNA directed RNA synthesis and for protein are useful for inhibiting RNA directed RNA synthesis and for protein are useful for probes and/or for the control of gene expression, as primers for amplification of nucleic acid molecules and as the standard of expression of the cDNA molecules and additionally, nucleotide and protein sequences are useful for suppression of undesired gene expression in humans and animals and the antibody is useful for in humans and animals and the antibody is useful for immunoprecipitation or immunolocalisation of the protein, identification immunoprecipitation or immunolocalisation of the protein, identification or immunolocalisation of the protein identification or immunolocalisation of the protein identification or immunolocalisation of the protein identification in the control of the protein identification or immunolocalisation identification in the control of the protein identification o
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nucleic acid molecule derived from a nucleic acid molecule which causes
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100.0%; Pred. No. 22;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB43113 standard; Peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0232366.
2000US-0234687.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             640 KAQEALE 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KACEALE 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB43113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
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AAM76838 standard; Protein; 18 AA.
572 KLSLRKS 578
                    8
                                                                                                                                                                                                                                                                                                26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                      12 KLSLRKS
                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                        04-FEB-2000;
                                                                                                                      06-NOV-2001
                                                                                                                                                                                                                                             09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM36944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                 AAM76838;
                                                                                                                                                                                                                                                                                                                                                                                                    Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 42
                                                       RESULT 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                                                         Human brain expressed single exon probe encoded protein SEQ ID NO: 36120.
         fetal liver. The present sequence is a pertide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon nucleic acid probes for analyzing gene expression in human
 gene expression in samples derived from human
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                             Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; SEQ ID NO: 36120; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 18;
                                                                                                  DB 22; Length 18;
                                                                                                                       Indels
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.6%; Score 7; DB 2
100.0%; Pred. No. 22;
ive 0; Mismatches
                                                                                                                       0; Mismatches
                                                                                                 0.6%; Score 7; I
100,0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank
                                                                                                                                                                                                                         AAM64015 standard; Protein; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-2000; 2000US-0207456.
30-UUN-2000; 2000US-0608408.
21-SEP-2000; 2000US-023366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-023559.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2001; 2001WO-US00667
                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.6
Best Local Similarity 100.
Matches 7; Conservative
 and displaying
                                                                                                                       7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-483446/52
                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel
                                                                             18 AA
                                                                                                                                             572 KLSLRKS 578
                                                                                                                                                           12 KLSLRKS 18
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26-MAY-2000; 2
30-JUN-2000; 2
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                    05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001
 measuring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                              AAM64015;
                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  brains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn
                                                                                                                         Matches
                                                                                                                                                                                                   RESULT 40
                                                                                                                                                                                                              AAM64015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide #10981 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; SEQ ID NO: 37144; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                              Human; bone marrow expressed exon; gene expression analysis; microarray; cancer; leukaemia; lymphoma; myeloma.
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100.0%; Pred. No. 22;
ive 0; Mismatches 0; Indels
Human bone marrow expressed probe encoded protein SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM36944 standard; Protein; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                               2000US-0180312.
2000US-0207456.
2000US-0632346.
2000US-0234687.
2000US-0234687.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488900/53
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nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      572 KLSLRKS 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 KLSLRKS 18
                                                                                                                                                                      WO200157276-A2.
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ID AAM3
XX
XX
AC AAM3
XX
XX
DT 17-C
XX
XX
XX
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Gaps

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Indels

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foetal liver; gene expression; single exon nucleic acid probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB44400 standard; Peptide; 24 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2002 (first entry)
                                                                                                                                      WPI; 2001-289830/30.
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                   Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             640 KAQEALE 646
                                                                                                                                                N-PSDB; AAD04382
                                                                                                (RIED/) RIEDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157277-A2.
                                                                                                                                                                                                 plant breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KAQEALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                35-MAR-1997;
                                                                    05-MAR-1997;
          US6218142-B1
                              17-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB44400;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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ABB44400
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                       Length 18;
Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide #2 obtained by micro-sequencing RdRP protein.
                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
                                                                                                                                                                                                                                                                                                                                                                                      Score 7; DB 22; Pred. No. 22; 0; Mismatches
                                                                                                                                                                                                                                                            analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                             Claim 27; SEQ ID No 37213; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Lys, Asn
/note= "Encoded by AAN"
17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Encoded by YTN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Encoded by WSN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Encoded by YIN"
                                                                                                                                                                                                           Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE00904 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                      h 0.6%; Sc.
Similarity 100.0%; Pi
7; Conservative 0;
                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                         04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-UNN-2000; 2000US-0608408.
03-MUS-2000; 2000US-0632366.
21-SEP-2000; 2000US-0238356.
27-SEP-2000; 2000US-0238359.
                                                                                       30-JAN-2001; 2001WO-US00663.
                                                                                                                                                                   04-OCT-2000; 2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                 human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lycopersicon esculentum
                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                              WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                    18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                              572 KLSLRKS 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 18
                                               WO200157272-A2
                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                           12 KLSLRKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-JUL-2001
                                                                   09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                           Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 43
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The present sequence is a peptide encoded by an oligonucleotide which is used to design RNA-directed RNA polymerase (RGRP)-specific PCR primers. Hases PCR primers are used to amplify a cDNA encoding tomato C-protein having RdRP activity. The peptide is obtained by micro-sequencing RdRP protein is capable of RNA-directed RNA synthesis, thus using RNA as a template for synthesising complementary RNA modecules. RGRP nucleic acid is useful for modulating gene expression in plants, humans and animals. This may lead to various physiological, developmental and/or morphological changes. Transgenic plants containing RdRP nucleic acid is especially useful in plant cell or tissue cultures and in plant breeding. RdRP is useful in gene therapy, particularly for treating a disease that is caused by the undestrable expression or overexpression of a gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecules encoding polypeptides with RNA-directed RNA polymerase enzymatic activity, useful in modulating gene expression in plants, humans and animals, as well as in plant cell/tissue cultures or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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100.0%; Pred. No. 22;
ative 0; Mismatches
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97US-0811583,
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                                                                                                                                                         (WASS/) WASSENEGGER M.
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04-OCT-2000
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                                                                                                Seguence
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                                                                                                                                                                                                                                                                                                                                                                                     Human brain expressed single exon probe encoded protein SEQ ID NO: 37583.
                                                                                                                       The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzhelmer's disease; multiple sclerosis; schizophrenia;
                                                                              genome-deriyed single exon nucleic acid probes useful for
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                                                                                                       Claim 27; SEQ ID NO 37035; 639pp + sequence listing; English.
                                                                                                                                                                                                                                DB 22; Length 24; . 29;
                                                                                                                                                                                                                                                  0; Indels
                                                                                       analyzing gene expression in human fetal liver
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Pred. No. 29;
0; Mismatches
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100.0%; Pre
0;
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                         (MOLE-) MOLECULAR DYNAMICS INC
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                                           Chen W,
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2000US-0207456.
2000US-0608408.
2000US-063366.
2000US-0234687.
2000US-0236359.
2000GB-0024263.
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Best Local Similarity 100.
Matches 7; Conservative
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                                                            WPI; 2001-483447/52
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                                           Hanzel
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27-SEP-2000;
04-OCT-2000;
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26-MAY-2000;
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03-AUG-2000;
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27-SEP-2000;
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                                          Penn SG,
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                                                                              Human
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                                                           probes which are derived from genomic sequences expressed in the human brain. They can be used from genomic sequences expressed in the human which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimær's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide #8452 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; microarray; gene expression; cervical epithelial cell;
                                                        present invention provides a number of single exon nucleic acid
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Example 4; SEQ ID NO: 37583; 650pp + Sequence Listing; English.
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analyzing gene expression in human cervical epithelial cells
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100.0%; Pred. No. 29;
iive 0; Mismatches
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2000US-0207456.
2000US-0608408.
2000US-0632366.
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2000US-0236359
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                        24 AA;
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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AAY18363

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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; antioonvulsant; antibeterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
                                                                                                                                                                                                                                                                        This sequence represents a fragment of human chromogranins A (CgA). The invention relates to an antibody having a reactivity specific to human CgA, which is prepared by immunising a warm-blooded animal, other than human, using this peptide. The antibody is useful in a method for detecting and/or measuring human CgA. The method can measure and detect human CgA with a high sensitivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
                                                                                                                                                                                                       New antibody - has reactivity specific to human chromogranins A
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100.0%; Pred. No. 36;
Live 0; Mismatches
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                                                                                                                                                                                                                                                   Claim 1; Page 2; 10pp; Japanese.
                                                                                                                                            (YANA-) YANAIHARA KENKYUSHO KK.
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                                                                                                                  97JP-0336452.
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99US-0169623.
                                                                                     97JP-0336452
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Best Local Similarity 100.
Matches 7; Conservative
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N-PSDB; AAC59408.
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Homo sapiens.
                          JP11153598-A.
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Pred. No.
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100.0%; Pred. No.
ive 0; Mismatch
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                            0.6%; Sco...
100.0%; Pre
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                                                                       Conservative
                       Query Match
Best Local Similarity
7, Conserve
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            24 AA;
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            Sequence
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568 Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant, corn, Arabidopsis thaliana; sequence-determined DNA fragment; SDF; genetic mapping; identification; promoter; structural gene; UTR; untranslated region; expression control.
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                                                                                                                                                                                                                  AAB33963-B34006 represent the amino acid sequences of 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                      Claim 11; Page 363; 410pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB25008 standard; Peptide; 40 AA.
Parkinson's diseases and cancers
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nes 7; Conservative
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20 FFFFLSS 26
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CC Arabidopsis thaliana. The SDFs are promoters, structural genes, contranslated regions (UTRs), or 3, termination sequences. They can be used for expressing gene product and controlling expression of a crarget gene, either as a promoter, a structural gene, an UTR or as a consider a squence. They are also useful as tools for genetic constering a group pf plants with a common trait. AAA78433 to AAA78630 con and AAA24605 to AAB25099 represent the specifically claimed considered and polypeptides encoded by them given in the conservation.

XX XX Squence 40 AA;

Query Match

Query Match

Query Match

At 130 FFFFLSS 136

Db 19 FFFFLSS 25

Search completed: November 6, 2002, 03:33:28

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NESOUR 1

NESOUR 62181-583-2

Sequence 2, Application US/08811583

Factor No. 6218142

GENERAL INFORMATION:
APPLICANT: Wassenger, Michael
APPLICANT: Schiebel, Winfried
APPLICANT: Reader, Hebra 1

TITLE OF INVENTION: RNA-DIRECTED RNA POLYMERASE (RRPP)

NUMBER OF SCHORNES: 13

CORRESPONDENCE ADDRESS: 13

CONDUTER: ISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STREET: 1251 Avenue of the Americas
CONDUTER: TEMP Compatible
OPERATING SYSTEM: PC-COMPATION
COMPUTER: Patentin Release #1.0, Version #1.30

COMPUTER: Patentin Release #1.0, Version #1.30

CONFURENT APPLICATION NDATA:
APPLICATION NUMBER: 15,794

REGISTRATION NUMBER: 27,794

REGISTRATION NUMBER: 27,794

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MPG-1

TELEPONMUNICATION INFORMATION:
TELEPANT 212-56-5000

TELEPHONE 212-56-5000

TELEPHONE 212-56-5000

TELEPANT STREET ST
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US-08-791-1158-27
US-08-791-1158-21
US-08-791-1158-25
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US-09-136-828-6
US-09-136-828-6
US-09-136-828-6
US-09-136-828-15
US-08-968-563-15
US-08-968-563-15
US-08-968-563-15
US-08-968-111-158-6
US-08-968-111-158-6
US-08-911-1158-6
US-08-791-1158-6
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LENGTH: 1114 amino acids
protein
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US-08-811-583-2
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13, Appl
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3132, Ap
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3132, Ap
3132, Appl
4, Appl
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110, Appl
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394.905 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                           1114
1 MGKTIQVFGFPYLLSAEVVK......RPVLNLSSLRAQLSHRLVLK 1114
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                                                                                                                                                                              2002, 03:36:48 ; Search time 83 Seconds
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1: /ogqu_G/ptodate/2/iaa/5A_COMB.pep:*
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6: /cgn2_G/ptodata/2/iaa/PcTUS_COMB.pep:*
                        GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-811-583-3
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US-08-941-583-13
US-08-941-583-13
US-08-949-202-4
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US-09-134-01C-3132
US-08-297-431B-4
US-08-297-431B-1

US-08-297-431B-16
US-08-297-431B-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262574 seqs, 29422922 residues
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Gapop 60.0 , Gapext 60.0
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Match Length DB
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                                                                                                                            protein search,
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Perfect score:
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Length 1114;

DB 4;

Score 1114;

100.0%;

Query Match

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ACTIVITY

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                                                                                                                                                                                                                        MOLECULES ENCODING
HAVING THE ENZYMATIC
RNA POLYMERASE (RGRP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 19.6%; Score 218; D8 4; Le
Best Local Similarity 100.0%; Pred. No. 7.4e-211;
Matches 218; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Version #1.30
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ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIBM PC COMPATIBLE
COMPUTER: LIBM PC COMPATIBLE
COMPUTER: LIBM PC COMPATIBLE
COMPUTER: DEATER PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-MR-1997
CLASSIFICATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MPG-1
TELECHOME: 212-596-9000
TELEFAX: 218-MINO acids
                                          1081 YDQLIQIKKDKARNRPVLNLSSLRAQLSHRLVLK
                                                                                             Sequence 3, Application US/08811583
Patent No. 6218142
GENERAL INFORMATION:
APPLICANT: Wasseneger, Michael
APPLICANT: Riedel, Leonhard
APPLICANT: Schebel, Winfried
APPLICANT: Sanger, Heinz
TITLE OF INVENTION: NUCLEIC ACID MOLE
TITLE OF INVENTION: PRA-DIRESTED RNA
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: FISH & NEAVE
STREET: 1251 Avenue of the Amarican
                                                                                                                                                                                                                                                                                          SSEE: FISH & NEAVE
: 1251 Avenue of the Americas
New York
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 218 amino acids amino acid
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TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-811-583-3
                                                                                                RESULT 2
US-08-811-583-3
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                                                                                                                                                      IQFGIGLKKFFFFLSSGSADYKLQLSYENIWQVVLHRPYGQNAQFLLIQLFGAPRIYKRL 180
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                                                                                                 IITLANNRLYFGSSYLKAWEMKTDIVQLRAYVDQMDGITLNFGCQISDDKFAVLGSTEVS 120
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                                                         1 MGKTIQVFGFPYLLSAEVVKSFLEKYTGYGTVCALEVKQSKGGSRAFAKVQFADNISADK 60
                 Gaps
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 Best Local Similarity 100.0%; Pred. No. 0; Matches 1114; Conservative 0; Mismatches
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Query Match 1.3
Best Local Similarity 100.
Matches 14; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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        Sequence 12, Application US/08811583
Fatent No. 6218142
GENERAL INFORMATION:
APPLICANT: Wassenegger, Michael
APPLICANT: Riedel, Leonhard
APPLICANT: Schiebel, Winfried
APPLICANT: Winfried
APPLICANT: New York
COUNTRY: USA
CITY: New York
COUNTRY: USA
COUNTRY: USA
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Patent No. 6218142

GENERAL INFORMATION:

APPLICANT: Wassenegger, Michael

APPLICANT: Riedel, Leonhard

APPLICANT: Schlebel, Whifried

APPLICANT: Schlebel, Winfried

APPLICANT: Schlebel, Winfried

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENZYMATIC ACTIVITY OF AN TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENZYMATIC ACTIVITY OF AN ADDRESSED: FISH & NEAVE

SCHRESPONDENCE ADDRESS:

ADDRESSEE: FISH & NEAVE

STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.5%; Score 17; DB 4; Length 17;
100.0%; Pred. No. 8.6e-10;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: PACENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,583
FILING DATE: 05-MAR-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MPG-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-900
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
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Matches 17; Conservative
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MOLECULE TYPE: peptide
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-08-811-583-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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COMPUTER READERS PROBLES CONF.

COMPUTER TREADERS PROBLES CONF.

CONFESSIONAL STATE CON
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APPLICANN: Mahalingam Sundarasamy
APPLICANY: Mahalingam Sundarasamy
TITLE OF INVENTION: GZ/M PHASE TRANSITION OF THE CELL CYCLE
TITLE OF INVENTION: GZ/M PHASE TRANSITION OF THE CELL CYCLE
NUMBER OF SEQUENCES:
ADDRESSES: Mondecock Washburn Kurtz Macklewicz & No. 6060587ris
STREET: One Liberty Place 46th floor
STREET: One Liberty Place 46th floor
CITY: Philadelphia
STREET: One Liberty Place 46th floor
STREET: Done Liberty Place 46th floor
CONNTRY: USA
CONNTRY: USA
COMPUTER: Teleppy disk
COMPUTER: TEMP Compatible
OPERATING SYSTEM: Windows NT
SOFTWARE: Wordperfect 6.
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/949,202
FILING DATE:
CLASSIFICATION NUMBER: US/06/949,202
FILING DATE:
APPLICATION NUMBER: US/06/949,202
TELEPHONE: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 341 amino acids
TYPE: APPLICATION acids
TYPE: APPLICATION STATES
TOPOLOGY: Incar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Weiner, David B
APPLICANT: Weiner, David B
APPLICANT: Weiner, David B
APPLICANT: Manad
APPLICANT: Manad
APPLICANT: Patel, Manad
APPLICANT: Patel, Manad
APPLICANT: Patel, Manad
APLICANT: Patel, Manad
TITLE OF INVENTION: CELLULAR RECEPTOR FOR HIV-1 VPR ESSENTIAL FOR
TITLE OF INVENTION: G2/M PHASE TRANSITION OF THE CELL CYCLE
NUMBER OF SEQUENCES: 4
CORRESSONDENCES: 4
CORRESSONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6060587ris
STREET: One Liberty Place 46th floor
CITY: Philadelphia
STREET: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windexible
OPERATING SYSTEM: Windexible
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Pred. No. 15;
0; Mismatches
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100.0%; Pre
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Patent No. 6060587
GENERAL INFORMATION:
                                                     APPLICANT: Weiner, David B
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Best Local Similarity 100.
Matches 8; Conservative
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US-08-949-202-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Readel, Leonhard
APPLICANT: Readel, Leonhard
APPLICANT: Schiebel, Winfried
APPLICANT: Schiebel, Wich
APPLICANT: Schiebel, Wich
APPLICANT: USA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                         1.3%; Score 14; DB 4; Length 14;
100.0%; Pred. No. 7.5e-07;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
COMPUTER: IBM FC COMPATIBLE
COMPUTER: IBM FC COMPATIBLE
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATA:
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/811,583
FILING DATE: 05-MAR.1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/08811583 Patent No. 6218142
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US-08-949-202-2
; Sequence 2, Application US/08949202
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NAME: HALGY, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MPG-
TELECOMMUNICATION INFORMATION:
TELECHONE: 212-596-9000
TELEPAX: 212-596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS: LENGTH: 13 amino acids
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                            14; Conservative
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Matches 10; Conservative
                                                                                                                                                                                                                                                                            1007 ASKTFDRRKDAEAI 1020
                                                                       TOPOLOGY: linear MOLECULE TYPE: peptide US-08-811-583-11
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MOLECULE TYPE: peptide
US-08-811-583-13
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Best Local Similarity
Matches 14; Conserva
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APPLICANT: Ayyavoo, Velpandi
APPLICANT: Ayyavoo, Velpandi
APPLICANT: Mahalingam
APPLICANT: Mahalingam
APPLICANT: Patel, Mamata
TITLE OF INVENTION: CELLUIAR RECEPTOR FOR HIV-1 VPR ESSENTIAL FOR
TITLE OF INVENTION: Q2/M PHASE TRANSITION OF THE CELL CYCLE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6172201ris
STREET: One Liberty Place 46th floor
CITY: Philadelphia
STATE: Pennsylvania
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                 0.7%; Score 8; DB 4; Length 341;
100.0%; Pred. No. 15;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 15;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 19103
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: Windows NT
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/418,175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILMS TO THE STATE OF THE STATE OF A PERIOR APPLICATION INDRER: 08/949, 202
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33, 229
REFERENCE/DOCKET NUMBER: UPAP-022
TELECOMMUNICATION INFORMATION:
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 minto acids
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                                                                                                                                                                                                                                                 Sequence 4, Application US/09418175 Patent No. 6172201 GENERAL INFORMATION:
Query Match
Best Local Similarity luv...
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Best Local Similarity
8; Conserva
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ZIP: 19103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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US-09-529-245-2
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APPLICANT: Meiner, David B
APPLICANT: Apyavoo, Velpandi
APPLICANT: Apyavoo, Velpandi
APPLICANT: Apyavoo, Velpandi
APPLICANT: Patel, Mamata
TITLE OF INVENTION: CELLULAR RECEPTOR FOR HIV-1 VPR ESSENTIAL FOR
TITLE OF INVENTION: G2/M PHASE TRANSITION OF THE CELL CYCLE
NUMBER OF SEQUENCES: 4
CORRESPONDENCES: ADDRESSES: Moodcock Washburn Kurtz Mackiewicz & No. 6172201ris
STREET: One Liberty Place 46th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                       Length 341;
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Pred. No. 15;
0; Mismatches
                        FILING DATE:
FILING DATE:
CLASSIFICATION: 536
ATORNEY/AGENT INFORMATION:
NAME: Debluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPAP-0222
TELECOMMUICATION INFORMATION:
TELEPRAX: 215-568-3100
TELEFRAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHRACTERIFICS:
LENGTH: 341 amino acids
TYPE: amino acid
TOPOLOCY: linear
TOPOLOCY: linear
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACTIBLE
OPERATING SYSTEM: Windows NT
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/418,175
FILING DATE:
CLASSPICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/949,202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UPAP-0222
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/949,202
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ATORNEY/AGENT INFORMATION:
NAME: DELUCA, MAIK
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPAP-
TELECHONICATION INFORMATION:
TELEPHONE: 215-568-3439
TELEFAX: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-418-175-2
; Sequence 2, Application US/09418175
; Patent No. 6172201
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.7%; Soc
Best Local Similarity 100.0%; P:
Matches 8; Conservative 0;
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                                                                                                                                                                                                                                                                                                       / TOPOLOGY: linear
// MOLECULE TYPE: protein
US-08-949-202-4
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Query Match 0.7%; Score 8; DB 4; Best Local Similarity 100.0%; Pred. No. 22; Matches 8; Conservative 0; Mismatches
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                    ; TYPE: PRT
; ORGANISM: Yeast
US-09-457-040B-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-09-134-001C-3012
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Sequence 4, Application US/09529245

Patent No. 6448078

GENERAL INFORMATION:

APPLICANT: Weiner, David B

APPLICANT: Mahalingam, Sundarasamy
APPLICANT: Patel, Manata

TITLE OF INVENTION: Cellular Receptor For HIV-1 VPR Essential for G2/M

TITLE OF INVENTION: Phase Transition of the Cell Cycle

TITLE OF INVENTION: Phase Transition of the Cell Cycle

CURRENT APPLICATION NUMBER: US/09/529,245

CURRENT FILING DATE: 1998-10-09

PRIOR PAPLING DATE: 1998-10-10

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 4

LENGTH: 341
APPLICANT: Patel, Mamata

TITLE OF INVENTION: Cellular Receptor For HIV-1 VPR Essential for G2/M

TITLE OF INVENTION: Dead of the Cell Cycle

FILE REFERENCE: UPAPO376

CURRENT APPLICATION NUMBER: US/09/529,245

CURRENT APPLICATION NUMBER: US/09/529,245

PRIOR APPLICATION NUMBER: US/09/529,202

PRIOR PILING DATE: 1997-10-10

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 341
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Sequence 17, Application US/09457040B
Sequence 17, Application US/09457040B
Sequence 10, Application US/09457040B
Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CORGANISM: Homo sapiens
US-09-529-245-2
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Sequence 3012, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: WOLLETC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC:
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 6/064,964
PRIOR APPLICATION NUMBER: US 6/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3012
LENGTH: 149
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCOCC
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCOCC
TITLE OF INVENTION: DEPLECATION STAPPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
LENGTH: 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Staphylococcus epidermidis US-09-134-001C-3012
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                  Sequence 7, Application US/09455960

Patent No. 636176

GENERAL INFORMATION:
TITLE OF INVENTION: Compositions isolated from M. vaccae and TITLE OF INVENTION: Compositions isolated from M. vaccae and TITLE OF INVENTION: their use in modulation of immune responses.
FILE REFERENCE: 11000.1047

CURRENT APPLICATION NUMBER: US/09/455,960

CURRENT FILING DATE: 1999-12-06

NUMBER OF SEQ ID NOS: 31

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 7

LENGTH: 165
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Patent No. 6136605
GENERAL INFORMATION:
APPLICANT: Fahl, William E
APPLICANT: Mancharan, T Herbert
APPLICANT: Puchalski, Ralph B
APPLICANT: Wasserman Wyeth W
TITLE OF INVENTION: NOVEL GLUTATHIONE S-TRANSFERASE ISOFORMS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                    Length 165,
                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/297,431B FILING DATE: August 26, 1994

CLASSIFICATION NUMBER: 36, 1994

CLASSIFICATION:

NAME: REGAL Jance E. REGISTRATION NUMBER: 3625

REGISTRATION NUMBER: 3625

REGISTRATION NUMBER: 3625

REGISTRATION INFORMATION:

TELEPHORE 215-972-8386

TELEPRAN: 215-972-838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1500 Market Street, 38th Floor STATE: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                0.6%; Score 7; DB 4
100.0%; Pred. No. 78;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                        ; TYPE: PRT; ORGANISM: Mycobacterium vaccae US-09-455-960-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 31: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 220 amino acids
amino acid
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Best Local Similarity 100.9
Matches 7; Conservative
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TOPOLOGY:
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US-08-297-431B-31
US-09-455-960-7
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                                                                                                                                                                                                                                                                                   APPLICANT: Fahl, William E
APPLICANT: Gulick, Andrew M
APPLICANT: Gulick, Andrew M
APPLICANT: Mancharan, T Herbert
APPLICANT: Macharan, T Herbert
APPLICANT: Masserman Wyeth W
TITLEOF INVENTION: NOVEL GLUTATHIONE S-TRANSFERASE ISOFORMS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saul, Ewing, Remick & Saul, LLP
STREET: 1500 Market Street, 38th Floor
CITY: Philadelphia
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Query Match 0.6%; Score 7; DB 4; Length 220;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1e+02;
1ve 0; Mismatches 0; Indels
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2 IP: 19102-2186

2 IP: 19102-2186

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,431B

FILING DATE: August 26, 1994

CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION INDMER: 36252
REFERENCE/DOCKET NUMBER: WARF F039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-972-8386
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-297-431B-4
Sequence 4, Application US/08297431B
Sequence 4, Application US/08297431B
Patent NO. 6136605
APPLICANT: Fahl, William E
APPLICANT: Gullck, Andrew M
APPLICANT: Manoharan, T Herbert
APPLICANT: Puchalski, Ralph B
APPLICANT: Kramer, Katharine
                                                                                                                                                                                                                                  Sequence 2, Application US/08297431B patent No. 6136605 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.0%,
100.0%; Pre-
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amino acid
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Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                  1089 KDKARNR 1095
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Fahl, William E
APPLICANT: Gulick, Andrew M

APPLICANT: Manoharan, T Herbert
APPLICANT: Kramer, Katharine
APPLICANT: Wasserman Wyeth W

ITLE OF INVENTION: NOVEL GLUTATHIONE S-TRANSFERASE ISOFORMS

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:
ADDRESSEE: Saul, Ewing, Remick & Saul, LLP

STREET: 1500 Market Street, 38th Floor

CITY: Philadelphia
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ZIP: 19102-2186

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATINE
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rc-Bos/MS-DOS
SOFTWARE: Patentin Rc-Bos/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,431B
FILING DATE: AUGUST 26, 1994
ATTONEY/AGENT INFORMATION:
ATTONEY/AGENT INFORMATION:
NAME: REGISTRATION NUMBER: 3625
REGISTRATION NUMBER: 3625
REGISTRATION NUMBER: 3625
REGISTRATION INFORMATION:
TELEPHONE: 215-972-8386
TELEFRAK: 215-972-8386
                                                                                                                                                                                                                                                                                                                                       DB 4; IL
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                                                                 WARF F039
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US-08-297-431B-8
'Sequence 8, Application US/08297431B
'Patent No. 6136605
            NAME: Reed, Janet E.
REGISTRATION NUMBER: 36252
REFERENCE/DOCKET NUMBER: WARI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-972-8386
TELEPHONE: 215-972-2292
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                       Query Match

Best Local Similarity 100.0%; P.
Matches 7; Conservative 0;
                                                                                                                                                            INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 221 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-297-431B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-297-431B-8
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APPLICANT: Wasserman Wyeth W
TILLE OF INVENTION: NOVEL GLUTATHIONE S-TRANSFERASE ISOFORMS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saul, Ewing, Remick & Saul, LLP
STREE: 1500 Market Street, 38th Floor
CITY: Philadelphia Street, 38th Floor
STREE: PA
CONTRY: US
ZIP: 19102-2186
COMPUTR: EBM PC Compatible
COMPUTR: IBM PC Compatible
COMPUTR: IBM PC Compatible
COMPUTR: IBM PC Compatible
COMPUTR: EPACHIC STREET: POSSIEM: PC-DOS/MS-DOS
SOFTWARE: PatentID Release #1.0, Version #1.25
CURRENT APPLICATION DATA: ASSISTING YSTEM: DECAMINES: USO/80/297,431B
FILLING DATE: August 26, 1994
ATTORNEYAGENT INFORMATION:
NAME: Reed, Janet E
REGISTRATION NUMBER: 36252
REGISTRATION NUMBER: 36252
REGISTRATION NUMBER: WARF F039
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TEMENATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Fahl, William E
APPLICANT: Gulick, Andrew M
APPLICANT: Gulick, Andrew M
APPLICANT: Manoharan, Therbert
APPLICANT: Manchalak, Ralph B
APPLICANT: Kramer, Katharine
APPLICANT: Wasserman Wyeth W
TITLE OF INVENSERMENCON: WOVEL GLUTATHIONE S-TRANSFERASE ISOFORMS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saul, EPWING, Remick & Saul, LLP
STREET: 1500 Market Street, 38th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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100.0%; Pred. No. 1e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 19102-2186
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,431B
FILLING DATE:
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 20
US-08-297-431B-6
Sequence, Application US/08297431B
Patent No. 6136605
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EBNGTH: 221 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLGY: linear
MOLECULE TYPE: protein
US-08-297-431B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION
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Best Local Similarity 100.
Matches 7; Conservative
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Patent No. 6136605
GENERAL INFORMATION:
APPLICANT: Fahl, William E
APPLICANT: Gulick, Andrew M
APPLICANT: Puchalski, Ralph B
APPLICANT: Puchalski, Ralph B
APPLICANT: Kamer, Katharine
APPLICANT: Kasserman Wyeth W
TITLE OF INVENTION: NOVEL GLUTATHIONE S-TRANSFERASE ISOFORMS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 221;
0. 1e+02;
ches 0; Indels
                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: DE-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,431B
FILING DATE: Adjust 26, 1994
CLASSIFICATION NUMBER: 36,57
FLING DATE: Adjust 26, 1994
TLING DATE: ADJUST 20, 1994
TLING DATE: ADJUST 20, 1994
TELEPHONE: 1000 NUMBER: 36,52
REFERENCE/DOCKET NUMBER: 36,52
TELEPHONE: 215-972-292
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 221 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: ADJUST 21 amino acids
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STREET: 1500 Market Street, 38th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: US
ZIP: 19102-2186
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,431B
FILING DATE: August 26, 1994
CCASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.6%; Score 7; DB 4 Best Local Similarity 100.0%; Pred. No. 1e+Matches 7; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 215-972-2292
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-297-431B-12
                             COUNTRY: US
ZIP: 19102-2186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1089 KDKARNR 1095
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US-09-297-431B-12
Sequence 12, Application US/08297431B
Patent No. 6136605
CENERAL INFORMATION:
APPLICANT: Fahl, William E
APPLICANT: Manoharan, T Herbert
APPLICANT: Manoharan, T Herbert
APPLICANT: Manoharan, T Herbert
APPLICANT: Wasserman Wyeth W
TILE OF INVENTION: NOVEL GLUTATHIONE S-TRANSFERASE ISOFORMS
NUMBER OF SUQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSES: Saul, Ewing, Remick & Saul, LLP
STREET: 1500 Market Street, 38th Floor
CITY: Philadelphia
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                                                                                                                                                                                                                                                                  APPLICANT: Fahl, William E
APPLICANT: Gulick, Andrew M
APPLICANT: Gulick, Andrew M
APPLICANT: Manoharan T Herbert
APPLICANT: Puchalski, Ralph B
APPLICANT: Kramer, Katharine
APPLICANT: Kramer, Katharine
APPLICANT: Nasserman Wyeth W
APPLICANT: Masserman Wyeth W
APPLICANT: Asserman Wyeth W
APPLICANT: Asserman Wyeth W
APPLICANT: SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSES: Saul, Ewing, Remick & Saul, LLP
STREET: 1500 Market Street, 38th Floor
CITY: Philadelphia
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100.0%; Pred. No. 1e+02;
ive 0; Mismatches 0; Indels
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MEDIUW TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATCHIN PC-DOS/MS-DOS SOFTWARE: PATCHIN DATA:

APPLICATION NUMBER: US/08/297,431B FILING DATE: AUGUST 26, 1994
CLASSIFICATION NUMBER: US/08/297,431B FILING DATE: AUGUST 26, 1994
CLASSIFICATION NUMBER: BC-DOS/MS-DOS/MS-SOFTWARE

REFERENCE/DOCKET NUMBER: WARF F039
TELECOMMONICATION IDFORMATION:

TELEPAX: 215-972-8386
TELEFAX: 215-972-8386
TEL
                                                                                                                                                              Sequence 10, Application US/08297431B Patent No. 6136605 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 0.6
Best Local Similarity 100.
Matches 7; Conservative
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125 KDKARNR 131
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COUNTRY: U
                                                                                                   RESULT 22
US-08-297-431B-10
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us-09-782-874-2.oli.rai

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ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36252
REFERENCE/DOCKET NUMBER: WARF
TELECOMMUNICATION INFORMATION:
TELEFHONE: 215-972-2292
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 221 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1089 KDKARNR 1095
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US-08-297-431B-16
Sequence 16, Application US/08297431B
Sequence 16, Application US/08297431B
Sequence 16, Application US/08297431B
SEQUENCE TAIL, William E
APPLICANT: Railick, Andrew M
APPLICANT: Manoharan, T Herbert
APPLICANT: Wandralski, Ralph B
APPLICANT: Wasserman Wyeth W
TITLE OF INVENTION: NOVEL GLUTATHIONE S-TRANSFERASE ISOPORMS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
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Nn. 1e+02;
0; Indels
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0.6%; Score 7; DB 4; Length 221;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATENTIN PATENTIN DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/297,431B
FILING DATE: August 26, 1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Saul, Ewing, Remick & Saul, LLP STREET: 1500 Market Street, 38th Floor CITY: Philadelphia STATE: PA
                                                                                                                                          0.6%; Score 7; DB 4
100.0%; Pred. No. 1e+
cive 0; Mismatches
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NAME: Reed, Janet E.
REGISTRATION NUMBER: 36252
REFERENCE/DOCKET NUMBER: WARF F039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-972-8386
TELEFRA: 215-972-8386
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Sequence 18, Application US/08297431B / Patent No. 6136605
SEQUENCE CHARACTERISTICS:
LENGTH: 221 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-297-431B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 221 amino acids
amino acid
                                                                                                                                        Query Match 0.6
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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US-08-297-431B-18
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Sequence 20, Application US/08297431B
Patent No. 6136605
GENERAL INFORMATION:
APPLICANT: Fahl, William E
APPLICANT: Manoharan, T Herbert
APPLICANT: Manoharan, T Herbert
APPLICANT: Puchalski, Ralph B
APPLICANT: Wasserman Wyeth W
TITLE OF INVENTION: NOVEL GLUTATHIONE S-TRANSFERASE ISOFORMS
MUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saul, Ewing, Remick & Saul, LLP
STREET: 1500 Market Street, 38th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: US
COUNTRY: US
ISTATE: PA
COUNTRY: US
COUNTRY: US
COUNTRY: US
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
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APPLICANT: Gulick, Andrew M
APPLICANT: Manoharan, T Herbert
APPLICANT: Puchalski, Ralph B
APPLICANT: Kramer, Katharine
APPLICANT: Kramer, Katharine
APPLICANT: Wasserman Wyeth W
TITLE OF INVENTION: NOVEL GLUTATHIONE S-TRANSFERASE ISOFORMS
CORRESPONDENCE: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 221;
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                                                                                                                                                                                                                                                                                                           COUNTRY: US

ZIP: 19102-2186

ZIP: 19102-2186

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OFFRATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/297,431B

FILLING DATE: August 26, 1994

CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.6%; Score 7; DB 4; 1
100.0%; Pred. No. 1e+02;
ive 0; Mismatches (
                                                                                                                                                               STREET: 1500 Market Street, 38th Floor STATE: Philadelphia
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Gaps
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Patent No. 6262242
GENERAL INFORMATION: Steck, Peter
APPLICANT: Steck, Peter
APPLICANT: Youse, Mark A.
APPLICANT: Young, W.K. Alfred
APPLICANT: Yung, W.K. Alfred
APPLICANT: Tavtigian, Sean V.
TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10023.3
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.6%; Score 7; DB 2; Length 322; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                       APPLICANT: Summers, R.G.
APPLICANT: Summers, R.G.
APPLICANT: State, L.
APPLICANT: State, L.
APPLICANT: State, M.J.
TITLE OF INVENTION: POLYKETIDE-ASSOCIATED SUGAR TITLE OF INVENTION: BIOSYNTHESIS GENES NUMBER, OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories STREET: 100 Abbott Park Road CITY: Abbott Park STREET: 1101 Abbott Park STREET: 1101 Abbott Park STREET: 100 Abbott Park STREET: MADUTER PARABLE FORM:
MEDIUM TYPE: Diskette COMPUTER: IBM COMPATIBLE OPSERATING STSTEM: DOS SCHEWARD S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION INDRES: US/08/576,626A
FILING DATE: 21-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY, AGENT INFORMATION:
NAME: Dianne Casuto
REGISTRATION NUMBER: P-40,943
REFERENCE/POCKET NUMBER: 5857.US.OI
TELECHONE: (847) 938-3137
TELEPHONE: (847) 938-2623
                                                                                                                                                                            Sequence 33, Application US/08576626A Patent No. 5998194 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33:
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; MOLECULE TYPE: No. 5998194e
US-08-576-626A-33
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SEQUENCE CHARACTERISTICS:
LENGTH: 322 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              604 RQLITLL 610
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                                                                                                                 RESULT 29
US-08-576-626A-33
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US-08-791-115B-27
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0.6%; Score 7; DB 1; Length 320;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.6%; Score 7; DB 4; Length 221;
100.0%; Pred. No. 1e+02;
1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ## APPLICANT: BAPLICATION US/08565386

| Sequence 17, Application US/08565386
| Patent No. 5741697
| GENERAL INFORMATION:
| APPLICANT: Bayoil, Patrik M. APPLICANT: Hsia, Ru-ching
| TITLE OF INVENTION: BACTERIOPHAGE OF CHLAMYDIA PSITTACI
| NUMBER OF SEQUENCES: 23
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
| STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: CLINCAL CACCOMPATER READABLE FORM:

MEDIUM TYPE: READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC COMPATED POSTANS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN BATA:
CURSTENT APPLICATION DATA:
APPLICATION NUMBER: US/08/55,386
FILING DATE: CLASSIFICATION:
CLASSIFICATION: 435
ATLASSIFICATION:
NAME: Timian, Susan J.
REFERENCE/DOCKET NUMBER: 176/60040
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
TENTY 320 amino acids
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRINT APPLICATION DATA:
CAPLICATION NUMBER: US/08/297,431B
FILING DATE: August 26, 1994
                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 3625
REFERENCE/DOCKET NUMBER: 3625
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-972-8386
TELEFRX: 215-972-8386
TELEFRX: 215-972-8386
SEQUENCE CHARACTICS:
LENGTH: 221 amino acids
TYPE: amino acid
TOPOLOGY: linear
MALECULE TYPE: protein
US-08-297-431B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 320 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 0.6
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                  FILING DATE: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 KDKARNR 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23. Application US/08791115B
Patent No. 6262242
GENERAL INFORMATION:
APPLICANT: Steck, Peter
APPLICANT: Pershouse, Mark A.
APPLICANT: Youg, W.K. Alfred
APPLICANT: Youg, W.K. Alfred
APPLICANT: Tavitijan, Sam V.
TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                               0.6%; Score 7; DB 4; Length 403; 100.0%; Pred. No. 1.8e+02; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: DC
CUNTAX: USA
ZIP: 22204

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OFFAATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/791,115B
FILING DATE: D3-DAN-1997
CLASSIFICATION NUMBER: US/08/791,115B
FILING DATE: O10-1997
ATTORNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 38,957
REPRENCE/DOCKET NUMBER: 38,957
RELEPRENCE/DOCKET NUMBER: 38,957
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701-E
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.6%; Score 7; DB 4; Len
ilarity 100.0%; Pred. No. 1.8e+02;
Conservative 0; Mismatches 0;
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US-08-791-115B-25
; Sequence 25, Application US/08791115B
  INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: ILENGTH: 403 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 403 amino acids amino acid
                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-791-115B-23
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Best Local Similarity
'-haq 7; Conserva
                                                                                                                                       linear
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US-08-791-115B-23
                                                                                                                                  ; TOPOLOGY:
US-08-791-115B-1
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Patent No. 626242
GENERAL INFORMATION:
APPLICANT: Steck, Peter
APPLICANT: Steck, Pater
APPLICANT: Jasser, Samar
APPLICANT: Tartiglan, Sam V.
TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10023.3
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 394;
                                                                                               COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER LIBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARR: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/791,115B

FILING DATE: 30-JAN-1997

CLASSIFICATION:

NAME: INFORMATION:

REGISTRATION NUMBER: 2318-134.A

TELEPHONE: 202-683-7031

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 394 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-791-115B-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ...LUKESSEE: ROTHWELL, FIGG, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701-E
STATE: DC
COUNTRY: USA
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C. STREET: 555 Thirteenth Street, N.W., Suite 701-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,115B
FILING DATE: 30-JAN-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.6%; Score 7; DB 4; Le Best Local Similarity 100.0%; Pred. No. 1.7e+02; Matches 7; Conservative 0; Mismatches 0;
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NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 38,957
REFERENCE/DOCKET NUMBER: 2318
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-683-6040
                                          Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    639 LKAQEAL 645
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US-08-791-115B-1
                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIE: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 35 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.6%; Score 7; DB 2; I Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 7; Conservative 0; Mismatches C
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COMPUTER: IEM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOCHWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,821
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REFERENCE/DOCKET NUMBER: P1130
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 6:
                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,115B
FILING DATE: 30-JAN-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08933821
Patent No. 5972338
GENERAL INFORMATION:
APPLICANT: GOGOWSKI, Paul J.
TITLE OF INVENTION:
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: This. Jeffrey L.
REGISTRATION NUMBER: 38,957
REFERENCE/DOCKET NUMBER: 2318
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-683-6040
TELEPHONE: 202-683-6040
                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-683-7031
| INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: 7: LENGTH: 430 amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGIH: 470 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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US-08-933-821-6
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US-08-791-115B-7
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APPLICANT: Steck, Peter
APPLICANT: Steck, Peter
APPLICANT: Dasser, Samar
APPLICANT: Tay, W.K. Alfred
APPLICANT: Tuny, W.K. Alfred
APPLICANT: Tavtigian, Sean V.
TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10023.3
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: S5 Thirteenth Street, N.W., Suite 701-E
Patent No. 6262242
GENERAL INFORMATION:
APPLICANT: Steck, Peter
APPLICANT: Pershouse, Mark A.
APPLICANT: Pershouse, Mark A.
APPLICANT: Tung, W.K. Alfred
APPLICANT: Tungidan, Sam v.
TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.6%; Score 7; DB 4; Length 403; Best Local Similarity 100.0%; Pred. No. 1.8e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FUGATE

MEDIUM TYPE: Floppy disk

COMPOTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/791,115B

FILING DATE: 30-JAN-1997

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Inhen, Jeffrey L.

REGISTRATION NUMBER: 2318-134.A

TELEPROCMMUNICATION INFORMATION:

TELEPROCMMUNICATION INFORMATION:

TELEPRACE/DOCKET NUMBER: 2318-134.A

TELEPRACE/DOCKET NUMBER: 2318-134.A

TELEPRACE/OSCET NUMBER: 2318-134.A

TELEPRACE/DOCKET NUMBER: 2318-134.A

TELERACE/DOCKET NUMBER: 2318-134.A
                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C. STREET: 555 Thirteenth Street, N.W., Suite 701-E CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-791-115B-7
; Sequence 7, Application US/08791115B
; Patent No. 6262242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 403 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: DC
COUNTRY: US
ZIP: 22204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-791-115B-25
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                                                                                                                                                                                                                                                                                                                                                                                                   Length 470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: INBW PC Compatible
COMPUTER: INBW PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Windratin (Genentech)
CURRENT APPLICATION NUMBER: US/09/332,928A
FILING DATE: 14-Jun-1999
CLASSIFICATION CURROWN>
PRIOR APPLICATION ATA:
APPLICATION NUMBER: 08/933,821
FILING DATE: CURROWN>
TRILNG DATE: CURROWN>
THING DATE: CURROWN>
THING DATE: WINDRATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REPERENCE/DOCKET NUMBER: P1130
TELEPHONE: 650/225-3216
TELEPHONE: 650/225-3216
TELEPHONE: 650/225-3216
TELEPHONE: GID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                   Score 7; DB 4; I
Pred, No. 2e+02;
0; Mismatches (
                                                                ATTORNEY AGENT INFORMATION:
NAME: Dreger R.
RECISTRATION NUMBER: 33.055
REFERENCE/DOCKET NUMBER: P1130R1A
TELECHOMUNICATION INFORMATION:
TELEPHONE: 650/255-3216
TELEPHONE: 650/952-9881
TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 470 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-136-828-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-332-928A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09332928A; Sequence 6, Application US/09332928A; Patent No. 636863
GENERAL INFORMATION:
GENERAL INFORMATION:
GUNDER, AUSTIN L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF ENQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREEF: LDAA WAY
CITY: South San Francisco
STATE: California
APPLICATION NUMBER: US/09/136,828 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 470 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                Query Match

Best Local Similarity 100.0%; Pr
Matches 7; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1024 VRALRKE 1030
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US-09-332-928A-6
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2e+02;
0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                               ZIF: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT AND SISTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/960,507
FILING DATE: CLASSIFICATION:
NAME: Dreger, Ginger R.
RECISTRATION NUMBER: 31,055
REFERENCE/DOCKET NUMBER: P1130p1
TELECHMONIACATION INFORMATION:
TELECHMONIACATION INFORMATION FOR SED ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 470 amino acids
TYPE: Amino Acid
                                                                                                        Sequence 6, Application US/08960507
Patent No. 6057435
GENERAL INFORMATION:
APPLICANT: GOGOWSKI, Paul J.
APPLICANT: GUTNEY, Austin L.
TILLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
COUNTRY: USA
ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09136828
Patent No. 6350450
GENERAL INFORMATION:
APPLICANT: GOGOWSKI, Paul J.
APPLICANT: GUNDEY, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
CORRESPONDER ADDRESS:
ADDRESSEE: Genertech, Inc.
STREET: 1 DNA WAY
CTTY: SOUTH SAN Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 100..
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93 VRALRKE 99
                                                                                 US-08-960-507-6
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CHARLES E. NAKAMURA
APPLICANT: CHARLES E. NAKAMURA
APPLICANT: CHARLES E. NAKAMURA
APPLICANT: AMY (KUANG-HUA) HSU
APPLICANT: RICHARD D. LA RRAU
APPLICANT: SHARON L. HAYNIE
APPLICANT: MARIA DIAZ-TORRES
APPLICANT: DONALD E. TRIMBUR
APPLICANT: DONALD E. TRIMBUR
APPLICANT: WASANTHA NAGRAJAN
APPLICANT: WASANTHA NAGRAJAN
APPLICANT: RAMEGHY N. PROPUCTION OF 1.3-PROPANEDIOL
APPLICANT: RAMEGHY N. PRODUCTION OF 1.3-PROPANEDIOL
TITLE OF INVENTION: METHOD FOR THE RECOMBINANT
TITLE OF INVENTION: METHOD FOR THE RECOMBINANT
TITLE OF INVENTION: PRODUCTION OF 1.3-PROPANEDIOL
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: DELAWARE
COUNTRY: WILMINGTON
STREET: DIAGNARE
COUNTRY: U.S.A.
2007
                                                             COMPUTER FALDABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.6%; Score 7; DB 4 Best Local Similarity 100.0%; Pred. No. 2e-Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: GENENCOR INTERNATIONAL, INC. STREET: 4 CAMBRIDGE PLACE STREET: 1870 SOUTH WINTON ROAD
                                                                                          MEDIUM.
COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-LUC-
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/332,929
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/93,821
FILING DATE:
ATTORREY/AGRAT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 91130
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEPHONE: 650/225-3216
TELEPHONE: 650/225-3216
TELEPHONE: GSO/225-3216
TELEPHONE: AMAINO ACIDS:
LENGTH: 470 amino acids
TYPE: Amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: ROCHESTER
STATE: NEW YORK
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15, Application US/08968563
Patent No. 6013494
GENERAL INFORMATION:
       California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1024 VRALRKE 1030
                               USA
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US-08-968-563-15
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. a-62;
. a-63 (). Indels
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100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DS/MS.DOS
SOFTWARE: WINPATIN (Genentech)
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                    APPLICANT: Godowsti, Paul J.
APPLICANT: Godowsti, Paul J.
APPLICANT: Gurney, Austin
APPLICANT: Gurney, Austin
APPLICANT: Godard, Convid
APPLICANT: Godard, Audrey
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Tumas, Daniel
APPLICANT: Schwall, Ralph
TITLE OF INVENTION: Tie Ligand Homologues
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Generiech, Inc.
STREET: I DAR May
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P1130P2
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Sequence 6, Application US/09332929;
Patent No. 6420542
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Garney, Austin L.
TITLE OF INVENTION: T1e Ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INPORMATION:
NAME: Dreger, Ginger R.
REGISTRATION UNDERS: 33.055
REPRENCE/DOCKET UNDERS: P1130
TELECOMMUNICATION INFORMATION:
TELEFRAN: 650/252-3216
INPORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                             RESULT 39
US-09-136-801-6
Sequence 6, Application US/09136801
Patent No. 6413770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 470 amino acids
Amino Acid
3%: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.6
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Godows
1024 VRALRKE 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1024 VRALRKE 1030
                                           93 VRALRKE 99
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Gaps

us-09-782-874-2.oli.rai

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0.6%; Score 7; DB 4; Length 501; 100.0%; Pred. No. 2.2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BULTHUIS, BEN A.
GATENEY, ANTHONY A.
HAYNIE, SHARON L.
HSU, AMY K.
LAREAU, RICHARD D.
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
GLYCEROL BY RECOMBINANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSES GENENCOR INTERNATIONAL, INC.
STREET: 4 CAMBRIDGE PLACE
1870 SOUTH WINTON ROAD
CITY: ROCHESTER
STATE: NEW YORK
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: DISKETTE, 3.5 INCH
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
ROPLICATION NUMBER: US/09/297,928
FILING DATE: 11 May-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION UNDERS: 60/03602
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AZAMETHY
REGISTATION UNDERS: 33,692
REFERENCE/DOCKET NUMBER: CR-9981-P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 43
US-09-297-928-11
Sequence 11, Application US/09297928
Patent No. 6388716
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEO ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 501 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 302-773-0164
TELEX: 6717325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 14618
COMPUTER READABLE FORM:
                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 501 amino acids TYPE: amino acid STRANDEDNESS: unknown
         TELEPHONE: 650-864-7620
TELEFAX: 650-845-6504
                                                                                                                                                                                                                                                                                                                  Query Match 0.69
Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                          SS: unknown unknown
                                                                                                                                                                             TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                    309 EHALEKL 315
                                                                                                                                                                                                                                                                                                                                                                                                                                               363 EHALEKL 369
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US-08-969-683A-15
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5. 2.2e+02;
cches 0; Indels
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/08969683A
Patent No. 6136576
GENERAL INFORMATION:
TITLE OF INVENTION: METHOD FOR THE RECOMBINANT
TITLE OF INVENTION: PRODUCTION OF 1,3 PROPANEDIOL
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A
ZIP: 14618
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,683A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 0.6%; Score 7; DB 3
Best Local Similarity 100.0%; Pred. No. 2.,
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 4 Cambridge Place
STREET: 4 Cambridge Place
STREET: 1870 South Winton road
CITY: Rochester
                                                                                                         FILING DATE:

CLASSIFICATION: 435

CLASSIFICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/030,601

FILING DATE: NOVEMER 13, 1996

ATORNEY/AGENT INFORMATION:

NAME: FLOYD, LINDA AXAMETHY

REGISTRATION NUMBER: 33,692

REFERENCE/DOCKET NUMBER: CR-9982

REFERENCE/DOCKET NUMBER: CR-9982

REFERENCE/DOCKET NUMBER: CR-9982

TELEPHONE: 302-892-812

TELEPHONE: 302-773-0164

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 501 amino acids

TYPE: amino acid

STANDEDMESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILLING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/20873
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: 60/030,601
FILING DATE: 13-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Glaister, Debra
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC 369-2
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 13-NOV-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: GLPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            309 EHALEKL 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363 EHALEKL 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-969-683A-15
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Sequence 49, Application US/09183266A

Sequence 49, Application US/09183266A

Sequence 49, Application US/09183266A

Sequence 49, Application

APPLICANT Stillman, Bruce

APPLICANT Williams, R. Sanders

APPLICANT WILLIAMS REPLICATION REGULATING GENES,

TITLE OF INVENTION: DNA REPLICATION REGULATING GENES,

TITLE OF INVENTION: ANTIBODIES THERETO AND DIAGNOSTIC APPLICATIONS THEREOF

FILE REPERENCE: CSSIL96-01A3

CURRENT APPLICATION NUMBER: DCT/US97/07333

FRIOR FILING DATE: 1997-05-05

PRIOR APPLICATION NUMBER: 08/648,650

PRIOR PLING DATE: 1996-05-15

PRIOR APPLICATION NUMBER: 08/648,650

PRIOR PLING DATE: 1996-05-15

PRIOR PLING DATE: 1996-05-05

SOFTWARE FELEX PRIOR DATE: 1996-05-05

SOFTWARE PRIOR DATE: 1996-05-05

SOFTWARE FELEX PRIOR DATE: 1996-05-07

SOFTWARE FELEX PRIOR DATE: 1996-05-05

SOFTWARE FELEX PRIOR DATE: 1996-0
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Sequence 6, Application US/08791115B

Patent No. 6262242

GENERAL INFORMATION:
APPLICANT: Steck, Peter
APPLICANT: Dershouse, Mark A.
APPLICANT: Jasser, Samar
APPLICANT: Tavitigian, Sean V.
ITILE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10023.3

CORRESPONDENCE ADDRESS:
ADDRESSEE: Rechmell, Figg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701-E
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONTAIN 22204
COMPUTER READABLE FORM:
MEDIUM TIPE Floppy disk
MEDIUM TIPE Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,115B
FILING DATE: 30-JAN-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAMM: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 38,957
REFERENCE/DOCKET NUMBER: 2318-134.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: S. cerevisiae
US-09-183-266A-49
               639 LKAQEAL 645
                                                                    308 LKAQEAL 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                     RESULT 45
US-09-183-266A-49
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: STURR, NIGEL K
APPLICANT: GRAY, IAN C
APPLICANT: GRAY, IAN C
APPLICANT: STEWART, LORNA M
TILLE OF INVENTION: DIAGNOSIS OF SUSCEPTIBILITY TO CANCER
TITLE OF INVENTION: DAT TREATMENT THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
                                                                    0.6%; Score 7; DB 4; Length 501;
100.0%; Pred. No. 2.2e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.6%; Score 7; DB 4; Length 565; Best Local Similarity 100.0%; Pred. No. 2.4e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,156A
CLASSIPICATION: A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/042,655
FILING DATE: US 60/042,655
FILING DATE: US 60/042,655
FILING DATE: US 60/033,147
FILING DATE: US 60/033,147
FILING DATE: US 60/003,47
FILING DATE: US 60/005,840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Translation of partial cDNA sequence US-08-906-156A-12
                                                                                                                                                                                                                                                                                                                                                                              RESULT 44
US-08-906-156A-12
US-08-906-156A-12
Sequence 12, Application US/08906156A
Patent No. 6287854
GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 565 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: SADOFF, B.J. S6,663 REGISTRATION NUMBER: 36,663
                                                                                                  Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide HYPOTHETICAL: NO
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CITY: ARLING
STATE: VA
COUNTRY: US!
ZIP: 22201
US-09-297-928-11
                                                                       Query Match
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Sequence 29, Application US/09143571

Sequence 29, Application US/09143571

Patent No. 6333153

GENERAL INFORMATION:

APPLICANT: GRADIA, SCOTT

APPLICANT: GRADIA, SCOTT

APPLICANT: GRADIA, SCOTT

TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR EFFECTING ADENINE

TITLE OF INVENTION: PROTEINS

FILE REFERENCE: 9885-601

CURRENT APPLICATION NUMBER: 60/093,935

EARLIER FILING DATE: 1998-09-28

EARLIER PILING DATE: 1997-11-28

EARLIER PRILING DATE: 1997-11-28

NUMBER OF SEQ ID NOS: 36

SEQ ID NO 29

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-143-571-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               366 EFSDDLH 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      728 EFSDDLH 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   619 VLEQKQK 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 VLEQKQK 199
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; ORGANISM: Human
US-09-741-150-4
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US-09-741-150-4
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APPLICANT: Steck, Peter
APPLICANT: Steck, Peter
APPLICANT: Yasser, Samrk A.
APPLICANT: Yung, W.K. Alfred
APPLICANT: Yung, W.K. Alfred
APPLICANT: Tavtigian, Sean V.
TITLE OF INVENTIONS: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701-E
                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 645; . 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 7; DB 4; Length 742;
Pred. No. 3.1e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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MEDIUM TYPE: Floppy disk

COMPUTER: FLOPPy disk

MEDIUM TYPE: Floppy disk

COMPUTER: ISM PC COMPALIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CUBRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/791,115B

FLING DATE: 30-JAN-1997

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: INFORMATION:

REFERENCE/DOCKET NUMBER: 2318-134.A

TELEPHONINICATION INFORMATION:

TELEPHONINICATION INFORMATION INFORMATION:

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100.0%; Pred. No. ...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                    Query Match 0.6%; Score 7; DB 4
Best Local Similarity 100.0%; Pred. No. 2.7
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08791115B Patent No. 6262242
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-683-6040
TELEFAX: 202-683-6031
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 645 amino acids
TYPE: amino acids
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Best Local Similarity
7, Conserve
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US-08-791-115B-6
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CITY: Washington
STATE: DC
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US-08-791-115B-5
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Gaps

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Score 7; DB 4; Length 834; Pred. No. 3.4e+02;

Mismatches

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GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLARED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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00.0%; Pred. No. 3.6e+02;
ve 0; Mismatches 0; Indels
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US-08-724-354D-22
Sequence 22, Application US/08724354D
Patent No. 5994119
GENERAL INFORMATION:
APPLICANT: Dietz, Harry C.
TITLE OF INVENTION: MAMMALIAN REGULATOR OF
TITLE OF INVENTION: NONSENSE-MEDIATED RNA DECAY
Sequence 4, Application US/09741150 Patent No. 6436689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.6%; So
Best Local Similarity 100.0%; P
Matches 7; Conservative 0;
```

RESULT 48

```
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4215 Excutive Square, Suite 1400
CITY: La 4215 Excutive Square, Suite 1400
CITY: La 4215 Excutive Square, Suite 1400
CITY: La 4215 Excutive Square, Suite 1400
STATE: CAA
COUNTRY: USA
ZIP: 92037
COMPUTER: LIBM COMPATIBLE
APPLICATION NUMBER: G0/O16,482
FILING DATE: 29-APR-1996
ATTORNEY/ARENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
RESTRENCE/COCKET NUMBER: 38,347
RELEPONDATION INFORMATION:
TELEPONDATION INFORMATION:
TELEPONDATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 971 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: MOLLOCULE TYPE: protein
US-08-724-1354D-22
```

Search completed: November 6, 2002, 03:40:49 Job time : 93 secs

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0; Gaps

Query Match

0.6%; Score 7; DB 2; Length 971;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels

994 KTEAEIL 1000 ||||||| 538 KTEAEIL 544

Title: Perfect score:

Seguence:

nucleic

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Scoring table:

Word size :

Searched:

Database :

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BI203182
EST51222 CTOS Lycopersicon esculentum CDNA clone CTOS1C7 5' end similar to putative RNA-directed RNA polymerase, mRNA sequence.
BI203182.1 GI:14680906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lycopersicon.

1 (bases 1 to 659)
van der Hoeven,R., Sun,H., Bezzerides,J., Cho,J., Utterback,R., Ronning,C. and Tanksley,S. Generation of ESTs from Tomato Suspension Cultures Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                      BO1111609
BPC52042
BC5204242
BC5204242
BC6507474
BC689665
BC689665
BC4832
BC689665
BC482389
BC689665
BC689665
BC689665
BC73389
BC73389
BC73389
BC738868
BC738888
BC738888
BC738888
AW649811
BF112386
BG594667
BQ111608
BE920043
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BH558896
BF621359
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BB446629
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tomato.
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
BI203182
; Search time 4531 Seconds
(without alignments)
13335.988 Million cell updates/sec
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                                                                                                      1 GAAATATTCTTTACTTACTT.......AGTTTCATCTTTCTTAAA 3731
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                                                                                                                                                                               32308132
       5.1.3
Compugen Ltd.
                                                                                                                                            16154066 segs, 8097743376 residues
                                                                                                                                                                               parameters:
       GenCore version
Copyright (c) 1993 - 2002
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                                                    5, 2002, 23:19:32
                                      nucleic search, using sw model
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                                                                                                                     OLIGO_NUC
Gapop 60.0 , Gapext 60.0
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em_gss_tun:*
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em_gss_pro:*
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em_esthum:*
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em_estpi:*
em_estpi:*
gb_est1:*
gb_est2:*
gb_est2:*
gb_est3:*
gb_est5:*
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Maximum DB seq length: 2000000000
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3731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length
                                                      November
                                                                                                                                                             0
```

Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.

Contact: CUGI

TITLE JOURNAL COMMENT

BI203182 EST521222 BE43532 EST406410 AM933692 EST359535 AI896465 EST265896 BE433646 EST400175 AW932918 EST358761

BI203182 BE435332 AW933692 AI896465 BE433646

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Result

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BG39467 EST443345
BG111608 EST443345
BG111608 EST44331289
BG597875 EST446553
BG597875 EST44689
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AV207607 AV207607
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FEATURES

BASE COUNT

Matches

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/note="Vector: pBluescriptsKmcVadapt; Site_1: EcoR1; Site_2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
                                                                                                                                                 1 (bases 1 to 618)
Albala, Verballov, White, R., van der Hoeven, R.S., Holt, I.E.,
Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M.,
Nierman, W., Fraser, C.M., Martin, G.B., Glovannoni, J.J. and Tanksley
                      Lycopersicon esculentum
Bukaryota; Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3250 CATTAGTGTTGCTGTGAGGGCCTTGAGGAGGAGGCAAGAGCCTGGTTCAAGAGGCGTAA 3309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2830 CAAAAAACTIGCIGAGCICIIIICAATIGCAGIGGACTIICCAAAGACIGGIGIICCCGC 2889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3010 ACCTCAGGCTAGCTCTATCGCGACCTTCACAAGAGATGTTGCAAGGAGATCATATGATGC 3069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2890 TGAAATACCATCTCAGTTGCGCCCTAAAGAATACCCAGACTTCATGGATAAGCCGGACAA 2949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Generation of ESTs from tomato fruit tissue, breaker stage Unpublished (2000)
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Email: http://www.genome.clemson.edu/orders/index.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db.xref="taxon:4081"
/clone="clb52569"
/clone_lib="tomato breaker fruit, TIGR"
/tissue_type="eericarp"
/dev_stage="breaker"
/lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.6%; Score 546; DB 10; I ilarity 100.0%; Pred. No. 2.3e-278; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                 Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prime sequence.
Location/Qualifiers
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Contact: CUGI
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  tomato.
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                                                                                                                                                                                                                           /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Suspension cultures of L.esculentum E6203 were grown
Im Murashige and Skoog based medium, supplemented with 15%
coconut milk (filter sterilized and added after
autoclaving), 2% saccharose, and Img/ml 2,4D (pH5.8).
Fresh medium was added every 7 days, and cultures were
shaking."
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EST406410 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
Clone CLEG26C9, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3180 AGGCTGAAATACTTAGTGGTGGCATTATGAAGGCATCAAAAACTTTTGACGCGCAGAAAAG 3239
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                                          /organism="Lycopersicon esculentum"
/cultivar="TA496, E6203"
/db_xref="taxon:4081"
                                                                                                                                                                           /tissue_type="suspension cultures"
/lab_host="SOLR"
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Location/Qualiflers
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                                                                                                                                                       /clone_lib="cTOS"
                                                                                                                             /clone="cTOS1C7"
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DEFINITION

RESULT 2 BE435332

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ACCESSION VERSION KEYWORDS

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2704 TGTCACAATTGAGGAAGTTGAAGAGTACTTCACCAACTATATTGTGAATGACAGTTTGG
                                                                                      2764 AATCATAGCAAATGCCCATGTCGTATTTGCAGACAGAGCAGGAACCTGATATGGCCATGAGTGA
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VERSION
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AI896465
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                                                                                                                                                                               AW933692 525 bp mRNA linear EST 18-MAY-2001 EST359535 tomato fruit mature green, TAMU Lycopersicon esculentum CDNA clone CLEF56C18 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                       l (bases 1 to 525)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Glovannoni,J. Generation of Esrs from tomato fruit tissue Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /close_lb="tonato fruit mature green, TAMU"
/tissue_type="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="80LR"
/note="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2:
Xhol; cLEF - Fruit were tagged at the 1cm stage and
harvested 5-f days prior to ripening. Fruit were cut in
half to verify the seeds were indeed 'immature' and the
seeds and locules were discarded prior to freezing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2643
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                      Gaps
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3310 TGATATAGATGACATGTTACCAAAGGCTTCGGCTTGGTACCACGTTACATCATCCTAC
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.1%; Score 525; DB 10; Length 525; llarity 100.0%; Pred. No. 3.3e-267; Conservative 0; Mismatches 0; Indels
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1. .525
/organism="Lycopersicon esculentum"
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/clone="cleF56C18"
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/db_xref="taxon:4081"
/clone="clEC15G23"
/clone="ib="tomato callus, TAMU"
/tissue_type="callus, TAMU"
/tissue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XL1-Blue MRF""
/note="vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Site_2:
/note="vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Si
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TAMU Lycopersicon esculentum cDNA clone
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Alcala, J. Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.
Alcala, J., Vrebalov, J., Craven, M.B., Bowman, C.L., Ahn, S., Ronning
C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
Generation of ESTs from tomato callus tissue
                                                                                                                                 2824 TCCATGCAAAAACTTGCTGAGCTCTTTTCAATTGCAGTGGACTTTCCAAAGACTGGTGT 2883
                                                                                                                                                                                                                                                                                                                                  TCCCGCTGAAATACCATCTCAGTTGCGCCCTAAAGAATACCCAGACTTCATGGATAAGCC 2943
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Lycopersicon esculentum
Bukaryots, Viridiplantes, Streptophyta; Embryophyta; Tra
Spermatophyta; Magnoliophyta; eudicotyledons; core eudic
Asteridae; euasterids I; Solanales; Solanacee; Solanum;
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100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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/organism="Lycopersicon esculentum"
/cultivar="TA496"
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100.0%; Pred. No. 6.5e-212;
iive 0; Mismatches 0;
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Clemson University Genomics Institute
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EST25896 tomato callus, TR
CLEC15G23, MRNA sequence.
A1896465
A1896465.1 GI:5602355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 570)
JACALAJ, Vrebalov, J., White, R., van der Hoeven, R.S., Holt, I.E.,
Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M.,
Nierman, W., Fraser, C.M., Martin, G.B., Glovannoni, J.J. and Tanksley
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                             2584 ITCTGGGAGTGATTTGGATGGGGATATCTACTTTGTTTGCTGGGATCAAGACATGATCCC 2643
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                                                                                                                                                                                                                                                                                                                                                                         2824 TCCATGCAAAAAACTTGCTGAGCTCTTTTCAATTGCAGTGGACTTTCCAAAGACTGGTGT 2883
                                                 1 TCCATGCTTGCATCCTGGTGATATTCGTGTTTTAAAGGCTGTAAATGTTCGAGCGCTGCA 60
                                                                                                                                                                                       181 GCCAAGGCAAGTCCAGCCGATGGAATATCCTCCAGCACCCAGCATACAGTTGGACCATGA
                                                                                                                                                                                                                                     TGTCACAATTGAGGAAGTTGAAGAGTACTTCACCAACTATATTGTGAATGACAGTTTGGG
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Lycopersicon esculentum'
/cultivar="TA496"
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/dev_stage="breaker"
/lab_host="SOLR"
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/clone="clEG16J9"
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Contact: CUGI
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Alcala J., Vrebalov, J., White, R., Matern, A.L., Holt, I.E., Liang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M. Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J. Generation of BSTs from tomato fruit tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Būkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                                                                              2369 CATGGAGAGTTTTCTGACGATTTACATCCATTTAATAACAGCAGATCCACCAACAGAAA 2428
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/cultivar="TA496"
/db_Arref="ta806"
/clone="cLEF50H7"
/clone_llb="tomato fruit mature green, TAMU"
/tissue_Lype="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
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                                                                  Length 570;
                                                                                                                   0; Indels
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                                                                  Score 398; DB 10; I Pred. No. 1.2e-199;
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100.0%; Pred. No. 1...
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  112 c
                                                                                         Best Local Similarity 100.0
Matches 398; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW649811 597 bp mRNA linear EST 18-MAY-2001 EST328265 tomato germinating seedlings, TAMU Lycopersicon escollentum cDNA clone cLE19L3 5', mRNA sequence.
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Sukaryota, Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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Alcala, J., Vrebblov, J., White, R., van der Hoeven, R.S., Holt, I.E.,
Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M.,
Nierman, W., Frsser, C.M., Giovannoni, J.J., Martin, G.B. and Tanksley
Xhol; CLEF - Fruit were tagged at the lom stage and harvested 3-5 days prior to ripening. Fruit were cut in half to verify the seeds were indeed 'immature' and the seeds and locules were discarded prior to freezing the
                                                                                                                                                                                                                                                                                                                                                                                                                                            GACTGGTGTTCCCGCTGAAATACCATCTCAGTTGCGCCCTAAAGAATACCCAGACTTCAT 2934
                                                                                                                                                              2635 CATGATCCCGCCAAGGCAAGTCCAGCCGATGGAATATCCTCCAGCACCCCAGCATACAGTT 2694
                                                                                                                                                                                                                     GGACCATGATGTCACAATTGAGGAAGTTGAAGAAGTACTTCACCAACTATATTGTGAATGA 2754
                                                                                                                                                                                                                                                                           CATGAGTGATCCATGCAAAAACTTGCTGAGCTCTTTTCAATTGCAGTGGACTTTCCAAA 2874
                                                                                                                                                                                                                                    61 GGACCATGATGTCACAATTGAGGAAGTTGAAGAGTACTTCACCAACTATATTGTGAATGA 120
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Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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                                                                                                                                    Indels
                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             esculentum"
                                                                                                        Score 358; DB 10;
Pred. No. 2.2e-178;
0; Mismatches 1;
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Clemson University Genomics Institute
Clemson University
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/cultivar="TA496"
/db_xref="taxon:4081"
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1. .597
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AW649811.1 GI:7411049
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                                                                                                        Query Match
Best Local Similarity
Matches 408; Conserv
                                                                  177
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AW649811
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BF112386 BST489976 tomato breaker fruit Lycopersicon esculentum cDNA clone cLEG41011 5' sequence, mRNA sequence.
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Skaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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Alcala, "Vrebalov, "J. White, R., van der Hoeven, R.S., Holt, I.E., Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley
/clone="clEIgL3".
/clone="lb="tomusing seedlings, TAMU"
/closue_lb="whole seedlings"
/tissue_type="whole seedlings"
/dev_stage="7 days post imbibtion"
/note="vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xhol; 7 days post imbibition on water-agar. Mixed stage
whole germinating seedlings from seed coat emergence up
to two centimeters in seeds not showing obvious signs of
germination were discarded."

a 12 c 138 g 159 t.
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                                                                                                                                                                                                                                                                                                                                                                          448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Generation of ESTs from tomato fruit tissue, breaker stage
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100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
Location/Qualifiers
1. 367
                                                                                                                                                                                                                                                                                  Length 597;
                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                               Score 341; DB 10;
Pred. No. 2.4e-169;
0; Mismatches 1;
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BF112386.1 GI:10942076
                                                                                                                                                                                                                                                                               9.1%;
ilarity 99.7%;
Conservative (
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Contact: CUGI
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Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Solanum tuberosum

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; eusasterids 1; Solanales; Solanaceae; Solanum.

(E 1 (bases 1 to 521)

Restrepo,S., Griffiths,H., Van der Hoeven,R., Tsai,J. and

Karamycheva,S. A.

Generation of a set of potato cDNA clones for microarray analyses

NI Unpublished (2002)

On Apr 17, 2002 this sequence version replaced gi:20163570.

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potatoftigr.org

This clone is available through the Research Genetics, contact the Research Genetics for further information 1-800-711-6195 or conact and seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST597184 mixed potato tissues Solanum tuberosum cDNA clone STMCB875 end, mRNA sequence.
BQ111608
BQ111608.2 GI:21915035
EST.
                                                                                                                                                                                                      /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2879 GGTGTTCCCGCTGAAATACCATCTCAGTTGCGCCCTAAAGAATACCCAGACTTCATGGAT 2938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2699 CATGATGTCACAATTGAGGAAGTTGAAGAGTACTTCACCAACTATATTGTGAATGACAGT 2758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332 AGIGATCCAIGCAAAAAACTIGCIGAGCTCTITICAAIIGCAGIGGACTITCCAAAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 CAIGAIGICACAATIGAGGAAGTIGAAGAAGTACTICACCAACTATATIGIGAATGACAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2819 AGTGATCCATGCAAAAACTTGCTGAGCTCTTTTCAATTGCAGTGGACTTTCCAAAGACT
                                                                                         /db_xref="taxon:4113"
/clone="cSTS8119"
/clone=lib="cSTS"
/tissue_type="sprouting eyes from tubers"
/dev_stage="sprouting eyes from tubers"
/dev_stage="l2-14 weeks post harvest"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                           5.2%; Score 195; DB 12;
1larity 99.6%; Pred. No. 1.1e-91;
Conservative 0; Mismatches 1;
                                                       /organism="Solanum tuberosum"/cultivar="Kennebec"
                                                                                                                                                                                                                                                                                                                                     187 t
Seq primer: M13F-R.
Location/Qualifiers
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les 245; Conserv
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Best Local S
Matches 245;
                                          source
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JOURNAL
COMMENT
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AUTHORS
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Solanum tuberosum
Solanum tuberosum
Solanum tuberosum
Solanum tuberosum
Solanum tuberosum
Solanum tuberosum
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; eussterids I; Solanales; Solanaceae; Solanum.

E I (bases I to 725)
S van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A.,
Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.
Generations of ESTs from sprouting potato eyes
U Upublished (2000)
Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
                                                                                                                                                       Anotes Tector: pBluescriptSKmCUadapt; Site_1: EcoR1; Site_2: XhoI; supplier: Boyce Thompson Institute; Site_2: XhoI; supplier: Boyce Thompson Institute; sequencing: The Institute for Genomic Research. Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
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                                                                                                                                                                                                                                                                                                                                                           Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
  /organism="Lycopersicon esculentum"
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                           Score 316; DB 12;
Pred. No. 4.4e-156;
0; Mismatches 1;
                                                                        /clone_lib="tomato breaker
/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
                                      /db_xref="taxon:4081"
/clone="cLEG41011"
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BG594667
BG594667.1 GI:
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BG594667
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/organism="Solanum tuberosum"
/cultivar="Kennebec or Binjte"
/db_rafe="taxon:4113"
/clone="STMCB87"
/clone="STMCB87"
/clone="stmcB87"
/clone="ib="mixed potato tissues"
/fissue_type="mixed tissues"
/fissues_mixed tissues_"
/fissues_mixed tissues_mixed tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissues_tissu
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1 (bases 1 to 434)

1 (bases 1 to 434)

1 Solanales; Solanaceae; Solanum.

1 (bases 1 to 434)

1 Restrepo's, Griffiths, H., van der Hoeven, R., Tsai, J. and Karamycheva, S.A. Griffiths, H., van der Hoeven, R., Tsai, J. and Karamycheva, S.A. Generation of a set of potato cDNA clones for microarray analyses

1 Onpublished (2002)

1 Contact: Robin Buell

1 The Institute for Genomic Research

2712 Medical Center Dr. Rockville, MD 20850, USA

Email: potatotetigr.org

This clone is available through the Research Genetics, contact the Research Genetics for further information 1-800-711-6195 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BQ111609 434 bp mRNA linear EST 17-APR-2002 EST597185 mixed potato tissues Solanum tuberosum cDNA clone STMCB87 3' end, mRNA sequence. BQ111609.1 GI:20163571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in the control of the contro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2873 AAGACTGGTGTTCCCGCTGAAATACCATCTCAGTTGCGCCCTAAAGAATACCCAGACTTC
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Seq primer: T7.
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                                                                                           /organism="Solanum tuberosum"
/cultiva=="Rennebec or Binjte"
/cultiva=="Rennebec or Binjte"
/db_arsf="raxon:4113"
/clone="STMCB87"
/clone=lib="mixed potato tissues"
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/clone_lib="mixed tissues"
/clone_rib="mixed tissues"
/clone_rib=
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1 (bases 1 to 610)

2 (c.M., Fry.W.E., Tanksley.S.D. and Baker.B.

2 (c.M., Fry.W.E., Tanksley.S.D. and Baker.B.

3 (contaction of ESTs from potato leaves and petioles

4 (2000)

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5 (contact: Cathy Ronning

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/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SolR"
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/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTB3D19"
Location/Qualifiers
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Best Local Similarity 100.0 Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                               Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      potato.
Solanum tuberosum
                                                                                                                                                mRNA sequence.
BG597875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 a
                                                                                                                                                                                                                                                                                                    potato.
                                                                                                                                      DEFINITION
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COMMENT
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                                         RESULT 14
BG597875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
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BQ507474
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AUTHORS
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="tromato developing/immature green fruit"
//clone_lib="tromato"
//dev_gree_"immature green (5-35 days post-anthesis)"
/lab_host="solia"
/lab_host
                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 18-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lycopersicon esculentum streptophyta; Embryophyta; Tracheophyta; Sukaryota; Viidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Aggnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 403)
Adala, Verballov, J., White, R., van der Hoeven, R.S., Holt, I.B.,
Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M.,
Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley
                                                                                                                           3291 CCTGGTTCAAGAGGCGTAATGATATAGATGACATGTTACCAAAGGCTTCGGCTTGGTACC 3350
                                                                                                                                                                                                                                                       3351 ACGTIACATATCATCCTACATATTGGGGTTGCTACAATCAGGGGTTGAAAAGAGCTCATT 3410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3281 GAGGCAAGACCTGGTTCAAGAGGGGTAATGATATAGATGATGTTACCAAAGGCTTCG 3340
                                                                                                                                                                                                                                                                                      419 CCTGGTTCAAGAGGCGTAATGATATAGATGATGATGTTACCAAAGGCTTCGGCTTGGTACC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST437289 tomato developing/immature green fruit Lycopersicon esculentum cDNA clone cLEM25110 5' sequence, mRNA sequence. BF052042.1 GI:10805938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generation of ESTs from tomato fruit tissue, immature green
                                                                                                                                                                                                                                                                                                                                                                                   3411 TCATTAGCTTTCCCTGGTGTTTTATGACCAGCTAATCCAGATTAAGAAGGA 3462
                                                                                                                                                                                                                                                                                                                                                                                                                  Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.9%; Score 110; DB 12; Length 403; 100.0%; Pred. No. 1.6e-46; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3341 GCTTGGTACCACGTTACATATCATCCTACATATTGGGGTTGCTACAATCA 3390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282 GCTTGGTACCACGTTACATATCATCCTACATATTGGGGTTGCTACAATCA 331
99.4%; Pred. No. 2.3e-52; wismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
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Clemson University
100 Jordan Hall, Clemson, SC 29634, US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="cleM25110"
                                  Best Local Similarity 99.4 Matches 171; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
Contact: CUGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 110; Conservative
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BF052042
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JOURNAL
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Anote—"Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26c in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from
BG597875 682 bp mRNA linear EST 12-APR-2001 EST496553 cSTS Solanum tuberosum cDNA clone cSTS19C12 5' sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BQ507474 177 bp mRNA linear EST 22-JUL-2002 EST614889 Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues Solanum tuberosum cDNA clone STMGQ59
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 681)

wan der Hoeven, R., Bezzeridaes, J., Sun, H., Cho, J., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B. Generations of ESTS from sprouting potato eyes

Contact: Cathy Ronning

The Institute for Genomic Research

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1 (bases 1 to 773)

1 Eals, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C., Restrepo, S., Grilfiths, H., van der Hoeven, R., Tsai, J. and Karamycheva, S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Solanum tuberosum"
/cultivar="Kennebec"
/cultivar="taxon:4113"
/clone_"cSTS19612"
/clone_lib="cSTS"
/tssue_yrpe="grouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_lost="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   600 CAAAATGCTCAGTTTCTCCTCATACAGTTATTGGTGCTCC 640
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Gaps

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/note="Vector: Bluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubbers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG592782 529 bp mRNA linear EST 12-APR-2001 EST491460 cSTS Solanum tuberosum cDNA clone cSTS2K4 5' sequence,
                                               /clone_lib="tomato flower buds 3-8 mm, Cornell University"
/tissue_type="flower"
/tissue_type="flower"
/tissue_type="flower"
/dev_stage="3-8mm buds"
/note="Vector: PBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; supplier: Tanksley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Solanum.

( (bases 1 to 529)
van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemingo,A., Boughilo,C., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B. Generations of ESTs from sprouting potato eyes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2955 GCTATATCTCAGAAAGAGTTATTGGAAAGCTTTTCAGGAAAGTGAAGGACAAAGCACCTC 3014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3015 AGGCTAGCTCTATCGCGACCTTCACAAGAGATGTTGCAAGGAGATCATATGATGCTGATA 3074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 GCTATATCTCAGAAAGAGTTATTGGAAAGCTTTTCAGGAAAGTGAAGGACAAAAGCACCTC 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
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0
                                                                                                                                                                                                                                                                                                                                                                                                          Length 443;
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Pred. No. 1.1e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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/organism="Solanum tuberosum"
/cultivat="Kennebec"
/db_xref="taxon:4113"
/clone="cSTS2K4"
/clone_lib="cSTS"
/tissue_type="sprouting eyes from tuber./dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                             Score 95; DB 10;
Pred. No. 1.5e-38;
0; Mismatches 1
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                       /clone="cTOB13P9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
BG592782
BG592782.1 GI:13610922
                                                                                                                                                                                                                                                                                                                                                                                                             2.5%;
ilarity 99.3%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 145; Conserv
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Best Local Similarity
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van der Hoeven, R.S., Bezzeredes, J.L., Matern, A.L., Holt, I.E., Liang
'F., Hansen, T., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W.,
Frasch, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
Generation of Ests from tomato flower tissue, 3-8 mm buds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues"
/lissue_type="mixed tissues"
/lab_host="SOLR"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 18-MAY-2001
Generation of a set of potato cDNA clones for microarray analyses Unpublished (2002)

On Jun 10, 2002 this sequence version replaced gi:21366343.
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potatofetig:.org
This clone is available through the Research Genetics, contact the Research Genetics for further information 1-800-711-6195 or
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Sukaryota, Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          577 TGGCAGGTTGTGCTCCATCGTCCATATGGTCAAAATGCTCAGTTTCTCCTCATACAGTTA 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW623969
443 bp mRNA linear EST 18-MAY
EST321914 tomato flower buds 3-8 mm, Cornell University
Lycopersicon esculentum cDNA clone cTOB13P9 5', mRNA sequence.
AW623969
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100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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2.6%; Score 98; DB 14; Length 773
Best Local Similarity 100.0%; Pred. No. 4.2e-40;
Matches 98; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Solanum tuberosum"
/cultivar="Kennebec or Binjte"
/db_xref="taxon:4113"
/clone="SIMGQ59"
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/db_xref="taxon:4081"
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1. .773
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Matches 128;
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AJ487433
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Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Solanum tuberosum
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
E. (bases I to 393)
Supermatoria of 393
Supermatoria of ESTs from dormant potato tubers
Generations of ESTs from dormant potato tubers
Unpublished (2001)
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@tesgen.com
Seq primer: Mis-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anote—"Netcor: Daluescript SK(-); Site_1: EcoRI; Site_2: XhoI; This library targets genes expressed in dormant tubers. This library was made from sections of dormant tuber. avoiding the buds and epidermis. Tubers were stored for one month post-harvest at 4oC. The tuber was peeled, well away from the surface. Then it was chopped into 1-2 mm cubes and immediately frozen in liquid nitrogen. This library is noted as P4 in Tanksley lab notebooks."
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                                                                                                                                                                                                                                                                                        BG889665 393 bp mRNA linear EST 30-MAY-2001 EST515516 cSTD Solanum tuberosum cDNA clone cSTD15C7 5' sequence, mRNA sequence.
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                                                                                                    2775 ATGCCCATGTCGTATTTGCAGACAGAGAACCTGATATGGCCATGAGTGATCCATGCAAAA 2834
                                 2715 AGGAAGTTGAAGAGTACTTCACCAACTATTGTGAATGACAGTTTGGGAATCATAGCAA 2774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 ATACAGGATATGGAACTGTATGTGCATTGGAGGTTAAACAGTCCAAAGGAGGATCTAGAG 329
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ilarity 100.0%; Pred. No. 4.2e-31;
Conservative 0; Mismatches 0; Indels
1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="dormant tuber"
/dev_stage="one month post-harvest"
/lab_host="SOLR"
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/cultivat="Kennebec"
/db_xref="taxon:4113"
/clone="GSTD1567"
0; Mismatches
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BG889665.1 GI:14266751
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 Matches 134; Conservative
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Matches 81; Conserva
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RESULT 19

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/dev_stage="1 to 3 days"
/dev_stage="1 to 3 days"
/lab_host="SoLR"
/lab_host="SoLR"
/lab_host="SoLR"
/note="Wector: pBlueScript SK(-); Site_1: EcoRl; Site_2:
Xhol; NRA was supplied by Christian Bachem & Beatrix
Horvath(Laboratory of plant Breeding, Dept. of Plant
Sciences, Wageningen University, The Netherlands). Total
RNA was isolated from developing axillary buds of potato
nodal stem cuttings cultured on medium for the
introduction of tuber formation as described in Bachem et
al. (plant Journal 1996). Tissue samples were taken of
stages or cresponding to growing stolons and the early
stages of tuber formation.

87 a 51 c 80 g 103 t
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AJ487433 I GI:22022186
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Solanum tuberosum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases I to 32)
2 (bases I to 32)
3 (bases I to 32)
3 (bases I to 32)
4 (bases I to 32)
5 (bases I to 32)
5 (bases I to 32)
6 (bases I to 32)
7 (bases I to 32)
8 (
BE340733 321 bp mRNA linear EST 17-JUL-2000 EST344811 potato stolon, Cornell University Solanum tuberosum cDNA clone cSTA12M12 similar to RNA-directed RNA polymerase [Lycopersicon esculentum] PIR[I30819] T30819 RNA-direc, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Solanum tuberosum"
/cultivar="Bintje"
/db_xref="taxon:4113"
/clone="cSTA12M12"
/clone_lib="potato stolon, Cornell University"
/tissue_type="axillary buds of stem explants, swelling stolons"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Generation of ESTs from potato swelling stolons Unpublished (1999)
Contact: Research Genetics, Libraries Division Tel: 1-800-711-6195
Email: cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualiflers
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VERSION
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Location/Qualifiers
1. .340
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BQ827639.1 GI:22133265
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   cdna@resgen.com
Seq primer: T7.
                                                                                                                                                                                                                                                             107
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        SM Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

I (bases 1 to 340)

Buell,C.R., Hart,A., Baker,B., Tanksley,S., Fry,W., Smart,C., Kestrepo,S., Griffiths,H., van der Hoeven,R., Tsai,J. and Karamycheva,S.A.

Generation of a set of potato cDNA clones for microarray analyses on Jun 10, 2002 this sequence version replaced gi:21368534.

Other_ESTs: EST617079

Contact: Robin Buell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BST617080 Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues Solanum tuberosum cDNA clone STMHE37 3' end, mRNA sequence.

BQS09665.2 GI:21925399
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3401 AGAGCTCATITCATTAGCTTTCCCTGGTGTGTTTATGACCAGCTAATCCAGATTAAGAAG 3460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       282 AGAGATCATTCATTAGCTTTCCTGGTGTGTTTATGACCAGCTAATCCAGATTAAGAAG 341
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                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Solanum tuberosum cv. Provita" 91 c 125 g 152 t
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1.9%; Score 71; DB 9; Length 550;
Best Local Similarity 99.2%; Pred. No. 9.2e-26;
Matches 121; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato@tigr.org
                                                                                                                                                                                                                                                                                                                                                      one="P3f8"
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BQ509665/c
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                           ORGANISM
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Leeds/Wash D Wooss Est Froject
Unpublished (1999)
Contact: Ralph Quatrano
Leeds/Wash U Moss Est Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 315 286 1800
Fax: 315 286 1810
Fax: 315 286 1810
Fax: 315 286 1810
Fax: 316 286 1810
Fax: 316 286 1810
Fax: 317 286 1810
Fax: 318 286 1810
Fax:
/organism="Solanum tuberosum"
/cultivar="Kennebec or Binjte"
/db_xref="taxon:4113"
/clone="same:7"
/clone="same:7"
/clone=lib="Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues"
/lab_host="SolR"
/lab_host="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: EcoRI; Sit
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Bukaryota, Vilidiplantae; Streptophyta; Embryophyta; Bryophyta;
Bukaryota, Vilidiplantae; Funatiales; Funatiaceae; Physiconitrella.

[ bases 1 to 541]
[ bases 1 to 541]
[ chases 1 to 541]
[ chases 2 to 541]
[ chases 2 to 541]
[ chases 3 to 541]
[ chases 4 to 541]
[ chases 5 to 541]
[ chases 5 to 541]
[ chases 6 to 541]
[ chases 6 to 541]
[ chases 7 to 641]
[ chases 7 to 641]
[ chases 7 to 641]
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                                                                                                           1. :541./
/organism="Physcomitrella patens"
/organism="Physcomitrella patens"
/db_xref="texon:3218"
/clone="PEB_SOURCE_ID:PPAS041205"
/clone_lib="Moss EST library PPAS"
/dev_stage="protonemata, 7day old ABA-treated"
/lab_nost="E.coli DH10b"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
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1.5%; Score 57; DB 14; 1
Best Local Similarity 100.0%; Pred. No. 2.4e-18;
Matches 57; Conservative 0; Mismatches 0;
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CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by Pieter de Jong"
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                                               52 g
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                                                                                                                                                                                                                           239 TIGAAGAAATTTTTTTTTTT 261
                                                                                                                                                                                                   572 TIGAAGAATTTTTTTTTTT 594
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BB013867/c
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S. Jao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
Jong,P. and Fraser,C.,
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
Other_GSSs: CH230-112K20.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 contact Pieter de Jong (pdejongémail.cho.org).
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/Dacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejongémail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.tlgr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 112 row: K column: 20
ECORI; 7-day-old protonemal tissue was incubated 10-4M ABA for Ich hours before RNA isolation. CDNA was synthesised from Amersham's CDNA Sythesis Plus kit and ligated with ECORI-NOLI linkers for cloning in the ECORI site of Lampda Zaplī (Stratagene). After packaging, the library was propogated in E. coli XL.I Blue cells and amplified. The library was excised by mass excision in SOLR cells and amplifilan resistant transforments selected. Approximately, 1,000,000 colonies were grown and recovered. The double stranded plasmid library was recovered and used to transform DHOD cells by electroporation. Clones corresponding to abundant transcripts were identified by colony hybridization using a cDNA probe derived from untreasted protonematal tissue, and eliminated from the library, by rearraying."
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CH230-112K20.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-112K20, DNA sequence.
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/cell_type="Brain"
/note="Vector: pTARBAC2.1; Site_1: BcoRI; Site_2: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Métazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/clone_lib="CHORI-230 Segment 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Rattus norvegicus"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
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1. .348
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Rattus norvegicus
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Best Local Similarity
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BH258389
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Beta vulgatis:

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.

(Eases 1 to 571)

(Eases 1 to 571)

(Eases 1 to 571)

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39-EB847-006-003-M09-T3 Sugar beet MPIZ-ADIS-006 Lambda Zap II
library Beta vulgaris CDNA clone M-9-3, mRNA sequence.
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Advistage="4 week old pot-grown plants"

Anote="Grgan: shoot and root; Vector: pBluescript SK- from lambda ZAP II; CDNA (lambda ZAP-II) library from sugar beet, whole plant mRNA, Prepared using the Stratagene unixAP CDNA kit, cloning sites ECORI-XhoI, primer sites and orientation:

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                                                                                                                                                                                                   0.6%; Score 23; DB 17; Length 348;
100.0%; Pred. No. 2.9;
.ive 0; Mismatches 0; Indels
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/db_xref="taxon:161934"
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Unpublished (2000)
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
Sciences Center (GSC), Yokohama Institute
Tel: 81-45-503-9222
Fax: 81-45-503-9222
Fax: 81-45-503-9226
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URL:http://genome-gsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp/
Carning.p. Nishiyama.y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N. Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Scl. U.S.A. 91 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki, Y. and Hayashizaki,Y., Asiyama,J., (1999)
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
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                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/clone_lib="RIKEN full-length enriched, adult male testis
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/organism="Mus musculus"
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Mus musculus
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Email: genome-resertc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Etwidda, S., Fukunishi, Y., Funayama, T., Hara, Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kidima, Y., Matsuyama, T., Nittsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shipayama, T., Nittsuma, H., Oda, H., Owa, C., Y., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watamatsu, M., Ogame, M., Yamamura, T., Yokota, T., Yoshino, M., RIKEN, Mouse, Ests.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/sex="male"
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                                                                                                                            Length 265;
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                               DB 10;
9.4;
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Contact: Chie Owa
Genome Science Laboratory
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REFERENCE AUTHORS

RESULT 27 AV045898/c

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Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itch.M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
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URL:http://genome-gsc.riken.go.jb,
Sasaki,N., Izawa,M., watahiki,W., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
Matsuura,S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome-resertc.riken.go.jp
thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length CDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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/note="Organ: mammary gland; Vector: pr7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                312 bp mRNA linear EST 23-NOV-1999
AV045898 Mus musculus adult C57BL/6J testis Mus musculus cDNA clone
bav04s007, mRNA sequence.
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/db_xref="taxon:10090"
/clone="1700049G07"
/clone_lib="Mus musculus adult C57BL/6J testis"
/sex="male"
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Pred. No. 9.6;
                                 DB 9; Length 308; 9.6;
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
                              0.6%; Score 22; DB illarity 100.0%; Pred. No. 9.6 Conservative 0; Mismatches
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AV045898.2 GI:4865563
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Best Local
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TITLE JOURNAL COMMENT

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FEATURES

BASE COUNT

us-09-782-874-1.oli.rst

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laevis
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E (Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akhyama, J., Fukuda, S., Fukudishi, Y., Funayama, T., Hara, A., Haytsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shiperno, M., Tamana, T., Sauzuki, H., Tagamo, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y., Yoshino, M., Contact: Chie Owa
                                  Email: genome-resetro.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
Thermostabilization and thermoactivation of thermolabile enzymes by
Trenholse and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
Please (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
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                                                                                                                                                                                                                                                                                                                                                                                              AV046870 356 bp mRNA linear EST 23-NOV-1999
V046870 Mus musculus adult C57BL/6J testis Mus musculus cDNA clone
1700064EI7, mRNA sequence.
AV046870
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                                                                                                                                                                                                   Length 332;
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                                                                                                                                                                                                   Score 22; DB 9;
Pred. No. 9.7;
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1700064E17"
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/dev_stage="adult"
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100.0%; Pred
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopodinae; Xenopodinae; Yacopus.

1 (bases 1 to 580)

2 lackshear, P.J., Lai, W.S., Thorn, J.M., Kennington, E.A., Staffa, N.G. Jr., Moore, D.T., Boulfard, G.G., Beckstrom-Sternberg, S.M., Touchman, J.W., Bonaldo, M.F. and Soarse, M.B.

The NIERS Kenopus maternal EST project: interim analysis of the first 13,879 ESTs from unfertilized eggs

Centact: Perry J. Blackshear of Signal Transduction office of Clinical Research and Laboratory of Signal Transduction office of Clinical Research and Laboratory of Signal Transduction National Institute of Environmental Health Schences

A2-05 NIERS, 101 Alexander Drive, Research Triangle Park, NC 27709, USA
adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
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Tel: 219 541-4899
Tex: 919 541-451
Email: blackOl096niehs.nih.gov
Clone is available through Research Genetics, Inc., 2130 Memorial
Parkway, Huntsville, AL 35901
Phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email
cdnafresgen.com
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                                                                                                                                                                                                                                                                     Length 356;
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/cell_type="unfertilized egg"
dew_stage="unfertilized egg"
/lab_host="DH10B"
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/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="PBX0139D05"
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BACKWARD: CAGGAAACAGCTATGACC
Plate: 0139 row: D column:
Seq primer: T7 primer.
Location/Qualifiers
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AW644365.1 GI:7401749
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AV207607/c
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                approaches to facilitate gene discovery', Genome Research 6:791-806, 1996. The first strand synthesis used a NotI-dTIB primer; double stranded cDNAs were ligated to ECORI adapters, digested with NotI, and directionally cloned into the NotI and ECORI digested pT713-Pac vector. The library contained approximately 7.2 X 10^5 recombinants, with average insert sizes of 1-1.5 kb."
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@gsc.riken.go.jp,
WLihttp://genome-gsc.riken.go.jp,
Saaski,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 275)
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                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
Soares, M.B. 'Normalization and subtraction: two
                                                                                                                                                                                                                                                                                                                    0.6%; Score 22; DB 10; Length 580; clarity 100.0%; Predch No. 11; Conservative 0; Mismatches 0; Indels
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es 22; Conserv
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/organism="Mus musculus"

source

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (basea 1 to 282)

E Konno.H., Alzawa.K.; Akahira.S., Akiyama.J.; Carninci.P.; Endo.T.; Konno.H., Alzawa.K.; Akahira.S., Rayatu.N.; Hirozane.T.; Hirozane.T.; Hirozane.T.; Hirozane.T.; Hirozane.T.; Ishii.Y.; Ishikawa.T.; Itoh.W.; Izawa.M.; Kadota.K.; Kagawa.I.; Kajama.J.; Kikuchi.N.; Kojima.Y.; Koya.S.; Kusakabe.M.; Matsuna.T.; Hirozane.T.; Cowa.C.; Ozawa.Y.; Saito.H.; Sano.M.; Sato.K.; Shibata.K.; Shibata.Y.; Shigemoto.Y.; Shiraki.T.; Soqabe.Y.; Sugahara.Y.; Slibata, Suzuki.H.; Takahashi.F.; Tateno.M.; Tominaga.N.; Tsunoda.Y.; Watahiki.A.; Washanbe.S.; Yammura.T.; Yasunishi.A.; Vookino.M.; Muramatsu.M. and Hayashizaki.Y.; Kitsu Mouse ESTS (Kono.H.; et al. 1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="6330543D06"
/clone_lib="RIKEN full-length enriched, adult male medulla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AV207607 AV207607 RIKEN full-length enriched, adult male testis Mus musculus CDNA clone 1700096A08 3', mRNA sequence.
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
Tel: 81-82-8461ro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Pax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                  Another Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                             /tissue_type="medulla oblongata"
/dev_stage="adult"
/lab_host="DH10B"
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100.0%; Pred. No. ...
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URL:http://genome.gsc.riken.go.jp/
/strain="C57BL/6J"
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                                                                                                                                  /sex="male"
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Matches 21; Conservative
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AUTHORS
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                                                      Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M.; Kitsunai, T.; Akiyama, J.; Shibata, K.; Izawa, M.; Kawai, J.; Yomaru, Y.; Carninci, P.; Shibata, Y.; Ozawa, Y.; Muramatsu, M.; Okazaki, Y. and Hayashizaki, Y. Automated filtration-based high-throughput plasmid preparation carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG379160 284 bp mRNA linear EST 12-MAR-2001 UI-R-BT1-bnk-e-09-0-UI.S1 UI-R-BT1 Rattus norvegicus cDNA clone UI-R-BT1-bnk-e-09-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RIKEN full-length enriched, adult male testis"
/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Site_1: XhoI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was GAGAGAGAGAGCACCAAGAGCTCTTTTTTTTTTTTTVN 3'], cDNA was
Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y., Matsuura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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100.0%; Pred. No. 32;
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Program for Rat Gene Discovery and Mapping
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                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1700096A08"
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97044477
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/lab_host="SOLR"
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es 21; Conserv
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BG379160/c
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University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 9250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tall. CDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) POLYA-Yes.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (base 1 to 32)

Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci
, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hivozane, T., Horl, F., Ishli, Y., Hara, A., Hayatsu, N.,
Izawa, M., Kadota, K., Kagawa, T., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
Matuyyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Odazaki, Y.,
Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,
Suzuki, H., Sazito, H., Sakai, C., Sato, K., Shibata, K., Shigemoto, Y., Watahiki, A., Watahashi, F., Tominaga, N., Toya, T., Tasunoda, Y., Watahiki, A., Yokata, T., Yamamura, T., Yamanaka, I.,
Yano, R., Yasunishi, A., Yokata, T., Yoshida, K., Yoshino
RIKEN Mouse ESTS (Konno, H., et al.)
Contact: Yoshihide Hayashizaki
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BB446629.1 GI:9289241
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., Miyata, A., Mitani, Y., Iida, K., Uesugi, H., Sugiyama, Y. and
                                                                                                                                                                                                        Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
1. 381
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66 c 77 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.00,
100.0%; Pre-
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BE581464.1 GI:9832406
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        ,M., Miya'
Nomoto,H.
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VERSION
KEYWORDS
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JOURNAL
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                                                                                                                Email: genome-resegac.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carlinci, P. Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
Carninci, P. Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
'N., Okazaki, Y., Muramatsu, M. and Haysshizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P., and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AV202914 381 bp mRNA linear EST 26-JUL-1999
AV202914 Yuji Kohara unpublished cDNA Caenorhabditis elegans CDNA
clone yks56e12 5', mRNA sequence.
AV202914 GI:5586685
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis;
1 (bases 1 to 381)
Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H., Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I." 75 c 57 g 110 t
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100.0%; Pred. No. 33;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualiflers
1. 323
/organism="Mus musculus"
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Matches 21; Conservative
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AV202914
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AUTHORS
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KEYWORDS
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(bases 1 to 426)
Mordater, J., Olifton, S., Chiapelli, B., Pape, D., Martin, J., Wylle, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvill, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
Washington University School of Medicine
Washington University School of Medicine
Tel: 314 286 1800
Fax: 314 286 1810
Fax
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/ds.rain="Rhabditiform larvae obtained from gerbils"
/db.xref="taxon:6248"
/clone_lib="TBN95TM-SSR"
/lab_host="XL-1 Blue MRF' (Stratagene)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Strongyloides stercoralis
Eukaryota, Metazoa, Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloididae; Strongyloides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="CB1489 him-8(e1489)"
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/clone="yk556el2"
/clone=lip="Yuji Kohara unpublished cDNA"
/sex="hermaphrodite, male"
/tissue_type="whole animal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 others
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Unpublished (1999)
Contact: McCarter JP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Caenorhabditis elegans"
Expressed genes in C.elegans Unpublished (1999)
Contact: Yuji Kohara Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan Tel: 81-559-81-6854
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.6%; Score 21; DB 9;
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Gaps

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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/clone_lib="NHEMGE.95"
/clone_lib="NHEMGE.95"
/clone_lib="hippocampus"
/lab_host="bHippocampus"
/lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 484)

NIH-MGC http://mgc.ncl.nih.gov/.

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gaphys-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshlyuki and Plearo Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov

Plate: LLAMI0725 row: d column: 19

High quality sequence stop: 398.

1. . . 484
                                                                                                                                                                                                                                                                                                                                                                                     602688174F1 NIH_MGC_95 Homo sapiens CDNA clone IMAGE:4820322 5', mRNA sequence.
BG705217
EG705217.1 GI:13979333
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                                                                             Similarity 100.0%; Score 21; DB 17; Length 440; Similarity 100.0%; Pred. No. 35; 1; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                               2788 ATTIGCAGACAGAGCAGCTGA 2808
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Best Local Similarity 100.0%; Pi
Matches 21; Conservative 0;
                                                                                                                                                                                                                                                      386 ATTTGCAGACAGAGCTGA 406
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                                                                                    Query Match
Best Local Sim
Matches 21;
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BG705217/c
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BI693834/c
LOCUS
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TITLE
JOURNAL
COMMENT
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS
                                                                                                                                                                                                                                                                               q
/note="Vector: Lambda Uni-ZAP XR (Stratagene); Site 1: ECORI; Site_2: XhoI; mRNA was purified from 2 x 10E3 rhabditiform larvae which had been isolated from gerbils experimentally infected with larvae originally isolated from experimentally infected dogs. cDNA was constructed and, using adaptors, was cloned undirectionally into the vector from the EcoRI site to the XhoI site. The library has an unamplified titer of 1 x 10E5 pfu/ml and an amplified, undiluted titer of 9 x 10E11 pfu/ml. The average insert size of the unamplified library is 675 bp (range, 100-170)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Fax: (206) 616-3887
Fmail: jWallacedu.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pleter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@tesgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 651 row: N column: 18
Seg primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ498746 11near GSS 28-APR-1999 HS_25075_B2_609_SP6E RPCI-11 Human Male BAC Library Homo sapiens AQ498746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 21; DB 10; Length 426;
Pred. No. 34;
0; Mismatches 0; Indels
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Location/Qualifiers
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l Similarity 100.0%; P:
21; Conservative 0;
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Best Local Similarity
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AQ498746
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Location, ---
1. :504
/organism="Saccharomyces unisporus"
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/clone="474.dhz57g01.sl"
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/note="Random genomic sequence"
71 c 75 g 184 t
                                                                                                                                                                                                                                               Similarity 100.0%; Pred. No. 35; Length 504; 21; Conservative 0; Mismatches 0; Indels
     Email: mj@genetics.wustl.edu
Class: random plasmid subclone.
Location/Qualifiers
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BI038396.1 GI:14445022
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Local Sim.
21;
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                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
E (Desses 1 to 500)
I (Dasses 1 to 500)
I (Dipublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CONTact: Robert Strausberg, Ph.D.
CONTaction of Collocation: Life Technologies, Inc.
CONTACTION AND TICYTE Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
High quality sequence start: 5
High quality sequence start: 5
High quality sequence stop: 500.
Location/Qualifiers
I. . 500
/organism-Wux mus musculus"
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101 c 103 g 131 t
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Pred. No. 35;
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Washington University Medical School
80x 8232, 4565 Scott Ave., St. Louis, MO 63110, USA
Tel: 314 362 2735
Fax: 314 362 7855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="FVB/N-3"
/db_xref="caxon:10000"
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/clone_lib="NCI_CGAP_Mam2"
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100.0%; Pred. No. .c..
... 0; Mismatches
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 BI693834.1 GI:15656450
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Best Local Similarity 100.'
Matches 21; Conservative
                                                                             Mus musculus
                                                           house mouse
ACCESSION
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AZ930706
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// 521 /-
// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="Homo 18606"
// Clone_lib="NT00266"
// Clone_lib="NT00266"
// Clone_lib="Organism="Homo: Vector: pucl8; Site_l: Smal;
// Note_"Organism="Homo: Vector: pucl8; Site_l: Smal;
// Site_2: Smal; A mini-library was made by cloning products
// Site_2: Smal; A mini-library was made by cloning products
// Site_2: Smal; A mini-library was made by cloning products
// Site_2: Smal; A mini-library was made by cloning products
// Organism Organism Organism of Institute for Cancer Research)
// Profiles into the pucl8 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
// Issue mRNA and cDNA amplification were performed under
// Organism                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Bukaryota, Martazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 521)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
Simpson, A.J., Soares, F., Brentani, R.R., Reis, L.F., de Soua, S.J. and
BI038396 521 bp mRNA linear EST 14-JUN-2001 RC5-NT0266-180101-021-A06 NT0266 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: +55-11-2704922
Email: asimpson@ludyig.org.br
Email: asimpson@ludyig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludyig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-NT0266-180101-021-A06643=2001-01-18&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
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Query Match Best Local S Matches 21

δ g RESULT 42 BIO41199 LOCUS DEFINITION

ACCESSION VERSION

SOURCE ORGANISM

KEYWORDS

REFERENCE AUTHORS JOURNAL MEDLINE COMMENT

TITLE

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AQ985038 630 bp DNA linear GSS 30-JAN-2000 EVCI-23-322G7.TJ RPCI-23 Mus musculus genomic clone RPCI-23-322G7,
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                                                                                                                                                                         house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Was musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 637)
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100.0%; Pred. No. 37;
Live 0; Mismatches 0; Indels
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AQ985038
AQ985038.1 GI:6818243
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AZ866201.1 GI:13067272
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AQ985038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

I bases I to 529

Buss Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                          BI041199 529 bp mRNA linear EST 14-JUN-2001 RC5-NT0266-220201-013-E01 NT0266 Homo sapiens cDNA, mRNA sequence.
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Mahall: salimpson@ludwig.org.br
This sequence was properly from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
Project. This wall way org.br/scripts/gethtml2.pl?tl-RC5&t2=RC5-NT0266-
220201-013-E01&t3=2001-0222&t4=1)
Seq primer: puc 18 forward
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                    Gaps
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20202663
                         Length 521;
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Pred. No. 36;
0; Mismatches 0; Indels
                                                                                    Indels
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                  0.6%; Score 21; DB 13;
100.0%; Pred. No. 36;
ive 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone_lib="NT0266"
/dev_stage="Adult"
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Location/Qualifiers
1. 529
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llarity 100.0%; P
Conservative 0;
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                                            l Similarity 100.
21; Conservative
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Gaps

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Query Match

Matches

ò g

BASE COUNT ORIGIN

RESULT 43 AQ985038/c

source

FEATURES

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(http://www.jax.orgyresources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qi|4732114|qb|AR123072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 755)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longarce, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly Islam, H., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Male"
//sab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resourant /Anamants/Anares/). The DN
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/db_cref="tuxon:10090"
/clone="tuxoc2M0176B12"
/clone=lib="Mouse 10kb plasmid UUGC1M library"
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Location/Qualifiers
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BH098015
     AUTHORS
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Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M., Tssgaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
AL Unpublished (1999)
Other_GSSS: RPCI-24-28N6.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 302 0200
Fa
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BOGYJ73TF BOGY Brassica oleracea genomic clone BOGYJ73, DNA
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Wector: pTARBAC1; produced by Pieter de Jong. The
Repress was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using Mbol partially digested male C57BL/6J
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Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Other_GSSs: BOGY173TR
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Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seg primer: TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.6%; Score 21; DB 17; Length 755; 00.0%; Pred. No. 38; ve 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-228N6"
/clone=lib="RPCI-24"
/sex="Male"
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1. .755
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les 21; Conserv
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BH608326/c
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Gaps

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954 bp mRNA linear EST 17-OCT-2001 HVSMEa0006K07f Hordeum vulgare seedling shoot EST library HVDDNA0001 (Cold stress) Hordeum vulgare cDNA clone HVSMEa0006K07f, BF621359 BF621359 IG:11885093
                                                                                                                                                                                                                                                                                                                                      BH558896 80B bp DNA linear GSS 14-DEC-2001
BOHLC24TR BOHL Brassica oleracea genomic clone BOHLC24, DNA
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Hordeum vulgare
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
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1 (bases 1 to 954)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Henry, D., Palmer, M., Rambo, T., Simmons, J., Oates, R., Choi, D.W., Fenton, R.D. and Main, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brassica oleracea.
Brassica oleracea.
Brassica oleracea.
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
I (bases I to 808)
Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea other_GSSs: BOHLC24TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sincator and a services

Location/Qualifiers

1. 808
/organism="Brassica oleracea"
/strain="Trol000bH3"
/db_xref="taxon:3712"
/clone="BCHLC24"
/clone="BCHLC24"
/clone="Tobellool"
/clon
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Tel: 301-383-3523
Fax: 301-388-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seg primer: TR
Class: sheared ends.
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BH558896.1 GI:17810676
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                   Conservative
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5160t3 NICHD Zebrafish normalized I Danio rerio cDNA clone 5160,
BG985828
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gactagttcttagatcgcgatcgcGGCCGCccttttttttttttttt. Second strand DNA was synthesized by E. coli DNA polymerase I in combination with E. coli RNAse H and E. coli DNA ligase. Double stranded cDNA was ligated with SalI adapter. These cDNAs were cloned into the SalI/NotI site of pBluescript KS+ and transformed into E. coli Electromax DH10B by
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/clone_lib="NICHD Zebrafish normalized I"
/dev_stage="bud to 10 somite stage embryos"
/note="Vector: pBluescript KS+; Site_l: NotI; Site_2: SalI
/RNA was reverse-transcribed to first strand oDNA using
SuperScriptII reverse-transcriptase and tagged oligo-dT
primer which contains several restriction sites including
NotI site:
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Kudoh,T., Tsang,M., Hukriede,N.A., Chen,X., Dedekian,M., Clarke
C.J., Klang,A., Schultz,S., Epstein,J.A., Toyama,R. and Dawid,I.B.
A gene expression Screen in zebrafish embryogenesis
Genome Res. 11 (12), 1979-1987 (2001)
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E 2188053

E 2188053

Contact: Dawid IB
Laboratory of Molecular Genetics
Laboratory of Molecular Genetics
National Institute of Child Health and Human Development, NIH
BldG.6B. Room 413, 9000 Rockville Pike, Bethesda, MD 20892 USA
Tel: 301 496 0243
Email: idawid@nih.gov
Seq primer: T3.

Enail: idawid@nih.gov
Seq primer: T3.

Location/Qualifiers

source
//organism="Danio rerio"
/db_xref="taxon:7955"
//clone="5160"
//lone_lib="NICHD Zebrafish normalized I"
                                                                                               /________Brassica oleracea"
/strain="TO1000BH3"
/db_xref="faxon:3712"
/clone="BGY4773"
/clone=lib="BBGY"
/clone=lib="BBGY"
/clone="vector: pHGS1; Site_1: BstXI; 2-3 kb sheared genemic DNA inserted into pHGs1 using BstXI linkers"
a 141 c 140 g 207 t
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llarity 100.0%; Pred. No. 38;
Conservative 0; Mismatches 0; Indels
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LOCUS

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

TITLE JOURNAL MEDLINE COMMENT

REFERENCE AUTHORS

RESULT 47 BG985828/c

BASE COUNT ORIGIN

Matches

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Gaps

source

FEATURES

BASE COUNT

ORIGIN

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Search completed: November
Job time: 4579 secs
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/clone_lib="Hordemu vulgare seedling shoot EST library
HVCDNA0001 (Cold stress)"
/lab host="rediing shoot"
/lab host="rediing shoot"
/lab host="rediing shoot"
/lab host="rediing stress) site_1: EcoR1; Site_2: Xho1;
Seeds were surface sterilized then germinated under axenic
conditions in the dark at room temperature on filter paper
conditions in the dark at room temperature on filter paper
conditions in the dark stroom temperature on filter paper
conditions in the dark stroom temperature on filter paper
conditions in the dark stroom seedlings were
incubated at 5cc for 2 days. Shoots were then harvested,
total RNA was prepared, poly(A) RNA was purified, one
primary unamplified cDNA library was made, and 600000 pfu
were in vivo excised to give pBluescript SK(-) cDNA
phagemids. These steps were performed in the TJ Close
laboratory at the University of California, Riverside
choi, Close, Fenton). Phagemids were plated and picked at
the Clemson University Genomics Institute (CUGI) (Begum,
Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations
, DNA sequencing and sequence analysis were performed at
CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main
). The sequence has been trimmed to remove vector sequence
above. For more details on library preparation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS 13-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R. Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/pgn/31/cover.html)" 248 c 213 g 325 t octhers
Development of a genetically and physically anchored EST resource for barley genomics: Morex cold-stressed seedling shoot cDNA
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100.0%; Pred. No. 39;
tive 0; Mismatches 0; Indels
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                                                                    Unpublished (2001)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 1288
Fax: 864 656 4293
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    954 //Organism="Hordeum vulgare" /cultivar="Morex"

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                                                                                                                                                                                                                                           Frail: rwing@clemson.edu
Total hq bases = 201
Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                        High quality sequence start: 110
High quality sequence stop: 461.
Location/Qualifiers
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/clone="HVSMEa0006K07f"
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AL196386.1 GI:7834536
GSS; genome survey sequence.
Tetraodon nigroviridis.
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6, 2002, 03:25:53

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Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
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Tetraodon nigroviridis
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
Tetraodontidae; Tol099
Roest-Crollius; H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Baurin,W. and Weissenbach,L.
Human gene number estimate provided by genome wide analysis using
                                                                                                                                                                                                                                                                                                                         2 (bases
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
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100.0%; Pred. No. 39;
.ive 0; Mismatches 0; Indels
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/db_xref="taxon:99883"
/clone="137820"
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Matches 21; Conservative
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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November 5, 2002, 17:42:07; Search time 9160 Seconds (without alignments) 11853.992 Million cell updates/sec US-09-782-874-1 3731 1 GAMATATICITTACTIACIT......AGITICAICTITCIAAA 3731 4109280 2054640 seqs, 14551402878 residues Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY_NUC Gapox 1.0 em_htg_other:*
em_htg_mus:*
em_htg_pln:*
em_htg_rod:* Minimum DB seq length: 0 Maximum DB seq length: 2000000000 gb_ro:*
gb_sy:*
gb_un:*
gb_vi:*
em_ba:*
em_fun:* em_sts:* em_un:* em_in:*
em_om:*
em_or:*
em_ov:* em_pat:* em_ph:* em_pl:* em_ro:* gb_ba:* gb_htg:* gb_in:* gb_ov:* gb_pat:* gb_pl:* gb_pl:* *: mo_dp GenEmbl:* Title: Perfect score: Sequence: Scoring table: Database : Searched: Run on:

is the number of results predicted by chance to have a Pred. No.

em_htgo_hum:* em_htgo_mus:* em_htgo_other:*

em_htg_vrt:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence scule Nicoti Petuni Genomi Arabido Oryza	AP004880 Oryza sat AF080120 Arabidops AL049876 Arabidops AL161531 Arabidops AL606653 Oryza sat AZ204840 Sequence AP004357 Oryza sat AK204819 Sequence AC012329 Arabidops AL032964 Arabidops AL032964 Arabidops	AY202084 Neurospor AY411016 Neurospor AC102931 Magnaport AC411017 Neurospor AF411018 Neurospor AF413073 Phomopsis AF468822 Diaporthe AF159143 Caenorhab	278419 Caenorhabdi 278419 Caenorhabdi 298533 S.pombe chr AJ011978 Triticum AF159144 Caenorhab 248334 Caenorhabdi AL132848 Caenorhabdi AV032878 Neurcospor AV049072 Diaporthe AJ314910 Dictyoste AF117611 Dictyoste AJ314909 Dictyoste AJ314909 Dictyoste AJ314909 Dictyoste AJ314909 Dictyoste AJ314909 Dictyoste AJ314909 Accorded AJ31490 Solanum tub AC099767 Caenorhab IG6494 Sequence 14 AC005169 Arabidops AJ133528 Neurcospor AX034425 Sequence	linear PAT 08-AUG-2001 nd Sanger, H.L. ides having the enzymatic se (RDRP)	
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Qy 961 GGT     Db 961 GGT	Qy 1021 TAG      Db 1021 TAG	Qy 1081 ATT       Db   1081 ATT	QY 1141 CTA      DD 1141 CTA			Qy 1321 TTC 	1381	1441	Qy 1501 AAT      Db 1501 AAT	QY 1561 AGT 	1621	1681	Oy 1741 GGT 		1861	OY 1921 AAA 	1981
1149 t	e 3731; DB 6; Length 3731; 1. No. 0; Smatches 0; Indels 0; Gaps 0;	TTGTGT 60	GTGATAATAAATTTGGTTGTGCTTCAGTTTCAGTCACTACTGCTGGGTAGTTTTAT 120 	18	GGTTTTCGGATTCCCTTATCTTCTCTGC 240	TACAGGATATGGAACTGTGTATGTGCATTGGA 300	ATTTGCCAAAGTTCAATTTGCCGACAACAT 360	TAACAGGCTGTATTTGGCTCTTATTT 420	4 4	ATCAGATGACAAGTTTGCAGTGTTGGGAAG 540		GGTTCAGCTGACTATAAACTTCAGCTTTCATATGAAAATATATGGCAGGTTGTGCTCCA 660	CCTCATACAGTTATTTGGTGCTCCTCGGAT 720		GTGAGGACAACAGATTTCCCTCCATCTTGGATAGGGCTATCTTCTAGCTTATGTTTGCA 840 	CGAGGAAAGITTTTTCCACTATGCAGAACG 900	CACCTITICGTCICTCAAAARCGGCTCT 960 
FEATURES Location/Qualifiers source 1.3731 /organism="unknown" BASE COUNT 1064 a 669 c 849 g	Query Match 100.0%; Score Best Local Similarity 100.0%; Pred. Matches 3731; Conservative 0; Mism	25 – 25	Qy 61 GTTGTGATAATAAATTTGGTTGTGCTTCAGT 	QY 121 TITGCATAACTICAGGGGTATICCAGTIGGTGTTAGCATITGAAAGICGAACTGCACTIT	QY 181 GGAATTIGGCTACAIGGGAAAGACAATTCAGGITTTCGGATTCCCTTATCTTTCTCTCTGC	QY 241 GGAAGTGGTTAAGTCATTCTTAGAAARATACAGGATATGGAACTGTATGGCATTGGA 	QY 301 GGTTAAACAGTCCAAAGGAGGATCTAGAGCATTTGCCAAAGGTCCAATTTGCCGACAACAT	QY 361 AAGTGCTGACAAAATCATCACTTTGGCTAATAACAGGCTGTATTTTGGCTCTTATTT 	Qy 421 GAAGGCTTGGGAAATGAAAACTGATATTGTCCAACTGGGGGCATATGTGGATCAGATGGA 	QY 481 TGGCATAACTTTGAATTTCGGATGTCAGATATCAGATGACAAGTTTGCAGTGTTGGGAAG	QY 541 TACAGAAGTITCAAFICAAFITGGCATIGGATIGAAAATITTTTTTTTTTTTTTTTTTTT	OY 601 TGGTTCAGCTGACTATAAACTTCAGCTTTCA 	QY 661 TCGICCATAIGGTCAAAATGCTCAGTITCTCCTCATACAGTTATTIGGTGCTCCTCGGAT	Qy 721 CTATAAGAGACTTGAAAACTCCTGTTATAGCTTCTTTAAGGAAACTCCTGATGATCAGTG	OY 781 GGTGAGGACAACAGATTCCCTCCATCTTGG 	OY 841 GITCCGIAGGGGTGTTCGTCTTCCAAATTTCGAGGAAAGTTTTTCCACTATGCAGAACG 1111111111111111111111111111111	OY 901 TGAAAACAATAITACTITACAGACIGGTTTCACCTTTTTCGTCICTCAAAAATGGGCTCT

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PLN 18-DEC-1998
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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1 (bases 1 to 3731)
Schiebel,W., Pelissler,T., Riedel,L., Thalmeir,S., Schiebel,R., Kempe,D., Lottspeich,F., Sanger, H.L. and Wassenegger,M.
Isolation of an RNA-directed RNA polymerase-specific cDNA clone
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3541 TICCAGICGAGCGITAAGCIGAIAIAIAIAIAAGGIAAAAGGIGIGAICAIAAGAAAAC 3600
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Wassenegger, M.
Direct Submission
Submitted (08-JAN-1997) M. Wassenegger, Max-Planck-inst. fuer
Blochemie, Viroidforschung, Am Klopferspitz 18a,
Planegg-Martinsried, 82152, FRG
Location/Qualifiers
1. .3731
                                                   TGTTATGCATTGTTGACTACCTTTTGTCTTTAAAACTGCATGAAGCTGCAACATATATGC
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Pred. No. 0;
); Mismatches
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194. .3538
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Best Local Similarity 100.0%;
Matches 3730; Conservative 0;
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194. .3538
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                             TGAAAACAATATTACTTTACAGACTGGTTTCACCTTTTTCGTCTCTCAAAAATCGGCTCT
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TGATTTTCGCAGATCAAGAATGTCGCAAAATATGCTGCCAGACTTGGT 	1 TGGTGGATATAAAGGTGTTGTGGGTGTTGATCGGATTCATCAATGAGTTGTCTTTGAG	1 AGATGAAGTTCTCGAACAGAAAGGAAGCTGTAGATCAGCTTGATGCTATTTGCA	1 GTTGCAAACCTTCCGCGCATCCAAGTTGCTCGATTTGCGGACTACATCAAGAATATTAT    IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	TAATAACAGCAGATCCACCAACAATTTCATTCTGAAGGAATGTGGTTGTTGCAAA	ATGITCTGGGAGTGATTTGGATGGGGATATCTACTTTGTTTGCTGGGATCAAGACATGATGATGATCTAGTTGTTTGCTGGGATCAAGACATGATGATGATCTACTTGTTTGCTGGGATCAAGACATGATGATGATGATGTTGTTTGT
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FKAKARDBRANDRYGTEREDGLIPPRQVGSNATTTHTYNGLYNDETRENDERDENDAGGNATOLT
FKAKARDBRANDRYGTTTHTYNGLYNDETRENDENDAGGLIPPROCUPERTOLT
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                                                                                                                                                                                                                                           Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spernatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 3505)
Wassenegger, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 3505)
Schiebel, W., Pelissier, T., Riedel, L., Thalmeir, S., Schiebel, R.,
Kempe, D., Lottspeich, F., Saenger, H.L. and Wassenegger, M.
Isolation of an RNA-directed RNA polymerase-specific cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCACTTGGAATTTGGCTACATGGGAAAGACAATTCAGGTTTTCGGATTCCCTTATCTTCT 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (16-OCT-1998) Wassenegger M., Max-Planck-Institut
Biochemistry Viroidresearch, Am Klopferspitz 18A, 82152
Martinsried, FRG
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                                Nicotiana tabacum mRNA for RNA-directed RNA polymerase. AJ011576. GI:4138281
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/db_xref="taxon:4097"
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20. .3370
/gene="RdRP"
20. .3370
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89.0%; Pred. No. 0;
11ve 0; Mismatches
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                                                                                                                                                                                    dRP gene; RNA-directed
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Matches 3137; Conservative
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                                                                                                                  ACCESSION
VERSION
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AUTHORS
TITLE
JOURNAL
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RdRP gene; RNA-directed RNA polymerase.
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Petunia x hybrida
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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(Dases i to 4579)
Wassenegger, M.
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Schlebel, W., Pelissier, T., Riedel, L., Thalmeir, S., Schlebel, R.,
Kempe, D., Lottspeich, F., Saenger, H.L. and Wassenegger, M.
Isolation of an RNA-directed RNA polymerase specific cDNA clone
of
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/number=2
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Arabidopsis thaliana.

Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Wagnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 132699)

Chao, Shinn, P., Dunn, P., Buehler, E., Kahn, S., Kim, C., Walker, M., Williams, S., Altafi, H., Araujo, R., Conn, L., Conway, A.B., Gonzalez, A., Hansen, N.P., Hulzar, L., Kremenerskala, I., Lenz, C., Li, J., Liu, S., Luros, S., Rowley, D., Schwartz, J., Toriumi, M., Vysotskala, V., Yu, G., Davis, R.W., Federspiel, N.A., Theologis, A. and
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(bases 1 to 132699)

Ecker, J.R.

Direct Submission
Submitted (25-FEB-1999) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th Street and
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
3. (bases 1 to 132699)
Ecker, J.R.

Direct Submission
Submitted (07-MAY-1999) Arabidopsis thaliana Genome Center,
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                                                                                                                  TIGATGICTCCTGGAGAGACACTAATATTCTCAAGGCAATGCTAAAACTGTGGTTATAAG
                                                                                                                                                                                CCTGATGCTGAGCCCTTTCTTTCAATGATGTTGCAAACCTTCCGCGCATCCAAGTTGCTC
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POPERTREAT OF BLOOKY, University of pennsylvania 19104 5019, USA

Hamilton Walk Philadeaphia, Pennsylvania 19104 5019, USA

Cheuk, S. Shinn, P., Brooks S., Kun, C., Aleafi, B., B., B., C., Chin, C., C.,
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join(26661 .26948,27454 .27610,27713 .27814,27911 .28038,2842 .28407,28565 .28632,28747 .28969)
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AGRGGHVNLKHAERRAITVNKIPSWVDNLIKKILLWEDDTRKSFLYDGVRLUSUTLEDY
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                                                                                                                                                                                                                                                                                                                                                                     KLTTRKOGEEEKRYRDOKKMODLLIKRRESIYGSKPSPRRSNSVRKTNGYNGDASVPP
TPRRNSAGATNNDIMTTPRSYSSHRONGYFKEVRRLSTAPLNFVAIPKEDSVSTYTSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 TIGGAATTIGGCTACATGGGAAAGACAATTCAGGTTTTCGGATTCCCTTATCTTCTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65693 AAAGTTAGACAACCAAAGAAGGTGGTCCAAGAGGTCTATGCCATTGTTCAATTCACATCT
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MHPLPMSTKRRGARISGRKMSQGAFKKVLEKLASDGFNFGNPIDLKSHWARHGTNKFV
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EQSLIVFSEESSFDEMVNNMKSQSELCVILAKIFGSIAVAIAVVYGVDYARKVLLPFV
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18300, .18406,18547, .18611,18742, .18950))
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63839 GAGGCICTIGGTTTAATGGCTCCAGGGAAAACACAAATATTCTCAAGGCATTGATCTTG 63780 64079 GIGGCIGIIGAICCAAACICAICAAGAAACIGICIGAGGAAGAGIAIGAGCAAAIIC 64020 2119 2299 63600 63540 63300 63180 63060 2477 63120 GAATCAGACAACATAAAGTTAGATGTCCTTGGATGGAGCAAATATCAGCCTTGTTATCTT 1999 64019 GAATCGGAGAACACCAAGCTTGATGTTCTGGCGTGGAGCAAGTACCAACCTTGTTATATG 2060 AAGCAAAAGGAAGCTGTAGATCAGCTTGATGCTATCTTGCATGATTCTTTGAAGGCACAG 2120 GAGGCTTTGGAATTGATGTCTCCTGGAGAACACTAATATTCTCAAGGCAATGCTAAAC AATCGTCAACTGATTACGCTCTTGTCTACACTTGGAGTGAAGATGAAGTTCTCGAACAG 63599 GATCCCATGAGGCCGGGAAGGCGATTCATCATCACGGACCTGTTGTTGTTGCCAAAAAC 2418 CCAACAGTAATTTCATTCTGAAGGGAAATGTGGTTGTTGCAAAAAATCCATGCTTGCATC 63539 CCATGCCTGCATCCTGGTGACGTGCTGTTCTTCAAGCTGTCAATGTCCCAGCTTTAAAT 63419 TGATTCGTGTTTTTTTCGAGCTTTTATTGTTTTAAGTCTCGAACTTTTCATTGGAATCTT 63119 GGTTTCCAGGAAGTTGAAGAGTACTTTGCGAACTACATTGTGTGATAGTTTAGGGATC 2180 TGTGGTTATAAGCCTGATGCTGAGCCCTTTCTTTCAATGATGTTGCAAACCTTCCGCGCA 2300 AIGGGAIGITIGGAIGAAICCAGAACCIIGGAAIAIGGICAGGIGIIIGGICAGIIIACI 2360 GGTGC--TGGACATGGAGGTTTTCTGACGATTTACATCCATTTAATAACAGCAGATCCA 2478 CIGGIGATATICGIGITITAAAGGCIGIAAAAIGITCGAGCGCIGCACCACAIGGI----------GGAAAAAGACCTCATCCGAATGTTCTGGGAGTGATTTGGATGGGGA 63359 GIGITCITITGIGCATAGGCCACACCAAAIGAAIGITCIGGGAGIGAITIAGAIGGAGA 63179 ATTIGATCACTITGGITATATTITIGITTTTTGGCGTTAGGAGATTGATTGGCTACCTT ATAGCAAATGCCCATGTCGTATTTGCAGACAGAGAACCTGATATGGCCATGAGTGATCCA TATCTACTTTGTTTGCTGGGATCAAGACATGATCCCGCCAAGGCAAGTCCAGCCGATGGA -----AGGAAGTIGAAGAGTACTICACCAACTATATIGIGAATGACAGTITGGGAATC TGCAAAAAACTTGCTGAGCTCTTTTCAATTGCAGTGGACTTTCCAAAGACTGGTGTTCCC ATATCCTCCAGCACCCAGCATACAGTTGGACCATGATGTCACAATTG------------AGATIGIGITGIATICCCICAGAAA-1940 2000 2668 2533 2608 63299 2715 2715 2768 2828 2558 63029 ö CO οy g ŏ Db Qγ 임 δλ g δ g òγ q δý g  $\delta \Delta$ 셤 à ga g g ò g g g ò å ò à g ò ò g Qγ

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Schiebel W., Pelissier,T., Riedel,L., Thalmeir,S., Schiebel,R.,
Kempe,D., Lottspeich,F., Saenger,H.L. and Wassenegger,M.
Isolation of an RNA-directed RNA polymerase specific obNA clone
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Biochemistry Viroidresearch, Am Klopferspitz 18A, 82152
Martinsried, FRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITGGTCAATCTTTTGGTTCCTCCAGAGACTTTGAGTGTTCTTAGGCATGAGATTGAA
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                                                                                                                                                                                                                                                                                                                                                                   Length 1538;
                                                                                                                                                                                                                                                                                                                                                               20.5%; Score 765; DB 8; Length 15
llarity 69.7%; Pred. No. 5.2e-171;
Conservative 0; Mismatches 425; Indels
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BAC

à

chromosome

Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA,
Clone:Ox1699_D12
Published Only in Database (2001)
2 (bases 1 to 80554)

Sasaki,T., Matsumoto,T. and Yamamoto,K. Direct Submission

Poaceae;

Poales;

Liliopsida;

Magnoliophyta; Oryzeae; Oryza.

Spermatophyta; Ehrhartoideae;

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Light Submitted (05-SEP-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Takuba, Daraki 305-8602, Japan (E-mail: tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-299-38-7468)

Tel:81-298-38-7441, Fax:81-299-38-7468)

The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the places is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

* This sequence will be replaced

* This sequence will be replaced

* This sequence will be prepared

* This secuence will be replaced

* The accession number will be preserved.

Location/Qualifiers

Location/Qualifiers
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Best Local Similarity 60.1%;
Matches 1108; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
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AUTHORS
TITLE
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AUTHORS
TITLE
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                                                                                                                         2435 CIGAAGGGAAAIGIGGTIGIIGCAAAAAICCAIGCIIGCAICCIGGIGAIAIICGIGII
                                                                                                                                              2495 TTAAAGGCTGTAAATGTTCGAGCGCTGCACCACATGGTAGATTGTGTTGTATTCCCTCAG
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                    TITGIAIGIAGCAICAAGAAIIGGIICCGCCAAGAACGICIGAACCAAIGGACIACACI
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/organism="Oryza sativa (japonica cultivar-group)"

/cultivar-"Nipponbare" /db_xref="taxon:39947"

/chromosome="2

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Length 80554;

Score 551.4; DB 2; Pred. No. 2e-120; 0; Mismatches 646;

/clone="OJ1699_D12" 16948 c 17802 g 22769

ď 23035 Indels

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734 GAAAACTCCTGTTATAGCTTCTTTAAGGAAACTCCTGATGATCAGTGGGGTGAGGACAACA 793
                                                GATTITACTICATCTICTAGCATTGGGCAATCATATATTTTATGTCTTGAGGTACCACGT
                                                                                                                                                                                                                                                          GGTGTTCGTCTTCCAAATTTCGAGGAAAGTTTTTCCACTATGCAGAACGTGAAAACAAT
                                                                                                                                                                                                                                                                                                                        8479 CGATGTGATCTCCCAAACATTCGTGACTACTTTTTTACTATCATGAGTACAATCATGAC
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                                                                                                                               GATITICCCTCCATCTT---GGATAGGGCTATCTTCTAGCTTATGTTTGCAGTTCCGTAGG
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta, Embryophyta; Tracheophyta;
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AP004143
Oryza sativa (japonica cultivar-group) chromosome 2 clone
Olis99_Dl2, *** SEQUENCING IN PROGRESS ***, in ordered pieces.

AP004143 AP004143.1 GI:15451464 HTG; HTGS_PHASE2.

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

ò	1211		
셤	œ	ACGICCAACCAICACCIAACAIAICITITITITAIG 888	
QY	1271	GTCCTAGTAACACCATGCAAAGTTTATTTTTGTGGTCCAGAGGTTAATGTTTCCAATCGG 1330	
à à	33.	TEAAGACATAAGATAACTTTCTTCGTGTTTTTTTTTTTTT	
γŏ	0.00	144	
QQ	8987	04	
Qy Dp	1449	-TCAGGACAAACATCTATGAGGATCTTATCAACTGGGGAAAGGCTTTGTAATTGGT 1507 	
Qy Db	1508	GATAAAAATTTGAATTTCTTGCATTTTCATCGAGCCAGTTGCGGGATAATTCAGTGTG 1567 	
Qy Dp	1568 9167	ATGITIGCATCAAGACCIGGCCTIACIGCAAAIGATAAAGAGCIIGGAIGGGIGAIITI 1627 	
Qy	1628	TCGCAGATCAAGAATGTCGCAAAATATGCTGCCAGACTTGGTCAATCTTTGGTTCCTCC 1687 	
Qy Db	1688	agagagactitgagigticttaggcatgagatigaagtiattcccgatgtaaggticat 1747 	
Oy Dp	1748 9344	GGAACCAGCTATGTTTTTCTGATGGAATTGGTAAAATATCTGGTGACTTTGCTCATAGA 1807 	
Oy Db	1808	GTTGCCTCAAAATGTGGCCTTCAATATACCCCATCTGCTTTCCAGATTCGTTATGGT 1864 	
Qy Db	1865 9464	GGATATAAAGGIGTTGIGGGIGTTGAICCGGATTCAICAATGAAGTIGTCTTIGAGAAAG 1924 	
Oy Op	1925 9524	agcatgtcgaaratatgaatcagacaacataaagttagatgtccttggatgga	
Oy Dp	1985 9584	CAGCCTTGTPATCCTAATCGTCAACTGATTACGCTCTTGTCTACACTTGGAGTGAAAGAT 2044 	
Qy Dp	2045	GAAGTICTCGAACAAAGGAAAGGAAGCIGIAGAICAGCIIGAIGCIAICTIGCAIGAI 2104 	
Oy Ob	2105	TCTTIGAAGGCACAGGAGCTTIGGAATIGATGICICCTGGAGAGAACACIAATATICIC 2164 	
Qy Db	2165 9764	AAGGCAATGCTAAACTGTGGTTATAAGCCTGATGCTGAGCCCTTTCTTT	
QY	2225	CAAACCTTCCGCGCATCCAAGTTGCTCGATTTGCGGACTAGATCAAGAATATTTATT	
γα	2285	atccagaaccttggaatatggtcaggtg 234	

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Sasaki,T., Matsumoto,T. and Yamamoto,K.

Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, PAC
clone:19048709

L Published Only in Database (2002)

CE 2 (bases 1 to 162558)

RS Sasaki,T., Matsumoto,T. and Yamamoto,K.

Direct Submission

AL Submitted (20-MAR-2002) Takuji Sasaki, National Institute of
Submitted (20-MAR-2002) Takuji Sasaki, National Institute of
Submitted (20-MAR-2002) Takuji Sasaki, National Institute of
Submitted (20-MAR-2002) Takuji Sasaki, National Institute of
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Submitted (20-MAR-2002) Takuji Sasaki, National Institute of
Submitted (20-MAR-2002) Takuji Sasaki, National Institute of
Submitted (20-MAR-2002) Takuji Sasaki, National Institute of
Tel:81-298-387-444, Fax:81-298-387-469

NOTE: It currently consists of 1 contids. Gaps between them
are based on estimates that have provided by the gaps between them
are based on estimates that have provided by the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
* NOTE: This is a "working draft, sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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HTG: HTGS_PHASE2.
Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
clone:P0487D09
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                               2345 TITGTICAGITIACIGGIGCIGGACAIGGAGAGITITCIGACGAITIACAICCAITIAAI 2404
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/organism="Oryza.sativa (japonica cultivar-group)"
                                                                                                                                                                                2405 AACAGCAGATCCACCAACAGTAATTTCATTCTGAAGGGAAATGTGGTTGTTGCAAAAAT
                                                                                                                                                                                                                                                                                    2465 CCATGCTTGCATCCTGGTGATATTCGTGTTTTAAAGGCTGTAAATGTTCGAGCGCTGCAC
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match 14.8%; Score 551.4; DB 2; Best Local Similarity 60.1%; Pred. No. 1.8e-120; Matches 1108; Conservative 0; Mismatches 646;
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a 36152 c 36022 g 45360 t
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/db_xref="taxon:39947"
                                                                                                                            9944 TTCATTCGAGCTACTTCGGGTGTAAATG-
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SOURCE
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AUTHORS
TITLE
JOURNAL
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TITLE
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92176	850 92236	910	n .	92353	2 2	1090	1150 92527	1210 92587	1270 92639	1330	1390	1448 92804	1507 92864	1567 92924	1627 92984	1687 93044	1747 93101	1807 93161	1864 93221
7 GAAGATCCATTATTCAACTATTTTAGGGATCATACAGATGATCAATGGACCAGGACAACG	4 GATTICCCTCCAICTTGGAIAGGGCTATCTICTAGCTTATGTTTGCAGTTCCGTAGG	1 GGTGTTGGTCTTCCAAATTTCGAGAAAGTTTTTTCCACTATGCAGAACGAAGAATATCGAGAACAATTTTTTTT				1 GTACACCATGGATACCTGGGCCAGCATTAAATGTCTACTTTTTCCGATTAGTTGAT	1 CCTCGAAGGAGAAATGTGGCATGCATTGAGCATGCCTTAGAGAACTGTACTATATAAG	1 GAGTGCTGTTATGATCCCGTGAGGTGGCTCACTGAGCAGTATGATGATGGTATCTCAAGGGT	AGACAACCTCCAAAATCTCCGTCCATCACTTTAGATGATGGGTTGGTGTATGTA	GTCCTAGTAACACCATGCAAAGTTTATTTTGTGGTCCAGAGGTTAATGTTTCCAATCGG	1 GITCICCGCAAITATICIGAAGACATAGATAACTITCITCGGGTTTCTTTGTTGATGAG	1 GAGTGGGAGAACTGTATTCTACAGACTTATTACCAAAGGAAGTGGGAAGTGGG	- TCAGGACAAACATCTATGAGAGGATCTTATCAACTCTGCGGAAAGGCTTTGTAATTGGT	GGTAAAAAATTIGAATITCTIGCATTITCATCGAGCCAGTIGCGGGATAATTCAGTGTGG	ATGITTGCATCAAGACCTGCCTTACTGCAAATGATATAAGAGCTTGGATGGGTGATTTT	TCGCAGATCAAGAATGTCGCAAAATATGCTGCCAGACTTGGTCAATCTTTTGGTTCCTCCCC	AGAGAGACITIGAGIGITCTIAGGCAIGAGAITGAAGTIAITCCCGAIGIAAAGGITCAI 	GGAACCAGCTATGTTTTCTGATGGAATTGGTAAATATCTGGTGACTTTGCTCATAGA 	GTTGCCTCAAAATGTGGCCTTCAATATACCCCATCTGCTTTCCAGATTCGTTATGGT 
9211.	794 92177	851	6 6	ν r-	92354	1031	1091 92468	1151 92528	1211 92588	1271 92640	1331 92685	1391	1449	1508 92865	1568 92925	1628 92985	1688 93045	1748 93102	1808
QQ	oy Db	oy da	δ ₀ 7	3 8	셤	OY DP	QY Dp	QY	QY Db	QY	QY DP	Qy Db	QY Dp	QY Db	QY	QY Db	QY Db	Oy Dp	Qy Dp

Arabidopsis thaliana.

Arabidopsis thaliana.

Arabidopsis thaliana.

Arabidopsis thaliana

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;

Sosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases I to 74406)

I (pases I to 74406)

S strong, C., Graves, T. and Duckels, G.

The sequence of A. thaliana F2P3

Unpublished (1998)

I Unpublished (1998)

I Unpublished (1998)

S strong, C., Graves, T. and Duckels, G.

The sequence of A. thaliana F2P3

Unpublished (1998)

I Oppublished (1998) PLN 15-SEP-1998 93777 CCITGCCTCCACCCAGGIGATATACGGATICTCCATGCIGTIGATGTTCCTGTTTTGCAC 93836 2104 2164 1865 GGATATAAAGGTGTTGTGGGTGTTGATCCGGATTCATCAATGAAGTTGTCTTTGAGAAAG 1924 2345 ITIGITCAGITIACIGGIGCIGGACAIGGAGAGITITICIGACGAITIACAICCAITIAAI 2404 2465 CCATGCTTGCATCCTGGTGATATTCGTGTTTTAAAGGCTGTAAATGTTCGAGCGCTGCAC 2524 2105 ICTITGAAGGCACAGGAGGCIIGGAAATIGAIGCICCIGGAGAGAACACIAATAIICIC 2045 GAAGTTCTCGAACAGAAGCAAAGGAAGCTGTAGATCAGCTTGATGCTATCTTGCATGAT CAGCCTTGTTATCTTAATCGTCAACTGATTACGCTCTTGTCTACACTTGGAGTGAAAGAT 93462 CCTCAAGCTGCTATCGAAGCAATTGAACTTATGCCCCATGGGAGAATAACAAATGCAGTT 2285 AATGGAAGAACAATGGTTGGGTTTTGGATGAATCCAGAACCTTGGAATATGGTCAGGTG 2405 AACAGCAGATCCACCAACAGTAATTTCATTCTGAAGGGAAATGTGGTTGTTGCAAAAAT linear 93837 CACATGTTTAACTGTGTCGTCTTTCCACAGGAACCAAGGC 93879 2525 CACATGGTAGATTGTGTTTTCCCTCAGAAAGGAAAAGAC 2567 DNA 93702 TICATICGAGCIACTICGGGIGTAAATG-----ďq 74406 b Arabidopsis thaliana BAC F2P3. AF080120 AF080120.1 GI:3600045 ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 9 F2P3/c LOCUS DEFINITION 1925 1985 2165 REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE AUTHORS g g ά q g g q g g g g 셤 ò δ Ωý δŽ δy ŏ ò ò ö a à

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// Abc.state="Grade-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-state-sta
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DHIRREHTLEHELKEREDGLYKWBYD
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FYKVDPSDIRGHEKEMSFLETCGKTEERCHWWRRALTDAANILGDHPQNWDNEAY
KITTISKDVLEKLNATPSRDFNDLVGMBAHIAKMESLLCLESGGVRIVGINGPAGVGK
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LEVSFESRGGLYKCEVKECGLQFLEPHETSEFRYLSPHLYLGGSWIGNSSSIEEIIH
VDQEESSDSEEIIYADQEESSGIEEIIHAEREGTNRRKSVMRWIKVGARKMGLSLE
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/gene="F2P3.9"
/note="similar to initiation factor IF2-beta (Pfam: GTP_EFTU.hum, score: 226.67)"
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/db_xref="G1:3600058"
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APEVAVDTKIFLPPPPRSNDPHGLHCSGGVVLASRDGKIVCENTLDARLDVAFRMKLP
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20653. .20791,21177. .21277,21393. .21494))
/gene="F2P3.10"
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/gene="F2P3.8"
/note="similar to several Arabidopsis thaliana disease resistance proteins"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
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/gene="F2P3.9"
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25791. .26654
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Submitted (24-JUL-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation-"MINOIYKQVFSFFLSVLLLQSSTVSYVPKSFDLKKPCKHFVLYL
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YNMKTNYNAWVAWTLVFNSTKHKGTFTIMDANPFGLQPARDLSIVGGTGDFLMTRGIA
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MFRVDLENGDNILGYICGKIRKNFIRILPGDKVKVEMSVYDSTKGRIIFRMSSRD"
complement(4455. .10458)
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1. .74406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The 3' clone is F8M12, 200 bp overlap. Actual start of this clone is at base position 1 of F2P3; actual end is at 23552 of F8M12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAPPING: Clones were assigned to the YAC map by hybridization by M. Lodhi, Cold Spring Harbor Laboratories, and fingerprinted by M. Marra, WashU, to pick the best candidates for sequencing.
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/codon_start=1
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/note="contains similarity to Pisum sativum disease
resistance response protein 206-d (GB:U11716)"
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                                                                                                                                                                                                                                                          Washington University
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                                                                                                                                                                                             Genome Sequencing Center
Department of Genetics, Washingto
St. Louis, Mo 63108, USA
e-mail: rwilson@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
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/product="tRNA-Tyr"
/note="codon recognized: UAC"
complement(2779. .3078)
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/protein_id="AAC35542.1"
/db_xref="G1:3600055"
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/protein_id="AAC35543.1"
/db_xref="G1:3600056"
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complement(2779. .3078)
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/clone="F2P3"
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3 (bases 1 to 108598)
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LFSDDDVFGFSTSMSESFGGDLFGDNLFADMSFGSGFGSGGGFSSWHVEDHFQDIG
                                                                                                                      /translation="METEKKVSLPRILRISVTDPYATDSSSDEEEEVDFDALSTKRRR
VKKYVKEVVLDSVVSDKEKPMKKRRKRVVTVPVVVTTATRKFRGVRQRPWGKWAAEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                      C. elegans
                                         domain containing
                                                                                                                                                                                                                              complement(join(37194. .37985,38074. .38224,38340. 40511. .41062))
/gene="F2P3.11"
/note="similar to hypothetical proteins in Schizosaccharomyces pombe (GB:298533) and C. elegan (GB:Z48334 and Z78419)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39583 AAGAACTTTGCAGAGCATGTCTCGGATTTCATGAGAGTTACTTTTGTGGAAGAAGATTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 314.6; DB 8;
Pred. No. 4e-64;
0; Mismatches 539;
                                         to AP2
/gene="F2P3.5"
25791. .26654
/gene="F2P3.5"
/note="contains similarity
                                                                               /evidence=not_experimental
/protein_id="AAC35537.1"
/db_xref="G1:3600050"
                                                                                                                                                                                       DLFGSDPVLTV"
complement(37194. .41062)
/gene="F2P3.11"
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                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 8.4%;
Best Local Similarity 55.2%;
Matches 689; Conservative
                                                        proteins
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Arabidopsis thaliana DNA chromosome 4, BAC clone T22B4 (ESSA
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Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 108598)
Bevan,M., Pohl,T., Weizenegger,T., Bancroft,I., Mewes,H.W.,
Lemcke,K. and Mayer,K.F.X.
                                                                                                                                                                                                                                                                                                                                                                                                                         -----CGCAAGATTGATGAGGAAACATCTGTGGTTATTGGGAAAGTGGTCGTGAAA 38450
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CATAGAGTTGCCTCAAAATGTGGCCCTTCAATATACCCCCATCTGCTTTCCAGATTCGTTAT 1861
                                     39103 AAGCAAGTTGCACAGAAGTGTGGATTGAGTCATGTCCCTTCTGCCTTTCAAATTGGATAC
                                                                                                                                                                     GGTGGCTACAAAGGTGTGTGTTGACCGCAGTTCCTTCCGAAAGTTGTTGCGT
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Bancroft,I., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.
Unpublished
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JUTILE Direct Submission  JUGNNAL Submitted (09-MAR-2000) MIPS, at the Max-Planck-Institut fuer Blochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: Blochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: Lemcke@mips.blochem.mpg.de,mayer@mips.blochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 70J Norwich, UK, E-mail: michael.bevan@bbsrc:ac.uk COMMENT Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosones 3, 4 and 5 can be viewed at: http://www.mips.blochem.mpg.de/proj/thal/.	rce 1108598 // Arabidopsis thaliana" // Variety="Columbia" // Varief="taxon:3702" // Chromosome="4" - 11121 // Chromosome="4" // Varief="taxon:3702" // Chromosome="4" // Varief="taxon:3702" // Varief="t	/note="Overlap to BAC F25124; please refer to this entry for analysis and annotation" gene 9990. 13999 /gene="AT4911030" join(9890. 10044,10569. 10632,10733. 10822,10923. 10979, 11065. 11113,11202. 11278,11375. 11414,11300. 11594, 11679. 11846,11933. 12043,12130. 12217,12335. 12401, 12475. 112550,12625. 12742,12815. 13060,13167. 13306,	13487. 13665,1342. 13861,13943. 13399) /gene="Ar4gil030" /note="Ar4gil030" /note="strong similarity to acyl-CoA synthetase - Brassica napus (rape), PID:e217854 Contains Putative AMP-binding domain signature AA228-239 contains EST gb.AI992650.1, N65639, T20845, T43231, N88362, H77281, H76835, A1999263.1, T45466, AA395246"	/product="putative acyl-CoA synthetase" /protein_id="CAB43038.1" /db_xref="G1.4850282" /translation="WTSQKRFIFEVEAAKEATDGNPSVGPVYRSTFAQNGFPNPIDG1 OSCWDIPFPAVERYPNNRAHGRREISNGKAKYWKTYKEVYDIVIKLGNSLRSCGIK GSCKOTISPRAVERYPNNRAHGRREISNGKYPLYDTLGAGAVEFIISHARSCGIK EGEKCGIYGINCCEWIISMEACNAHGIXCVPLYDTLGAGAVEFIISHARSCGIK EGEKCGIYGINCCEWIISMEACNAHGIXCVPLYDTLGAGAVEFIISHARSSIGENC KIPELFKTCPNSTKYRKTVVSFGGVKPEQKEAEKLGLVIHSWDEFLKLGEGKQYELP IKKRSDICTINTNSGTTGORFGVKILIEDIGELKPSIFCANPRYLDRVYTGLQ QKLSGGGFFKKKYPDVARSYKFGNMKKGGSHVAASPFCDKLYFNKYVRGGGGGGNVRIIL SGAAPLASHIESFLRYVACCVTLGGYGLTESCAGTFATFDELDMLGTVVRUNDI RLESPERVYDDISTNYNYGORGITESCAGTFATFDELDMLGTVVGGENVPINDI RLESPERVYDDISTNYNSOVEUTESTUNYGNSFESFLVAINAPA NGSMKIIDRKKNIFKLAGGEYVAVENVENVESTWYVGNSFESFLVAINAPA	QQTLERWAVENGVNGDFNSICQNAKAKAFILGELVKTAKENKLKGFEIIKDVHLEPVA FDMERDLLTPTYKKKRPQLLKYYQNVIHEMYKTTKESLASGQ" 988010044 /gene="AT4911030"	intron 1004510568 /gene="AT4911030" /number=1 exon 1056910632 /gene="AT4911030"	intron 10633. 10732 /gene="AT4911030" /number=2 exon 10733. 10822 /gene="AT4911030"	intron 10823 .10922 /gene="Ar4g11030" /number=3 exon 10923 .10979 /gene="Ar4g11030"	intron /number-4 /number-4 /gene="AT4g11030" /number-4 exon 11065 11113

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ATCHRIV31 198301 bp DNA linear PLN 16-MAR-2000
Arabidopsis thaliana DNA chromosome 4, contig fragment No. 31.
ALI61531
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Arabidopsis thaliana
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brasslcaceae; Arabidopsis.
Poblic: (Passa 1 to 81065)
Poblic: Weizenegger.T.; Mewes, H.W., Lemcke, K. and Mayer, K.F.X.
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Volckaert, G., Grymonprez, B., Voet, M., Robben, J., Mewes, H.W.
Lemcke, K. and Mayer, K.F.X.
Unpublished
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                                          54371 GATAGTATGCTTAAATTTGACTCGAACAACAGGATGCTGAACGTTACCAGGTGGACGAG
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Lemcke, K. and Mayer, K.F.X.
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16931...18437

190in(16931...17069,17349...17821,17991...18142,18314...

190in(16931...2000)

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ilarity 55.2%; Pred. No. 3.8e-64;
Conservative 0; Mismatches 539;
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13862. .13
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A (bases 152454 to 156565; 171236 to 172629) Robben,J., Grymonprez,B., Volckaert,G., Mewes,H.W., Lemcke,K. and Mayer,K.F.X. Onpublished 5 (bases 1 to 198301) EU Arabidopsis sequencing,project. Direct. Submission Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemckefnips, blochem.mpg'de, mayer@mips.blochem.mpg'de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 70J Norwich, UK,	E-mail: michael.Devanebbsrc.ac.uk Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/ this fragment has an overlap with ATCHRIV30 at the 5' end and an overlap with ATCHRIV32 at the 3' end. Location/Qualifiers	/organism="Arabidopsis thallana" /organism="Arabidopsis thallana" /variety="Columbia" /db_xref="taxon:3702" /chromosome="4" 5133. 7500"	/gene="Aragilo80" (51355242,53385422,54995590, complement(join(51355242,53385422,54995590, 56755845,59356000,60906195,62846690,72047509)) /gene="Aragilo80" complement(join(51355242,53385422,54995590, 56755845,59356000,60906195,62846690,72047509)) /gene="Aragilo80" /gene="Aragilo	/product="98b" like protein" /product="98b" like protein" /protein_id="CAB812109.1" /db_xref="G17267807" /db_xref=	EHECTINGSTYTHISEKWHEIGEEEKGVYNSKAAELMEAYKEVEE COMPLEMENT(51355242) /gene="AT4g11080" /number=1 complement(52435337)				complement(59556000) /gene="AT4g11080" /number=5
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BOSNMNKETLSQLENPLVRRLGDTSSLSIPAKKQKSSGPSSFRQWPMFQRAGGVNIQTE
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                                                                                                                                                                                                                                                                                                                                           Arabidopsis thallana, PIR2:T01112
Contains Prokaryotic membrane lipoprotein lipid attaci
site AA405-415; Trp-Asp (WD-40) repeats signature
AA799-813; Trp-Asp (WD-40) repeats signature
contains EST gb.A199586.1, T46420, AA404849"
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ilarity 55.2%; Pred. No. 3.6e-64;
Conservative 0; Mismatches 539; Indels 21; Gaps
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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1802 CATAGAGTIGCCTCAAAAIGIGGCCTICAAIATACCCCATCTGCTTICCAGATICGTTAI 1861
                                                                                                                                                                 TCGATGCCTTGCTTAAACCGGGAGATCATTTGCCTTTTGTCGACCCTTGGAATAGAA
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Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (http://www.softberry.com/), genescan (http://ccR-081.mit.edu/GENSCAN.html), Genemark.htmlogy.gatech.edu/GeneMark/), tRNAscan-SE (Sean (http://genemark.biology.gatech.edu/GeneMark/), tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/), searches of the complete sequence against NCBI none redundant protein database (nr) (ftp://ncbi.nlm.uh.gov/blast/db) and the EST database at NCGR.

Location/Qualifiers

1. 12149
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Hong,G.F.

Direct Submission
Submitted (27-JUN-2002) Han Bin, National Center for Gene Research,
Chinese Academy of sciences, 500# Cao Bao Road, Shanghai 200233,
CHINA. E-mail enquiries: bhan@ncgr.ac.cn. Clone requests:
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                                                                          Dhanemogr.ac.cn
Oryza sativa japonica (nipponbare) genomic DNA, chromosome
clone: OSJNBD0048E02.
On Jul 12, 2002 this sequence version replaced gi:15594110.
Web site: http://www.ncgr.ac.cn
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Best Local Similarity 52.8%; Pred. No. 4.7e-64;
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SSVRIAQLWGLREKSRIFVTSGRWLMGCLDBAGILEHGQCFIQVSKPSIENCFSKHGS
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LANEQLGTICNAHYVHADRSEYGAMDEBCLLLAELAATAVDFPKTGKIVSMPFHLKPK
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FEYLIPEANGHKCLYDGTLGLLGYRKYGKEBEIPTGHIWSMPYTSKRQGELKERLK
HSYNGLKKBFRKYFBETIPPHENLSFEEKNILTYEKRASMYHYTYHPBWYKKSLELQD
PDESSHAAMLSFAWIAADYLARIKIRSREMGSIDSAKPVDSLAKFLAQRL"
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/db_xref="GI:15394185"
/translation="MGSEGNMKKSVVTQVSIGGFGESTTAKQLTDYLEDEVGIVWRCR
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ta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                   CCAATCAACTGAGAGACCGCTCTGCATGGTTCTTTGCTGAAGACGGGAAAACACGTGTGT
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Orysas sativa (japonica cultivar-group) genomic DNA, chromosome 1, APO04357
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1, Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
clone:B1074C08.
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2 (bases 1 to 165701)
Sasaki,T., Mateumoto,T. and Yamamoto,K.
Direct Submission
Submitted (19 NOV-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai
                                         2599
                                                                              2660
                                                                                                   CGATGGAATATCCTCCAGCACCCAGCATACAGTTGGACCATGATGTCACAATTGAGGAAG 2720
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                                                                                                                                                                                                                                                                     2720 TAATCGATTTCTTTGCAAGAACTTGGCGAATGAGCAGTTGGGCACAATTTGCAATGCAC 2779
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
clone:B1074C08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2961 TCTCAGAAAGAGTTATTGGAAAGCTTTTCAGGAAAGTGA---AGGACAAAGCACCTCAGG
                                                                                                                                                                                            2660 CCATGCATTATGATGCAGCTGAAGAGAGAGTTTAGGCCGTGCTGTCAACCACCAGGACA
TCCCTCAGAAAGGAAAAGACCTCATCCGAATGAATGTTCTGGGAGTGATTTGGATGGGG
                                     2540 TCCTCAGAAAGGTGATAGGCCGCATACAAACGAAGCTTCTGGCAGTGACCTTGACGGGG
                                                                                                                                                                                                                                                                                                                                                                                           2841 CTGAGCTCTTTTCAATTGCAGTGGACTTTCCAAAGACTGGTGTTCCCGGTGAAATACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                3018 CTAGCTCTATCGCGACCTTCACAAGAGATGTTGCAAGGAGATCATATGATGCTGATATGG
                                                                            ATATCTACTTTGTTTGCTGGGATCAAGACATGATCCCGCC-----AAGGCAAGTCCAGC
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Eukaryota: Viridiplantae: Streptophyta; Em
Spermatophyta; Magnoliophyta; Lillopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ehrhartoideae; Oryzeae; Oryza.
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12-1-7: TRANSALIANDA IDEACH, 1967-660. PUTCHALD: //rgp.dna.affrc.go.jp/, rel. 181-289-1974. Parabalians as affec go, py UTCHALD: //rgp.dna.affrc.go.jp/, rel. 181-289-1974. Parabalians as for comparable and rel. 2003 This sequence wersion replaced quiltologic of Lasarxi. O. slashing and the comparable of the following: COCCODET 1999 version). The genomic sequence was searched against (COCCODET 1999 version). The genomic sequence was searched against (COCCODET 1999 version). The genomic sequence was searched against (COCCODET 1999 version). The genomic sequence was searched against (COCCODET 1999 version). The genomic sequence was searched against the landing the protein name to indicate the homology local parabase in a corresponding DDBJ accession no. and RGP clone ID.

A gene with indirative or significant homology to a protein the protein name to indicate the homology local significant homology to any protein but with EST homology (COCCODET 1999 vor any protein but with EST homology (COCCODET 1999 vor any protein but with EST homology (COCCODET 1999 vor any protein but with EST homology (COCCODET 1999 vor any protein but with EST homology (COCCODET 1999 vor any protein but with EST homology (COCCODET 1990 vor any with a gene predicted with a gene predicte
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              LLGGCWPRSDEVFKATRPCHHEWFSLYRNVEQEEIPVHDIGNVMVVQSRDSCTRTYMI
PASRDFAALGSRNAFYYLWKQFDAGGSYNALFKKCLASEVLTFVKRLPEDWKLSDEWF
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region(s) in CDS
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/note="hypothetical protein"
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Pred. No. 1.8e-46;
0; Mismatches 658;
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/note="5' LTR
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Best Local Similarity 51.9%;
Matches 760; Conservative
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KQEQITAPLVAKKUDRRGGYIVDENSSKOEKKPKSYNFDGFPTRVLLIRNWYGPGEV
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 4013)
Wourrain,P., Beclin,C., Elmayan,I., Feuerbach,F., Godon,C.,
Worrain,B., Jouette,D., Lacombe,A.W., Nikic,S., Picault,N.,
Remoue,K., Sanial,M., Vo,T.A. and Vaucheret,H.
Arabidopsis SGS2 and SGS3 genes are required for
posttranscriptional gene silencing and natural virus resistance
Cell 101 (5), 533-542 (2000)

2 (Dasses 1 to 4013)
Beclin,C., Mourrain,P., Vaucheret,H. and Elmayan,T.
Direct Submission
Submitted (28-FEB-2000) Biologie Cellulaire, INRA, Route Saint-Cyr, Versailles 78026, France
Location/Qualifiers

0850495

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REFERENCE
AUTHORS
TITLE
JOURNAL
ORGANISM
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MEDLINE
PUBMED
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AUTHORS
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                                                              112114 ATCAGETTTGCTGGCTTCAAGGGTGTCATAGCTGTCTGGCAAGGACATGGTGATGGGACA 112055
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 1736 GTAAAGGTTCATGGAACCAGCTATGTCTTTTCTGATGGAATTGGTAAAATATCTGGTGAC 1795
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                                                                                                                                                          1853 AITCGITAIGGIGGATAIAAAGGIGTIGIGGGIGI-----IGAICCGGAITCAIGG
                                                                                                                                            AAGTTGTCTTTGAGAAAGAGCATGTCGAAATATGAATGAGCAACATAAAGTTAGATGTC
                                                                                                                                                                                                                                       2027 ACACTTGGAGTGAAAGATGAAGTTCTCGAACAGAAGCAAAAGGAAGCTGTAGATCAGCTT
                                                                                                                                                                                                                                                                                                                                   2147 GAGAACACTAATATTCTCAAGGCAATGCTAAACTGTGGTTATAAGCCTGATGCTGAGCCC
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                                                TITGCTCATAGAGTTGCCTCAAAATGTGGCCTTCAATATACC---CCATCTGCTTTCCAG
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/ / COGOLI-STAITE.
/ COCOLIS-STAITE.
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/ PECCHIOLS-STAITE.
/ CLASS TAIL TOI.-**MCSEGNAKKS VYTQVS IGGEGES TTAKOLIDYLEDEVGIVWRCR
/ LEAST ALD TENTENDEN PRINED TENTENT PRANED STAFANDER STARABADAGONLIL
LDGGOPHYCKFCFRKSTAFSFKDANMAN VINOPYKLELLVRDICTVROYKTLHGFVLIL
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/ MDESMOTINSAMFFARDGRTRVSDIKTWAGFKRONVAKCAARMGLCFSSTATVDVM
/ PHARUTSPYDIER RRYNTRYSDIKTWAGFKRONVAKCAARMGLCFSSTATATVDVM
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11 Similarity 51.5%; Pred. No. 1.4e-41;
733; Conservative 0; Mismatches 641;
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AF239718 4013 bp DNA lir Arabidopsis thaliana SGS2 gene, complete cds. AF239718 AF239718.1 GI:8164027

Arabidopsis thaliana

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                                                                                       1539 CGAGCCAGTTGCGGGATAATTCAGTGTGGGATGTTTGCATCAAGACCTGGCCTTACTGCAA 1598
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Search completed: November 5, 2002, 22:34:30 Job time : 11044 secs

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Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

November 5, 2002, 19:16:42; Search time 142 Seconds

(without alignments)

8057.824 Million cell updates/sec

Title:

Sequence:

1 GAAATATTCTTACTTACTT.....AGTTTCTTCTAAA 3731

Scoring table:

IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched:

441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters:

882724

Minimum DB seq length: 200000000

Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%

Listing first 45 summaries
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Issued_patents_NA:*

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| 'cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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| cgn2_6/ptodata/2/ina/FCTUS_COMB.seq:*
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Database :

## SUMMARIES

		Description	Sequence 1, Appli	Sequence 1, Appli	74	H	ď	7	ď	14,	194	ų	342	4	4	19,	19	17,	17,	ທ	'n	ò	ø	H	m	2	4	2	m
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US-08-961-527-86 US-09-004-838-62	US-09-221-017B-395	US-08-465-995A-1	US-08-465-994C-1	US-08-966-145-1	US-08-101-593-1	US-09-345-882-21	US-09-377-557-3	US-09-134-001C-1660	US-09-134-078-59	US-08-118-101A-1	US-08-961-527-73	US-08-212-188-3	US-08-970-725-3	PCT-US95-02708-3	US-08-755-587-26	US-09-134-001C-1983
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Dp 3	Oy 2 Db 2	2 2 Db 2	Oy 2 Db 2	OY 2 Db 2	oy 2	Qy 2	Qy 2 Db 2	0y 2 Db 2	Oy 2	Oy 2 Db 2	6y 2	Qy 2 Db 2	0y 2 0b 2	ος 2 α	Oy . 3	. dg	yo, ag	oy oy

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3421 TCCCTGGTGTTTATGACCAGCTAATCCAGATTAAGAAGGACAAAGCACGTAACAGGCC 3480
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US-08-100-874-1/C
US-08-100-874-1/C
Sequence 1. Application US/08100874
; Patent No. 5498533
; GENERAL INFORMATION:
    APPLICANT: POOVAIAN, B. W.
    APPLICANT: Han, T. J.
    APPLICANT: Han, T. J.
    APPLICANT: Han, T. J.
    APPLICANT: AN, G. H.
    TITLE OF INVENTION: Potato Plants
    UNDRES OF SEQUENCES: 2
    CORRESPONDENCES: 3
    CORRESPONDENCES: 4
    CORRESPONDENCES:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100, 874
FILING DATE: ULL/ 800
ATTORNEY/AGENT IMPORMATION:
NAME: SMITCH DAAMN F.
REFERENCE/DOCKET NUMBER: 7555-00004
TELEFORMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFORM: (313) 641-10270
TELEFER: 267637 Harness UR
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; TOPOLOGY: linear; IMMEDIATE SOURCE: CLONE: pTZgpt-F1s US-08-232-463-14
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                                                                                                                                                                                                                                                                                                                                                            Query Match
1.5%; Score 57.2; DB 1; Length 906;
Best Local Similarity 88.6%; Pred. No. 1.5e-06;
Matches 62; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SCHEIFLINGER, F
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS.
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26 AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 39472/114 IMMU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                   ORGANISM: Solanum tuberosum INDIVIDUAL ISOLATE: p-PCM-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 899149
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 906 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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81..530
                                                                                                      CDNA
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                                                                                TOPOLOGY: linear MOLECULE TYPE: CDN: HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                    linear
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STRANDEDNESS:
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                                                                                                                                                                                                     ; NAME/KEY:
; LOCATION:
US-08-100-874-1
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RESULT 4

US-09-345-882-1

Sequence 1, Application US/09345882

Sequence 1, Application US/09345882

Sequence 1, Application US/09345882

GENERAL INFORMATION:

TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.

TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.

TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.

CURRENT APPLICATION NUMBER: US 60/091,315

PRIOR APPLICATION NUMBER: US 60/091,315

PRIOR APPLICATION NUMBER: US 60/111,909

PRIOR PILING DATE: 1998-10-10

PRIOR FILING DATE: 1998-112-10
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                                                                                                                                     3027 TCGCGACCTTCACAAGAGATGTTGCAAGGAGATCATATGATGCTGATATGGAAGTTGATG 3086
                                                                                                                                                                                                                                                                                3087 GATTTGAAGATTACATTGACGAAGCTTTTGACTACAAAACTGAATATGACAAGAAGCTGG 3146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3267 GGGCCTTGAGGAAGGAGGCAAGAGCCTGGTTCAAGAGGCGTAATGATATAGATGACATGT 3326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGAAGGCATCAAAAACTTTTGACCGCAGAAAAGATGCTGAGGCCCATTAGTGTTGCTGTGA
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    Length 7218;
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Query Match 1.4%; Score 53.4; DB 1; I
Best Local Similarity 5.2%; Pred. No. 5.6e-05;
Matches 21; Conservative 219; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : polymorphic
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FEATURE:
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OTHER INFORMATION: 5-124-273
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SOFTWARE: Patent.pm
SEQ ID NO 1
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LOCATION: 90842
OTHER INFORMATION:
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LOCATION: 72794
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LOCATION: 88073
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polymorphic	: polymorphic	polymorphic	polymorphic	polymorphic	polymorphic	polymorphic	polymorphic	polymorphic	polymorphic	polymorphic	polymorphic	polymorphic	polymorphic	polymorphic	polymorphic	polymorphic	polymorphic	
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5-128-60	99-1442-22	5-129-144	5-130-257	5-130-276	5-131-395	5-133-375	5-135-155	5-135-198	5-135-357	5-136-174	5-140-120	5-140-348	5-140-361	5-143-84	5-143-101	5-145-24	5-148-352	.72817
LOCATION: 93714 OTHER INFORMATION: FEATURE:	NAME/KEY: allele LOCATION: 97122 OTHER INFORMATION: FEATURE:	NAME/KEY: allele LOCATION: 97152 CTHER INFORMATION:	NAME/KEY: allele LOCATION: 99098 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 99117 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 103806 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 106940 OTHER INFORMATION:	FEATURE: NAME/KEY: allele LOCATION: 108106 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 108149 OTHER INFORMATION: FFATURE:	NAME/KEY: allele LOCATION: 108308 OTHER INFORMATION:	FEATURE: NAME/KEY: allele LOCATION: 108471 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 134134 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 134362 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 134374 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 146328 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 146345 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 150329 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 160031	FEATURE: NAME/KEY: allele LOCATION: 727717;

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PRATURE: 110.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10.000 | 10
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REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3152 TTAATGGACTACTATGGCATAAAAACAGAGGCTGAAATACTTAGTGGTGGCATTATGAAG 3211
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Pred. No. 2.1;
0; Mismatches 130; Indels 0
                                                                     LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
                                                                                                                                                                                                                                          LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
FEATURE:
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MEDIUM TYPE: Floppy disk
COMPUTER:
COMPUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: polymorphic fragment 5-135-155
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STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-676-967-2
| Sequence 2. Application US/08676967
| Patent No. 5747317
| GENERAL INFORMATION:
| APPLICANT: COLLINS, KATHLEEN
| TITLE OF INVENTION: Human Telomerase
| NUMBER OF SEQUENCES: 10
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASZIFICATION: 530
ATTONEX/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.1%;
Best Local Similarity 47.6%;
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           108084..108130
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                                                                                                                                  FEATURE:
NAME/KEY: allele
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LOCATION: 108084
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NAME/KEY: allele
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COUNTRY: US!
ZIP: 94104
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2943 CGGACAAGACCAGCTATATCTCAGAAAGAGTTATTGGAAAGCTTTTCAGGAAAGTGAAGG 3002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 ITYWSNATGYINGARGAYGINCARMGNGCNYINAARGARAIHACNACNTIYGARGGNIGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2277;
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                                                                                                                                                                                                                                                                                                                                       Query Match
1.0%; Score 36.8; DB 1;
Best Local Similarity 27.4%; Pred. No. 1.8;
Matches 113; Conservative 66; Mismatches 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Science & Technology Law Group STREET: 268 Bush Street, Suite 3200 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Telomerase
                          UCB96-055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-676-974-2
; Sequence 2, Application US/08676974
; Patent No. 5770422
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
                    REFERENCE/DOCKET NUMBER: UCBS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELERAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: COLLING, KATHLEEN
TITLE OF INVENTION: Human Tel
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
36,627
                                                                                                                                                                                                                                                              , MOLECULE TYPE: CDNA
US-08-676-967-2
                                                                                                                                                                                                                                                linear
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FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   512 INAARGGNATGAAYATGAARGARATHAARGGNMGNACNGTNGCNGTNGAYTGG 564
                                                                                                                                                                                                                                                       Length 2277;
                                                                                                                                                                                                                                                     ; Score 36.8; DB 1; Length 2; Pred. No. 1.8; 66; Mismatches 232; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Science & Technology Law Group STREET: 268 Bush Street, Suite 3200 CITY: San Francisco STATE: CA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Telomerase
                   UCB96-055
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APPLICATION NUMBER: US/09/098,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09098487;
Patent No. 5917025;
GENERAL INFORMATION:
APPLICANT: COLLINS, Kathleen
TITLE OF INVENTION: Human Telomer.
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
           REFERENCE/DOCKET UNMER: UCB9-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEPAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                   1,0%;
nilarity 27.4%;
Conservative 66
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MOLECULE TYPE: CDNA

US-08-676-974-2
                                                                                                                                                                                                                                                                       Similarity
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Matches 113;
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3183 CTGAAATACTTAGTGGTGGCATTATGAAGGCATCAAAAACTTTTGACCGCAGAAAAGATG 3242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 TIYWSNATGYINGARGAYGINCARMGNGCNYINAARGARATHACNACNIIYGARGGNIGY 213
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                                                                                                                                                                                                                                                                                                                                 1.0%; Score 36.8; DB 2; Length 2
27.4%; Pred. No. 1.8;
Live 66; Mismatches 232; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Foley & Lardner STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/08232463;
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TILLE OF INVENTION: RECOMBINANT FOW
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB/
TELECOMMUNICATION INFORMATION:
TELEFRAX: (415)343-434
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
                                                                                                                                                                                                                                                                                                                                      1.09
Best Local Similarity 27.49
Matches 113; Conservative
                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA
US-09-098-487-2
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ZIP: 22313-0299
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Sequence 1, Application US/09415946
Patent No. 6376751
GENERAL INFORMATION:
SUND, Z. Renee
APPLICANT: SUND, Z. Renee
APPLICANT: Chen, Lingling
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Nucleic Acids That Control Reproductive Development in
TITLE OF INVENTION: Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2943 ACCTITCCTAAAGAAGTCAGTATTITGAAAACTTGTACTTTGTAGGTGGATCAGNAAAT 3002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320 GGATCTAGAGCATTTGCCAAAGTTCAATTTGCCGACAACATAAGTGCTGACAAAATCATC 379
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APPLICANT: Rosenberg, Martin
APPLICANT: Ward, Judith
TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides,
TITLE OF INVENTION: Polypeptides and Their Uses
NUMBER OF SEQUENCES: 534
CORRESPONDENCE ADDRESS:
ADDRESSE: SINTHKILINE Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IDENCINE COMPATIBLE COMPUTER: IDENCINE COMPATIBLE COMPUTER: IDENCINE COMPATIBLE COMPUTER: IDENCINE COMPATIBLE COMPATIBLE CONTRACT CONTRAC
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Pred. No. 2.8;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 49.0%;
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-08-936-165A-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 3191 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                            ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       610-270-5090
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US-09-415-946-1/C
                                                                                                                                                                                                                                                                         CITY: King
STATE: PA
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                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       761 GAAACTCCTGATGATCAGTGGGTGAGGACAACAGATTTCCCTCCATCTTGGATAGGGCTA 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTTCTAGCTTATGTTTGCAGTTCCGTAGGGGTGTTCGTCTTCCAAATTTCGAGGAAAGT 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITITICCACTATGCAGAACGTGAAAACAATATTACTTTACAGACTGGTTTCACCTTTTTC 940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  581 TTTTTTTTTTTTTTTATCTAGTGGTTCAGCTGACTATAAACTTCAGCTTTCATATGAAAAT 640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
1.0%; Score 36.6; DB 1; Length 7
Best Local Similarity 10.1%; Pred. No. 3.8;
Matches 48; Conservative 204; Mismatches 223; Indels
                                                                                                                                                                                                              TELEBOOK NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEBOOK: (703)836-9300
TELEBOX: (703)83-4109
                                                                                                                      APPLICATION NUMBER: EP 91 114 300. FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 194, Application US/08936165A
Patent No. 6348582
GENERAL INFORMATION:
APPLICANT: Black, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lonetto, Michael
Nicholas, Richard
Pratt, Julie
Reichard, Richard
                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burnham, Martin
Hodgson, John
Knowles, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-936-165A-194
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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Sequence 342, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: DEPLOEMENTS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT FILING DATE: 1999-08-13
PRIOR PPLICATION NUMBER: US 60/064,964
PRIOR PLING DATE: 1997-11-08
PRIOR PLING DATE: 1997-11-08
PRIOR PLING DATE: 1997-11-08
PRIOR PLING DATE: 1997-11-08
FROM PRIOR PLING DATE: 1997-10-08-14
NUMBER OF SEQ ID NOS: 5674
SED ID NO 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3040 AAGAGATGTTGCAAGGAGATCATATGATGCTGATATGGAAGTTGATGGATTTGAAGATTA 3099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3100 CATTGACGAAGCTTTTGACTACAAAACTGAATATGACAAGAAGCTGGGTAATTTAATGGA 3159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     813 AATGGTTTCTACAGGTAGCTTAGAAATTGAGCATGGAGATGCAAATGAAGGTGTAGAATT 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           873 GCTAAAACAAGCCTTAGAAGTCGAFAATGCATATCATGAACCATTGTTGATTTTAAGTGA 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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Sequence 4, Application US/08911445

Patent No. 5876713

APPLICANT: TAKEDA CHEMICAL INDUSTRIES, LTD.

APPLICANT: TAKEDA CHEMICAL INDUSTRIES, LTD.

ITILE OF INVENTION: NOVEL GLUTAMINE:FRUCTOSE-6-PHOSPHATE

ITILE OF INVENTION: AMIDOTRANSFERASE, ITS.PRODUCTION AND USE

NUMBER OF SEQUENCES: 25

CORRESSONDEMICE ADDRESS:

STREET: P.O. BOX 2999, STATION D

STREET: P.O. BOX 2999, STATION D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.9%; Score 35; DB 4; Length 1248; Best Local Similarity 51.6%; Pred. No. 4.3; Matches 80; Conservative 0; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,445
FILING DATE: 12-AUG-1997
CLASSIFICATION: 435
PROOF APPLICATION 1935
PROOF APPLICATION NUMBER: US/08/911,445
FILING DATE: 13-AUG-1996
FILING DATE: 13-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3160 CTACTATGGCATAAAACAGAGGCTGAAATACTTA 3194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              933 TITATATCGTAATGAAGAGACTATGAATCAATTA 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA CORGANISM: Staphylococcus epidermidis US-09-134-001C-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: OTTAWA
STATE: ONTARIO
COUNTRY: CANADA
ZIP: KIP 5Y6
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                    Db 10180 TACTTTTGT 10172
                                       1295 TATTTTGT 1303
                                                                                                                                                                                              US-09-134-001C-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10240 TGTGCCTTGGAAGGAATTGTGTGTGTTCAGAAGAAAGACATTGTAACCCTTCCAAAGGT 10181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1115 ATTGAGCATGCCTTAGAGAAACTGTACTATATAAAGGAGTGCTGTTATGATCCCGTGAGG 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1175 TGGCTCACTGAGCAGTATGATGGGTATCTCAAGGGTAGACAACCTCCAAAATCTCCGTCC 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1235 ATCACTTTAGATGATGGGTTGGTGTATGTAAGAAGGGTCCTAGTAACACCATGCAAAGTT 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: genomic DNA (Ecotype Columbia) from CD82 clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.9%; Score 35.4; DB 4; Length 17341; 49.2%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                          LUCKATION: join(4241..4335, 4448..4623, 4704..4823, 4903..4956, OTHER INFORMATION: EMBRYONIC FLOWER 1 (EMF1)
LUCKATION: (3202)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
; FILE REFERENCE: 018941-000110US
; CURRENT APPLICATION NUMBER: US/09/415,946
; CURRENT FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,696
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 1
; LENGTH: 17341
                                                                                                                                                                                                                                                                     ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , OTHER INFORMATION: exon 8 US-09-415-946-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (4160)..(4335)
OTHER INFORMATION: exon 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (4903)..(4956)
OTHER INFORMATION: exon 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (5046)..(6307)
OTHER INFORMATION: exon 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (3202)..(3265)
OTHER INFORMATION: exon 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: exon 3 NAME/KEY: intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (4704)..(4823)
OTHER INFORMATION: exon 4
NAME/KEY: intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (6448)..(8065)
OTHER INFORMATION: exon 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: intron
LOCATION: (3266)..(4159)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: intron
LOCATION: (4957)..(5045)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (4336)..(4447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (4624)..(4703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (4824)..(4902)
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LOCATION: (8066)..(8300)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: exon
LOCATION: (4448)..(4623)
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Matches 93; Conserva
                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: exon
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3130 ATATGACAACAAGCTGGGTAATTTAATGGACTACTATGGCATAAAAACAGAGGCTGAAAT 3189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19, Application US/08911445
Sequence 19, Application US/08911445
Patent No. 5876713
GENERAL INFORMATION:
APPLICANT: TAKEDA CHEMICAL INDUSTRIES, LTD.
TITLE OF INVENTION: NOVEL GLUTAMINE:FRUCTOSE-6-PHOSPHATE
TITLE OF INVENTION: AMIDOTRANSFERASE, ITS PRODUCTION AND USE
NUMBER OF SEQUENCE: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: FETHERSTONHAUGH & CO.
STRRET: P.O. BOX 2999, STATION D
CITY: OTTAWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.9%; Score 35; DB 2; Length 1458;
llarity 52.4%; Pred. No. 4.7;
Conservative 0; Mismatches 70; Indels
                                                    Ouery Match 0.9%; Score 35; DB 4; Length 1275; Best Local Similarity 52.4%; Pred. No. 4.3; Matches 77; Conservative 0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: OTTAWA
STATE: OTTAWA
STATE: ONTARIO
COUNTRY: CANADA
ZIP: KRADABLE FORM:
MEDIUM TYPE: FIDOPY disk
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDOPY disk
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,445
FILING DATE: 12-AUG-1997
CLASSIFICATION NUMBER: US/08/911,445
FILING DATE: 13-AUG-1997
APPLICATION NUMBER: JS 213944-1996
ATTORNEY/AGENT INFORMATION:
REPERENCE/COCKET NUMBER: 28605-30
TELEPHONE: (613)-232-2486
TELEPHONE: (613)-232-2486
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHRRACTERISTICS:
LENGTH: 1016 Base pairs
                                                                                                                                                                                                                                                                                                                                                    3250 CATTAGTGTTGCTGTGAGGGCCTTGAG 3276
                                                                                                                                                                                                                                                                                                                                                                                              492 CATTACGTTTTCAACGTTGGTCGAGAG 518
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Matches 77; Conserve
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STRANDEDNESS:
TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-08-911-445-19
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       US-09-182-983-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3190 ACTTAGTGGTGGCATTATGAAGGCATCAAAAACTTTTGACCGCAGAAAAGATGCTGAGGC 3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      432 AGATACAGAGACCATCGCCAAGCTGATTAAATATGTGTTCGACAACAAGAAAAACTGAGGA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 AAATTACAAAGATCTGAGGAAATTTCTGGAAAGCAAAGGCTACGAGTTTGAGTCAGAAAC 431
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09182983
Sequence 4, Application US/09182983
Sequence 4, Application US/09182983
Sequence 4, Application US/09182983
Settent No. 6207431
GENERAL INFORMATION:
APPLICANT: TAKEDA CHEMICAL INDUSTRIES, LTD.
TITLE OF INVENTION: AMIDOTRANSFERASE, ITS PRODUCTION AND USE TITLE OF INVENTION: AMIDOTRANSFERASE, ITS PRODUCTION AND USE NUMBER OF SEQUENCES: 25
CORRESPONDENCES ADDRESS:
ADDRESSEE: FETHERSTONHAUGH & CO.
STREET: P.O. BOX 2999, STATION D
CITY: OTTAM.
STREET: ONTARIO
COUNTY: CAMADA
ZIP: KIP 5V6
COMPUTER: ELAPPABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: BADABLE FORM:
COMPUTER: BADABLE FORM:
COMPUTER: BADABLE FORM:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
CHARGA TELLING DATE:
CHARGA TELLING DATE:
CHARGA TELLING DATE:
CHARGA TELLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.9%; Score 35; DB 2; Length 1275; Best Local Similarity 52.4%; Pred. No. 4.3; Matches 77; Conservative 0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: FETHERSTONHAUGH 6 CO.,
REFERENCE/FOCKET UNMERR: 28605-30
TELEPHONE: (613)-232-2486
TELEPHONE: (613)-232-2486
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1275 base pairs
ATTORNEY/AGENT INFORMATION:

NAME: FETERESTONHAUGH & CO.,

REFERENCE/DOCKET NUMBER: 28605-30

TELEPHONE: (613)-232-2486

TELEPHONE: (613)-232-2486

TELEPHONE: (613)-232-2486

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1275 base pairs

TYPE: nucleic acid

STANNEDNESS: double

TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3250 CATTAGTGTTGCTGTGAGGCCCTTGAG 3276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            492 CATTACGTTTTCAACGTTGGTCGAGAG 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/911,445
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0.9%; Score 35; DB 4; Length 1458;
Best Local Similarity 52.4%; Pred. No. 4.7;
Matches 77; Conservative 0; Mismatches 70; Indels
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REFERENCE 1 (bases 1 to 3731) AUTHORS Wassenegger,M., Riedel,L., Schiebel,W. and Sanger,H.L. TITLE Nucleic acid molecules encoding polypeptides having the enzymatic activity of an RRA-directed RRA polymerase (RDRP) JOURNAL Patent: US 6218142-A 1 17-APR-2001; FEATURES Location/Qualifiers 1. 3731 Source /organism="unknown" BASE COUNT 1064 a 669 c 849 g 1149 t	Query Match 100.0%; Score 3731; DB 6; Length 3731; Best Local Similarity 100.0%; Pred. No. 0; Matches 3731; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	GAANTATUCTTACTTACTTCACCAGGGATTGACTCATCACTCCCCTCAAGTCTTTGTGT 6	77777 77777 71111	TTTGCATAACTTCAGGGGTATTCCAGTTGGTGTTAGCATTTGAAAGTCGAACTGCACTT 18	OY 181 GGAATTIGGCTACATGGGAAAGACAATTCAGGTTTTCGGATTCCCTTATCTTCTCTGC 240	OY 241 GGAAGTGGTTAAGTCATTCTTAGAGAAATATACAGGATATGGAACTGTATGTGCATTGGA 300 	OY 301 GGTTAAACAGTCCAAAGGAGGATCTAGAGCATTTGCCAAAGTTCAATTTGCCGACAACAT 360 	QY 361 AAGTGCTGACAAAATCATCACTTTGGCTAATAACAGGCTGTAITTTGGCTCTTCTTATTT 420 Db 361 AAGTGCTGACAAATCATCACTTTGGCTAATAACAGGCTGTATTTGGCTCTTCTTATTT 420	OY 421 GAAGGCTTGGGAAATGAAAACTGATATTGTCCAACTGCGGGCATATGTGGATCAGATGGA 480	OY 481 TGGCATAACTTTGAATTTCGGATGTCAGATATCAGATGACAAGTTTGCAGTGTTGGGAAG 540 Db 481 TGGCATAACTTTGGATGTCAGATATCAGATGACAAGTTTGCAGTGTTGGGAAG 540	QY 541 TACAGAAGTITCAATICAGCAIIGGATIGAAAAAATITITITITITITAICIAG 600 	OY 601 TGGTTCAGCTGACTATAAACTTCAGCTTTCATATGAAAATATATGGCAGGTTGTGCTCCA 660 	Qy 661 TCGTCCATAIGGTCAAAAIGCTCAGTTTCTCCTCATACAGTTATTIGGIGCTCCTGGGAT 720	OY 721 CTATAAGAGACTIGAAAACTCCIGTIATAGCTICTITAAGGAAACTCCTGATGATCAGTG 780	OY 781 GGTGAGGACAACAGATTTCCCTCCATCTTGGATAGGGCTATCTTCTAGCTTATGTTTGCA 840	Oy 841 GTICCGTAGGGGTCTTCCTCCAAATTTCGAGGAAGTTTTTTCCACTATGCAGAACG 900

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oy Op	2041	AGATGAAGTTCTCGAACAGAAGCAAAAGGAAGCTGTAGATCAGCTTGATGCTATCTTGCA 210 
5 S	2101	TCTTTGAAGGCACAGGAGGCTTTGGAATTGATGTCTCCTGGAGAAGAACACTAATAT 216
୍ଦ ବୁଦ	2161	CAATGCTAAACTGTGGTTATAAGCCTGATGCTGAGCCCTTTCTTCAATGAT 222 
oy Op	2221	GTTGCAAACCTTCCGCGCATCCAAGTTGCTCGATTTGCGGACTAGATCAAGAATATTAT 2280 
oy Db	2281	TCCAAATGGAAGAACAATGATGGGATGTTTGGATGAATCCAGAACCTTGGAATATGGTCA 2340 
QY Db	2341	GGTGTTTGTTCAGTTACTGGTGCTGGACATGGAGAGTTTTCTGACGATTTACATCCATT 2400 
S G	2401	TAATAACAGCAGATCCACCAACAGTAATTICATTCIGAAGGGAAATGTGGTTGTTGCAAA 2460 
Oy Dp	2461	AAATCCATGCTTGCATCCTGGTGATATTCGTGTTTTAAAGGCTGTAAATGTTCGAGCGCT 2520 
S d	2521	GCACCACATGGTAGATTGTGTTGTATTCCCTCAGAAAGGAAAAAGACCTCATCCGAATGA 2580 
0y Dp	2581	AIGITCIGGGAGIGATITGGAIGGGGAIAICIACITIGTITGCIGGGAICAAGACAIGAI 2640 
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QY Db	2701	TGATGTCACAATTGAGGAAGTTGAAGAGTACTTCACCAACTATATTGTGAATGACAGTTT 2760 
oy D	2761	GGGAATCATAGCAAAIGCCCATGTCGTATTIGCAGACAGAACCTGATATGGCCATGAG 2820 
9y Dp	2821	TGATCCATGCAAAAACTTGCTGAGCTCTTTTCAATTGCAGTGGACTTTCCAAAGACTGG 2880 
QY	2881	CTAA
QY	2941	GCCGGACAAGACCAGCTATATCTCAGAAAGAGTTATTGGAAAGCTTTTCAGGAAAGTGAA 3000 
QY Db	3001	GGACAAAGCACCTCAGGCTAGCTCTATCGCGACCTTCACAAGAGATGTTGCAAGGAGATC 3060 

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PLN 18-DEC-1998
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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Schiebel, W., Pelissier, T., Riedel, L., Thalmeir, S., Schiebel, R.,
Kempe, D., Lottspeich, F., Sanger, H.L. and Wassenegger, M.
Isolation of an RNA-directed RNA polymerase-specific cDNA clone
                3061 ATATGATGATGATAGGAAGTTGATTTGAAGATTACATTGACGAAGCTTTTGACTA 3120
                                                                                                                                                                                                                                        3301 GAGGCGTAATGATAGATGACATGTTACCAAAGGCTTCGGCTTGGTACCACGTTACATA 3360
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ATATGATGCTGATATGGAAGTTGATGGATTTGAAGATTACATTGACGAAGCTTTTGACTA 3120
                                                         3121 CAAAACTGAATATGACAACAAGCTGGGTAATTTAATGGACTACTATGGCATAAAAACAGA
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Wassenegger, M.
Direct Submission
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Submitted (08-JAN-1997) M. Wassenegger, Max-Planck-inst. fuer
Biochemie, Viroidforschung, Am Klopferspitz 18a,
Planegg-Martinsried, 82152, FRG
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TGATAAAAATTTGAATTTCTGCATTTTCATCGGGCCAGTTGCGGGATAATT ATGTTTGCATCAAGACCTGGCCTTACTGCAAATGATAAAAGAGCTTGGATGG	AGTGTGGATGTTTGCATCAAGACCTGGCCTTACTGCAAATGATAAAGAGCTTGGATGG		81 TICCICCAGAGAGACITIGAGIGIICITAGGCAIGAGAIIGAAGITATICCGGAIGIAAA 1740 	41 GGTTCATGGAACCAGCTATGTCTTTCTGATGGAATTGGTAAAATAICTGGTGACTTTGC 1800 	01 TCATAGAGTTGCCTCAAAATGTGGCCTTCAATATACCCCATCTGCTTTCCAGATTGGTTA 1860	61 IGGTGGATATAAAGGTGTTGTGGGTGTTGATCGGATTCATCAATGAAGTTGTCTTTGAG 1920 	1 AAAGAGCATGTCGAAATATGAATCAGACAACATAAAGTTAGATGTCCTTGGATGGA	1 ATATCAGCCTTGTTATCTTAATCGTCAACTGATTACGCTCTTGTCTACACTTGGAGTGAA 2040	1 AGATGAAGTTCTCGAACAGAAGGAAGCTGTAGATCAGCTTGATGCTTGCA 2100 	1 IGATICTITGAAGGCACAGGAGGCTTIGGAATIGATGTCTCCTGGAGAGACACTAATAT 2160 	61 TCTCAAGGCAATGCTAAACTGTGGTTATAAGCCTGATGCTGAGCCCTTTCTTCAATGAT 2220 	GTTGCAAACCTTCCGGCATCCAAGTTGCTGATTTGCGGACTAGATCAAGAATATT	1 TCCAAATGGAAGAACAATGATGGGATGTTTGGATGAATCCAGAACCTTGGAATATGGTCA 2340 	1 GGTGTTTGTTCAGTTTTACTGGTGCTGGACATGGAGAGTTTTCTGACGATTTACATCCATT 2400	1 TAATAACAGCAGATCCACCAACAGTAATTTCATTCTGAAGGAAATGTGGGTTGTTGCAAA 2460 	61 AAATCCATGCATCCTGGTGATATTCGTGTTTTAAAGGCTGTAAATGTTCGAGCGCT 2520 	1 GCACCACATGGTAGATTGTGTTGTATTCCCTCAGAAAGGAAAAAAAGACCTCATCCGAATGA 2580	4 4.
Db 15(	Db 156.		Qy 168: Db 168:	Oy 17,	Oy 180 Db 180	Qy 186. Db 186	Oy 192 Db 192	Qy 198: Db 198:	Qy 204.	Oy 2101 Db 2101	Oy 21	Qy 2221 Db 2221	Oy 228: Db 228:	QY 2341 Db 2341	Oy 2401 Db 2401	Oy 246 Db 246	Qy 2521 Db 2521	Qy 258: Db 258:

2820 2880 2880 2940 2940 3000 3060 3120 3120 3180 3240 3240 3300 3300 3360 3420 3480 3480 3540 3540 3000 3060 3600 GGAATCATAGCAAATGCCCATGTCGTATTTGCAGACAGAGAACCTGATATGGCCATGAG SATCCATGCAAAAAACTTGCTGAGCTCTTTTCAATTGCAGTGGACTTTCCAAAGACTGG **ACAAAGCACCTCAGGCTAGCTCTATCGCGACCTTCACAAGAGATGTTGCAAGGAGATC** SCTGAAATACTTAGTGGTGGCATTATGAAGGCATCAAAAACTTTTGACCGCAGAAAAGA NGGCGTAATGATATAGATGATGATGTTACCAAAGGCTTCGGCTTGGTACCACGTTACATA STICTCAACTIGICATCICICAGGGCICAACTGAGTCACAGATTAGTGITGAAATGAGA CCAGTCGAGCGTTAAGCTGATATATATAATGTAATAGGGTGTGTGATCATAAGAAAAC TACTCTAAGAAACAGATGTACAGCTAAGTACTAATATGTGTATGTGATTTGAGTTTCATC SATGTCACAATTGAGGAAGTTGAAGAGTACTTCACCAACTATATTGTGAATGACAGTTT STICCCGCTGAAATACCAICTCAGIIGCGCCCIAAAGAAIACCCAGACTICAIGGAIAA CGGACAAGACCAGCTATATCTCAGAAAGAGTTATTGGAAAGCTTTTCAGGAAAGTGAA

PLN 07-JAN-1999

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YVGTKTRAFFLLSGTIMFARSYTPDLEVDGFEDYIDERFENTYRKREDIDDLLAK
ASAWYAA HPTYWGCYNEGLKRDHFISFPWCVXD"
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relula hybrida RdRP gene, partial.

ION AJ011979

SON AJ011979.

RdRP gene; RNA-directed RNA polymerase.

Petunia x hybrida.

Fetunia x hybrida.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Petunia.

E 1 (bases 1 to 4579)

Solanaceae; Petunia.
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Submitted (16-0CT-1998) Wassenegger M., Max-Planck-Institut of
Biochemistry Viroidresearch, Am Klopferspitz 18A, 82152
Martinsried, FRG
2 (bases 1 to 4579)
Schiebel,W., Pelissier,T., Riedel,L., Thalmeir,S., Schiebel,R.,
Kempe,D., Lottspeich,F., Saenger,H.L. and Wassenegger,M.
Isolation of an RNA-directed RNA polymerase-specific CDNA clone
1342 ATTTGAATTTCTTGCATTTTCATCGAGCCAGTTGCGGGATAATTCAGTGTGGATGTTGC 1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="RdRp"
john(<1. .1451,2420. .2570,3856. .>4579)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=experimental
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                                                                       1402 ATCAAGACCTGGCCTTACTGCAAATGATATAAGA 1435
                                                1576 ATCAAGACCIGGCCTTACTGCAAATGATATAAGA 1609
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SGANDDFLIEGNVYARNPCLHPGDITVLARANDPALHHWNOCVPFFORGKREHPNE
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DEBRYKSFYDNKLGANLMDYYGIKTEREILSGGIMRASKTPDRRKDERAIGYNYRCLK
KERREDIDMLAKASAWTHYTYHHTYWGLYNBGLKDEAIGYNYRCLLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 3505)
Schlebel, W., Pelissier, T., Riedel, L., Thalmeir, S., Schlebel, R.,
Kempe, D., Lottspelch, F., Saenger, H.L. and Wassenegger, M.
Isolation of an RNA-directed RNA polymerase-specific cDNA clone
from Tomato
Unpublished
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Submitted (I-CCT-1998) Wassenegger M., Max-Planck-Institut of
Blochemistry Viroidresearch, Am Klopferspitz 18A, 82152
Martinsried, FRG
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                                                                                                                                         Nicotian tabacum mRNA for RNA-directed RNA polymerase.
AJ011576 AJ011576.1 GI:4138281
GRP gene; RNA-directed RNA polymerase.
common tobacco.
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Similarity 100.0%; Pred. No. 2.7e-39;
04; Conservative 0; Mismatches 0;
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20. .3370
20. .3370
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     3721 TTTCTTCTAAA 3731
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BASE COUNT ORIGIN

Best Loc Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTCAM 906 bp mRNA linear PLN 15-AUG-1995 Solanum tuberosum clone PCM1 calmodulin mRNA, complete cds. J04559 GI:169476
                                                                                                                                                                              PAT 07-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           calmodulin.
Solanum tuberosum (strain Russet Burbank) cDNA to mRNA.
Solanum tuberosum (strain Russet Burbank) cDNA to mRNA.
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 906)
Jena, P. K., Reddy, A.S. and Poovaiah, B.W.
Molecular cloning and sequencing of a cDNA for plant calmodulin:
Molecular cloning and sequencing of a cDNA for plant calmodulin:
Proc. Natl. Acad. Sci. U.S.A. 86 (10), 3644-3648 (1989)
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Draft entry and printed copy of sequence [1] kindly submitted by B.W.Poovalah, 16-MAY-1989.
Location/Qualifiers
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1 (bases 1 to 906)

Poovalah, B. W., Takezawa, D., Han, T.-J. and An, G.H.
Control of growth and development of potato plants
Patent: US 5498533-A 1 12-MAR-1996;
Location/Qualifiers
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                                                                                                                                                                                   linear
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282
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Sequence 1 from patent US 5498533.
I18797
I18797.1 GI:1599152
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151 c 219 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLN 07-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thale cress. Arabidopsis thaliana Arabidopsis thaliana Eukaryota; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases I to 1538) Wassenegger, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 1538)
Schlebel, W., Pelissier, T., Riedel, L., Thalmeir, S., Schlebel, R.,
Kempe, D., Lottspeich, F., Saenger, H.L. and Wassenegger, M.
Isolation of an RNA-directed RNA polymerase-specific cDNA clone
from Tomato
                                                                                                                                                                                                                                           of
                                                                                                                                                          Gaps
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Direct Gib-Ocr-1998) Wassenegger M., Max-Planck-Institut
Biochemistry Viroldresearch, Am Klopferspitz 18A, 82152
Martinsried, FRG
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                                                                                                         Length 4579;
                                                                     .0%; Score 73; DB 8; Length 4.57.0.0%; Pred. No. 96-28;
                           2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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0.9%; Score 35; DB 8; Le
Best Local Similarity 100.0%; Pred. No. 7.2e-07;
Matches 35; Conservative 0; Mismatches 0;
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1. 1538
//Organism="Arabidopsis thaliana"
/cultivar="Columbia"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATHOI1977 1538 bp DNA Arabidopsis thaliana RdRP gene, partial. AJ011977. GI:4127462 RdRP gene; RNA-directed RNA polymerase.
                                                                                                      Query Match 2.0%; Score 73; DB Best Local Similarity 100.0%; Pred. No. 9e-Matches 73; Conservative 0; Mismatches
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1. .1538
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                           943 g
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/gene="RdRP"
<1. .>1538
/gene="RdRP"
     /number=3
789 c
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Length 25; Indels

DB 6;

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Rattus.

10 (bases 1 to 112247)

Raturoks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Blanbaria, J., Benton, J., Buratunge, R., Blankenburg, K., Bonnin, D., Burbaria, J., Benton, J., Burkett, C., Burrell, K.L., Byrd, N. C., Carroh, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Carroh, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Carroh, T.F., Carter, M., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davila, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Day-Carroll, L., Dederich, D. A., Davila, M., Davis, C., Day-Carroll, L., Dederich, D. A., Earnhart, C., Edgar, D., Edards, C.C., Elbaj, C., Escotto, M., Earls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Falls, T., Garcia, A., Ganrer, T., Garca, R., Ganrer, T., Garca, R., Garrell, J. H., Guevara, W., Mill, R., Havlak, P., Hawes, A., Hernandez, J., Honkaile, K., Gao, J., Garcia, A., Ganrer, T., Garca, N., Garrell, J. H., Guevara, W., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Howard, S., Huber, J., Hulk, S., Hame, J., Jackson, L. E., Howard, S., Khan, U., King, L., Korvar, J., Garcis, L., Korvar, J., Lu, X., Lude, S., Joudah, S., Jacobson, B., Jia, Y., Johnson, R., Jollvet, S., Joudah, S., Liu, M., Lu, X., Luder, M., Ludis, L., Kurtovic, J., Lu, X., Luder, R., Ludis, R., Ludis, M., Matchine, P., Martin, R., Mapua, P., Martin, R., Mayen, M., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oraga, M., Nickerson, E., Nwokenkwo, S., Oguh, M., Olyueon, I., Pickens, R., Pitt, L., Coulles, R., Peters, L., Pickens, R., Pitt, L., Coulles, R., Peters, L., Pickens, R., Pitt, L., Coulles, R., Peters, L., Pickens, R., Pitt, L., Shooshtarit, N., Rojas, A., Rojubokan, I., Rojas, A., Rojubokan, I., Rojas, A., R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC095524 112247 bp DNA linear HTG 10-JUL-2002 Rattus norvegicus clone CH230-7M23, *** SEQUENCING IN PROGRESS ***, 54 unordered pieces.
                                                                                                                                                         1 (bases 1 to 25)
Wassenegger,M., Riedel,L., Schiebel,W. and Sanger,H.L.
Nucleic acid molecules encoding polypeptides having the enzymatic
activity of an RNA-directed RNA polymerase (RDRP)
Patent: US 6218142-A 5 17-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentla; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                       0.6%; Score 24; DB
100.0%; Pred. No. 1;
ive 0; Mismatches
Sequence 5 from patent US 6218142.
AR145906
AR145906.1 GI:15109095
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9 c 4 g
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AC095524.3 GI:21716983
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                                                                                                                                                                                                                                                                                                                                                                                           Unknown...
Unknown...
Unknown...
Unclassified.

I (bases I to 25)

Nassenegger, M., Riedel, L., Schiebel, W. and Sanger, H.L.

Wassenegger, M., Riedel, L., Schiebel, W. and Sanger, H.L.

Nucleic acid molecules encoding polypeptides having the enzymatic activity of an RNA-directed RNA polymerase (RDRP)

Patent: US 6218142-A 4 17-APR-2001;

Location/Qualifiers
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Massenegger, M., Riedel, L., Schiebel, W. and Sanger, H.L.
Nucleic acid molecules encoding polypeptides having the enzymatic activity of an RNA-directed RNA polymerase (RDRP)
Patent: US 6218142-A 6 17-APR-2001;
Location/Qualifiers
1. 25
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                     Length 906;
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Pred. No. 0.29;
0; Mismatches 0; Indels
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0.7%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                0; Indels
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                Query Match 0.8%; Score 30; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 30; Conservative 0; Mismatches
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AR145907
AR145907.1 GI:15109096
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Sequence 4 from patent US 6218142.
AR145905 1 GI:15109094
                                                                                                            3687 TAAGTACTAATATGTATGTGATTTGAGTTT 3716
                                                                                                                                      47 TAAGTACTAATATGTATGTGATTTGAGTTT 18
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5 c 10 g
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Best Local Similarity 100.0%; Pr
Matches 25; Conservative 0;
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AR145907/c
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AR145906/c
LOCUS
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AR145905/c
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Weinstock, G. and Gibbs, R.
Direct Submission
L. Unpublished
E. 2 (hence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

E 3 (bases 1 to 112247)

Morley, K.C.

Direct Submission

L Submitted (10-UL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 9, 2002 this sequence version replaced gi:17942040.

Center: Baylor College of Medicine

Center: Baylor College of Medicine

Center code: BCM
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Arabidopsis thaliana.

Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases I to 132699)

Chao.O., Shinn, P., Dunn, P., Buehler, E., Kahn, S., Kim, C., Walker, M., Gonzalez, A., Hansen, N.F., Huizar, L., Kremenetskaia, I., Lenz, C., Liu, S., Luros, S., Rowley, D., Schwartz, J., Toriumi, M., Vysotskaia, W., Yu, G., Davis, R.W., Federspiel, N.A., Theologis, A. and Ecker, J.R.

Genomic sequence for Arabidopsis thaliana BAC F1086 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132699 bp DNA linear PLN 28-JUN-2000 Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence.
AC006917
AC006917.6 GI:4757662
HTG.
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Department of Biology, University of Pennsylvania, 38th Street and
Hamilton Wealk, Philadelphia, Pennsylvania 19104-6018, USA
(Dases 1 to 13269)
Cheuk, R., Shinn, P., Brocks, S., Buehler, E., Chao, C.,
Chonson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C.,
Chiou, J., Chon, E., Conn, L., Lee, J., Lenz, C., Li, J., Liu, A., Hansen, N.,
Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J.,
Schwartz, J., Southwick, A., Thaveri, A., Torlumi, M., Vaysberg, M.,
Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-FEB-1999) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA (bases 1 to 132699)
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA On May 7, 1999 this sequence version replaced g1:4731042.

1. 132699
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                                                                                                                                                                                                                                                                                                                                                Query Match 0.6%; Score 23; DB 2; Length 112247; Best Local Similarity 100.0%; Pred. No. 2.2; Matches 23; Conservative 0; Mismatches 0; Indels 0;
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103993: contig of 4525 bp in length
104093: gap of unknown length
108379: contig of 4286 bp in length
108479: gap of unknown length
112247: contig of 3768 bp in length
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2 (bases 1 to 132699)
Ecker,J.R.
Direct Submission
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MHPLPMSTKRRGARISGRKMSQGAFKKVLEKLASDGFNFGNPIDLKSHWARHGTNKFV
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Purch, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Banna, N., Bastien, V., Boqualavi, L., Boukhgalter, B., Anderson, S., Banna, N., Bastien, V., Boqualavi, L., Chazaro, B., Brown, A., Camarata, J., Campojano, A., Chang, J., Chasaro, B., Cooke, Y., Canarata, J., Campojano, A., Chang, J., Cooke, A., Cooke, Y., Dewar, K., Dewar, T., S., Dodge, S., Farco, S., Fartalano, K., Dewar, K., Diaz, J.S., Dodge, S., Farco, S., Fartalano, K., Dewar, K., Diaz, J.S., Cooke, A., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hullme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Kells, C., Lanceque, K., Lanczares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Mcaratas, A., Kells, C., Lanccque, K., Lamazares, R., Major, J., Marquis, N., Maneus, L., Mihova, T., McKernan, K., Major, J., Marquis, N., Maneus, L., Mihova, T., Merwan, P., McKernan, K., Major, J., Marquis, N., Maneus, L., Mihova, T., Peterson, K., Phukhang, P., Pierre, N., Pollara, V., Raymond, C., Rosett, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rostaus, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Severy, P., Sohner, S., Schupback, R., Seaman, S., Sanner, M., Traytis, N., Trighlio, J., Yassillev, H., Viel, R., Wilson, B., Warman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Santice, Canbridge, MA 02141, USA

B. Charles Street, Cambridge, MA 02141, USA

Severy, P., Subramsian, C., Lander, E., Ali, A., Allen, N., Alter, R., Richol, M., Mischelle, M., A., Misch, M., Mischelle, M., A., Misch, M., A., Misch, M., A., Misch, M., A., Misch, B., Stanger, Cannoni, Cannoni
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Mus musculus clone RP23-17D24, WORKING DRAFT SEQUENCE, 12 ordered
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
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AL732358_3 300001 354683
Continuation (4 of 4) of AL732358 from base 300001 (AL732358 Homo sapiens chromosome
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Homo sapiens chromosome 11 clone RP11-96012 map 11, LOW-PASS
SEQUENCE SAMPLING.
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1 (bases 1 to 62512) Brimates; Catarrhini; Hominidae; Homo.
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 11, clone RP11-96012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 29;
0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                      1103 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.6%; Score 22; DB 2; Best Local Similarity 100.0%; Pred. No. 7.4; Matches 22; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      vector_side:right"
40877 c 39993 g 62817 t
                           117292. 155491
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155592. 204160
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22804. .23139
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210000
310000
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AC103999.1 GI:17223287
HTG; HTGS_PHASE0
HOMO Sapiens
HOMO Sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.6%; Sc.
Best Local Similarity 100.0%; P:
Matches 21; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                         59370 a
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                                                                 misc_feature
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1749 1749 1759 Contrig of 673 bp in length 18167 18266 contrig of 673 bp in length 1822 19012 and 190 bp in length 1822 19013 gap of 100 bp in length 18022 19013 gap of 100 bp in length 19022 19033 contrig of 652 bp in length 19024 19739 gap of 100 bp in length 19034 20457; contrig of 683 bp in length 20458 20558 21240: contrig of 683 bp in length 20458 20501 contrig of 681 bp in length 20412 22111 gap of 100 bp in length 20412 22112 22111: gap of 100 bp in length 20412 2213 22501 contrig of 687 bp in length 22112 22801 gap of 100 bp in length 23565 gap of 100 bp in length 23565 gap of 100 bp in length 2452; gap of 100 bp in length 2517 25265 gap of 100 bp in length 2517 25265 gap of 100 bp in length 2518 2527 2527 contrig of 663 bp in length 2518 2527 2527 gap of 100 bp in length 2518 2527 gap of 100 bp in length 2518 2528 gap of 100 bp in length 2518 2527 gap of 100 bp in length 2528 2527 gap of 100 bp in len
9148 9771: contig of 624 bp in length 9772 9811: gap of 100 bp 10519 10618: gap of 100 bp 10519 10618: gap of 100 bp 11261: contig of 647 bp in length 11262 11361: gap of 100 bp 11362 12014: gap of 100 bp 11362 12014: gap of 100 bp 12015 12114: gap of 100 bp 12015 12114: gap of 100 bp 12015 12129: gap of 100 bp 1364 13563: contig of 658 bp in length 12793 12892: gap of 100 bp 13664 14328: gap of 100 bp 13664 14328: gap of 100 bp 14329 15989: gap of 100 bp 16999: gap of 16999 bp in length 15999: gap of 100 bp 16999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15867: contig of 669 bp in length 67; gap of 100 bp 10644: contig of 677 bp in length 44: gap of 100 bp 17393: contig of 649 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33519 33618: gap of 100 bp
33619 34274: contig of 656 bp in length
34275 34374: gap of 100 bp
34275 35024: contig of 650 bp in length
35025 35124: gap of 100 bp
35125 35783: contig of 659 bp in length
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36563: contig of 680 bp
63: gap of 100 bp
37338: contig of 675 bp
                                                                                                                                                                         11262 11361; gap of 11362 12014; contil 12015 12114; gap of 12115 12792; contil 12793 12892; gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15968 16644: cont. 16645 16744: gap of 17645 1749: cont. 17394 17493: gap of 17494 18166: cont. 18167 18266: gap cont. 18167 18266: gap cont. 1867
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v: gap of
15867:
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13564 13663:
13664 1438:
14329 14428:
15099 15099
15199 1598:
15186 15967:
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10619 112
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36564 36663:
36664 373
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35784 35883
              Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgaller, B., Barcaro, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgaller, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chastor, B., Choppel, Y., Colangelo, M., Campopiano, A., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreitz, P., Filzhugh, W., Gage, D., Galagan, J., Gardyna, S., Gord, S., Goyette, M., Graham, L., Grand-Peire, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kanata, A., Kastas, A., Kalls, C., Lakocque, K., Lamazares, R., Landers, T., Lenders, T., Mencar, A., Kastas, A., Kalls, C., Lakocque, K., McCarlhy, M., McCarlhy, M., McEvan, P., McKernan, K., Morbeefers, R., Mathriwy, C., McCarlhy, M., McEvan, P., McKernan, K., Morbeefers, R., Mathrim, J., Morbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Stance, B., Stange-Thomann, N., Stolanovic, N., Strauss, N., Subramanian, A., Kank, M., Travis, N., Wyman, D., Ye, W.J., Young, G., Shhmitted, (nl. DRC.) (nl. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (01-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This record contains 82 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. Will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L21922
Center clone name: 96_0_12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         674 773; gap of 100 bp 774 1448; contig of 675 bp in length 1449 1548; gap of 100 bp 1549 2277; gap of 100 bp 1788 2277; gap of 100 bp 1788 2277; gap of 100 bp 1789 2279; gap of 100 bp 1789 pp 18897; contig of 610 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   00 bp
677 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6080: gap of 100 bp 6751: contig of 671 bp in length 6851: gap of 100 bp 7512: contig of 661 bp in length
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of 610 bp in length
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3764; gap of 100 bp
4429; contig of 665 bp in length
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666 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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5980: co
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8283: co
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4530 5195: co
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7512: '
       (bases 1 to 62512)
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JOURNAL
REFERENCE
                                            AUTHORS
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COMMENT

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Homo sapiens clone RP11-14M16, LOW-PASS SEQUENCE SAMPLING.
ACO22577
ACO22577
HTG 13-JUL-2000
corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL: Sw.; SWISSPROT; TI., TREMBL; Wp., WORMPEP: Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/HGP/Chrx
RP13-146A14 is from the library RPCI-13.1 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 86478) Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-14M16
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28;
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VECTOR: pBACe3.6.
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20519 a 11789 c 11900 g 19971
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /chromosome="X"
/clone="RP13-146A14"
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llarity 100.0%; Pr
Conservative 0;
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Best Local Similarity
Matches 21; Conserv
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SOURCE
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AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
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VERSION
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AC022577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (13-MAY-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on MAY 25, 2002 this sequence version replaced gi:20803513.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 64179)
Heath,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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100.0%; Pred. No. 28;
ive 0; Mismatches 0; Indels (
   39 37438; gap of 100 bp 38099; contig of 610 bp in length 3869; contig of 610 bp in length 3869; contig of 670 bp in length 3869; gap of 100 bp in length 42 3741; gap of 100 bp in length 41182; contig of 672 bp in length 615; gap of 100 bp in length 6182; gap of 100 bp in length 1282; gap of 100 bp in length 1282; gap of 100 bp in length 1283; gap of 100 bp in length 1284; gap of 100 bp in length 1285; contig of 652 bp in length 1285; gap of 100 bp in length 1285; contig of 652 bp in length 1285; contig of 653 bp in length 1285; gap of 100 bp in length 1285; contig of 675 bp in length 1285; gap of 100 bp in length 1285; contig of 675 bp in length 1285; contig of 675 bp in length 1285; contig of 675 bp in length 1286; gap of 100 bp in length 1286; ga
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49579: contig of 676 bp in length
49679: gap of 100 bp
50346: contig of 667 bp in length
50446: gap of 100 bp
51070: contig of 624 bp in length
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52571: contig of 660 bp in length
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human.

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

DEFINITION RESULT 16 AL627224

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ACCESSION

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Gaps

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us-09-782-874-1.oli.rge

TITLE COMMENT

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1985; gap or

44824: contig of 835 pr

44824: gap of 100 bp

45912: contig of 888 bp in length

45912: contig of 888 bp in length

46787: contig of 875 bp in length

3 4687: gap of 100 bp

8 47800: contig of 913 bp in length

31 47900: gap of 100 bp

64895: gap of 100 bp

796 48895: gap of 100 bp

8 49767: contig of 872 bp in length

796 4895: gap of 100 bp

8 49767: contig of 872 bp in length

8 6 49767: contig of 872 bp in length
      23255: contig of 860 bp in length 26 23255: contig of 860 bp in length 100 bp 242256: contig of 901 bp in length 100 bp 27 25267: contig of 871 bp in length 27 25267: contig of 871 bp in length 27 25267: contig of 871 bp in length 27 25267: contig of 875 bp in length 27 255: gap of 100 bp 27 25150: contig of 875 bp in length 27 255: gap of 100 bp 27 2515: contig of 897 bp in length 27 2525: gap of 100 bp 27 2525: gap of
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51918; contig of 905 bp in length
51918; gap of 100 bp
52792; contig of 874 bp in length
52892; gap of 100 bp
53779; contig of 887 bp in length
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42906: contig of 901 bp in length
4306: gap of 100 bp
43885: contig of 879 bp in length
43985: gap of 100 bp
44824: contig of 839 bp in length
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35090: contig of 875 bp in length
35190: gap of 100 bp
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34115: contig of 929 bp
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contig of 845 bp
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37002: con
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                                                              Genome
                                                                                                                                                                                                                                                                  Research
                                                              for
Zimmer, A. and Zody, M.

Direct Submission

Bubritted (NoFEB-2000) Whitehead Institute/MIT Center for

Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This record contains 88 individual
sequencing reads that have not been assembled into
contigor. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
voverlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
be preserved.
                                                                                                                                                                                                                                                                                                                 Web Site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------- project Information
Center project name: 13423
Center clone name: 14_M_16
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of 882 bp in length
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of 877 bp in length
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383 bp in length
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958 1852: contig of 895 bp in length

1853 1952: gap of 100 bp

1853 2811: contig of 859 bp in length

2812 2911: gap of 100 bp

2812 2911: gap of 100 bp
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of 862 bp in length
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2 7751: gap of 100
8643: contig of 8
8743: gap of 100
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5710: contig of 8
5810: gap of 100
6692: contig of 8
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17413: contig of
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20387: contig of
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9620: contig of
9720: gap of 10
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18415: con
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7651: cor
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Gaps

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2; Length 101706; 0; Indels

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RATURE

(Dases 1 to 122685)

MURATUD M., Adamas C., Adio-Oducla, B., Ali-osman, F.R., Allen, C., Adamas, C., Adamas, C., Ade., Oducla, B., Ali-osman, F.R., Allen, C., Adamas, C., Burkett, C., Carron, T.C., Carron, T.C., Carron, C., Coyle, M.D., Dethorne, S.R., David, R., Delaney, K.R., Harnandez, C., Harris, K., Delaney, K., Major, K., Parims, E., Pull, J., Delles, M., Major, K., Parims, E., Pull, J., Delect, S., Soctt, G., Pare, R., Parims, E., Pull, J., Delect, S., Soctt, G., Pare, R., Parims, R., Manier, S., Wallianson, A., Statek, A., Stanker, J., Taylor, C., Taylor, T., Telffods, M., Ten, M., Major, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACUSYNO2 122685 bp DNA linear HTG 12-JUL-2002 Rattus norvegicus clone CH230-183A24, *** SEQUENCING IN PROGRESS ***, 54 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                              Location/Qualifiers
1. .101706
1. .001706
.001816="Oryza sativa (japonica cultivar-group)"
.cultivar="Nupponbare"
.db.xref="taxon:39947"
./chromosome="2"
./chromosome="2"
.2928 c 22675 g 28253 t 151 others
                                                                                                                                                                                                                                                                                                                                                                                               DB 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.6%; Score 21;
Best Local Similarity 100.0%; Pred. No.
Matches 21; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 29464 AATTTTTTTTTTTATCTA 29484
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Rattus norvegicus
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                                                                                                                                                                                                                                                                                           27699 a
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DEFINITION
                                                                                                                                                                                                                                                                                           BASE COUNT
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AC099102
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KEYWORDS
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Tel:81-298-38-7441, Fax:81-298-38-7468)
The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a "working draft' sequence."
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Clone:OJ1067_B01.
Clyrza sativa (japonica cultivar-group)
Eukayota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea.
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OJ1067_B01, *** SEQUENCING IN PROGRESS ***, in ordered pleces.
AP004079
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Orgas astitva nipponbare(GA3) genomic DNA, chromosome 2, BAC clone:OJ1067_B01

Published Only in Database (2001)

2 (bases 1 to 101706)

Sasaki,T., Matsumoto,T. and Yamamoto,K.

Direct Submission
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                                   $8897; contig of 877 bp in length 1988 $897; gap of 100 bp 59551; contig of 854 bp in length 552 $9851; gap of 100 bp in length 152 $9851; gap of 100 bp in length 152 $6173; contig of 892 bp in length 1823; gap of 100 bp in length 1824 $62748; contig of 892 bp in length 1824 $62748; contig of 892 bp in length 1824 $62748; contig of 892 bp in length 1825; gap of 100 bp in length 1825; contig of 879 bp in length 1825; contig of 879 bp in length 1825; contig of 879 bp in length 1825; contig of 857 bp in length 1825; contig of 868 bp in length 1825; contig of
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8897: gap of 8.
59751:
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69656: ~...
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HTG; HTGS_PHASE2.
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tes 21; Conserv
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TITLE
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COMMENT

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of 2505 bp in 1
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of 1652 b
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of 1895 b
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of 1416 b
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unknown lof 1272 b
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unknown of 1870 k
unknown of 1575 k
unknown of 1575 k
unknown of 2499 k
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of 2051 k
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of 2160 k
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of 1529 b
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of 31791
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Direct Submission

Submitted (12-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 11, 2002 this sequence version replaced gi:20976259.

Center: Baylor College of Medicine

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Center: Project Information

Center project In
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NOTE: This is a 'working draft' sequence. It currently consists of 54 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                          Direct Submission
Submitted (09-NOV-2001) Human Genome Sequencing Center, Department
Of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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Worley, K.C.
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                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Libert Submitted (27-JAN-1999) Sanger Centre, Hinxton, Cambridgeshire, Caudinited (27-JAN-1999) Sanger Centre, Hinxton, Cambridgeshire, Call 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Dec 19, 1998 this sequence version replaced gi:4007559.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequence with only a small overlap as described above.

This sequence is the entire insert of clone 960017. The true right end of clone 47R8 is at 100 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.sanger.cc.uk/HGP/ChrX 960017 is from the library RPCI5 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacper.med.buffalo.edu/ VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                             HS960017 129226 bp DNA linear PRI 23-NOV-1999 Human DNA sequence from clone 960017 on chromosome Xp11.21-11.22 Contains EST, CA repeat(DXS991), STS, GSS, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
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/note="match: GSS AQ024874"
4609. 4853
/note="LIME3 repeat: matches 5910. .6160 of consensus"
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Norde-"HALl repeat: matches 343. .524 of consensus"
7796. .3944
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Anche-"HALI repeat: matches 685. .820 of consensus"
5491. .5783
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                                                                       ch 0.6%; Score 21; DB 2; Length 122685; I Similarity 100.0%; Pred. No. 27; 21; Conservative 0; Mismatches 0; Indels 0
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/note="LIM4c_repeat; matches 1497. 1709
117249: gap of unknown length
122685: contig of 5436 bp in length.
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/db_xref="taxon:9606"
/chromosome="X"
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/clone_lib="RPCI-5"
1. .3727
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AL022166.1 GI:4034471
HTG; repeat polymorphism.
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Pavitt, R.
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                                                                            Query Match
Best Local Similarity
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117150
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                                                                                                                                                                                                                                                                                                     RESULT 20
HS960017/c
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VERSION
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AUTHORS
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// (10 Le ... M. M. / Lepeat: matches 1: ... 1970; Consensus 1. 1577.
// (10 Le ... L. 1577.
// (10 Le ... L. 1577.
// (10 Le ... L. 1592.
// (10 Le ... L. 1593.
// (10 Le ... L. 1593
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7note="L1Mhl0 repeat: matches 5765. .6319 of consensus"
14021. .14527 ------ 5789 .6284 of consensus"
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Anote="LiM4 repeat: matches 2851. .3019 of consensus" 7033. 7459

Anote="LiM4 repeat: matches 4387. .4834 of consensus" 7583. .7888

Anote="AluJo repeat: matches 1. .298 of consensus" 7800-7934

7890. .7934

7953. .8030
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'note="LIM1 repeat: matches 1815. .1832 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .1908 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .1769 of consensus"
                                                                                                                                                                                                 .4843 of consensus"
                                                                                                                                    .2530 of consensus'
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                                                                                                                                                                                                                                                                        6617. .6877 _______ matches 39. .298 of consensus 6878. .7031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .2748 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="AluSx repeat: matches 1. .295 of consensus" 3148. .13430 force="L1 repeat: matches 4789. .5073 of consensus" 1448. .14011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="L2 repeat: matches 2658. .2748 of consensus" 8084. .8359 //note="Luub repeat: matches 1. .288 of consensus" 8558. .8776
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'note="AluJb repeat: matches 1. .293 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oŧ
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/note="LLM1 repeat: matches 1398.
21415. .21515
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20912
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                                                                                                                                                                                                 matches 4632.
                                                                                                                                2340.
                                                                                                                                       matches
                                       491. .5581
/note="Single clone region"
                                                                                                                                              6199, .6397

/note-"LIM4 repeat: m 6505, .6616

/note-"LIM4 repeat: m 6617, .6817
                                                                                  // 10128 // 10128 // 100te="LIM4 repeat: 6199, .6307
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/note="LlM1 re
20620. .20912
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552 te="L1	- a c	, ä.	1110	96	e="I	(i) <del></del>	ote="LiPPAll repeat: matches 46876161 of consensus" 56027895	ī.,	· ⊷ ·	ote="L1M4 repeat: matches 27404562 of consensus" 15931561	ote="L1M4c repeat: matches 10442037 of consensus" 57535678	ote="LiPAi3 repeat: matches 24946151 of consensus" 57935990	obe="Alugg repeat: matches 1, .312 of consensus" 991, .38399	ote="LiPAl3 repeat: matches 10, ,2494 of consensus" 10838560	ote="LiM4c repeat: matches 9121066 of consensus"	occ35528 50 "LiMer repeat: matches 5771 of consensus" 9339954	ote="MER5A repeat: matches 10189 of consensus" 246. 41985	ote="LIMA8 repeat: matches 55426288 of consensus"	ovaor ote="MLTIF repeat: matches 403541 of consensus" 188 42321	120. 1212.1 2016 "Aludb repeat: matches 1137 of consensus" 113 .42583	The "MLTIF repeat: matches 268431 of consensus" 56 42850	ote="MLTIS" but="MLTIF repeat: matches 1293 of consensus"		WE		te="LiHS repeat: matches 14686146 of consensus" 22850835	e="match: STS L41742"	prement()1130>313 te="match: GSS AQ202 95 52406	חו עני	-"MLT11 repeat: ement(539505	-"match: STS G0386754513	"MLT1B repeat: matches 4.	
21855 /note	പോര	/note		/note 24891	110	not 509	/note 26560	/note= 27921	/note 28397	/note: 30159	/note 31575	/note	/note 35991	/note	/note	/note=7	/note:	/note='	/note	/note='	/note=	/note	/note:	note	a Äler	/note:	/note=		/note=	note Omp]	/note 54275	/note= 54610	/note
reg	repeat_region	creat_reg.	epeat redi	epeat_redi	at_reqi	t_reqi	epeat_regio	t regi	t_regi	eat_reg	repeat_region	t red	t_reqi	t reqi	l	t_regi	epeat redi	1 4	t redi	t regio	epeat regio	1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	4FC4-1-69-	at redi	featu	foatur	3C_1		isc_fe		repeat_region	

Medicago.

12 (Dases I to 131310)

Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Medicago truncatula BAC Clone mth2-13e5
Unpublished

12 (Dases I to 131310)

Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.

Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.

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The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA

Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.

Submitted (21-AUG-2002) Department of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA Medicago truncatula clone mth2-13e5, WORKING DRAFT SEQUENCE, 19
AC126008 GI:22380755
HTG: HTG 21-AUG-2002 Medicago truncatula Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnollophyta, eudicotyledons; core eudicots; Rosidae, eurosids I; Fabales; Fabaceae, Papilionoideae, Trifolieae, * NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. 2: contig of 2042 bp in length
2: gap of unknown length
3: contig of 2481 bp in length
3: gap of unknown length
3: gap of unknown length
4: contig of 2010 bp in length
5: contig of 2019 bp in length
5: gap of unknown length
6: contig of 2019 bp in length
7: contig of 2019 bp in length
7: gap of unknown length
7: contig of 2014 bp in length
7: contig of 2684 bp in length
7: contig of 3684 bp in length bp in length length bp in length length HTG; HTGS_PHASE1; HTGS_DRAFT.
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Length 129226; Indels

DB 9; 27;

Query Match 0.6%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 27; Matches 21; Conservative 0; Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135458 bp DNA linear HTG 18-JUL-2002 stattus norvegicus clone CH230-387J16, *** SEQUENCING IN PROGRESS AC117166
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Rodentia; Sciurognathi; Muridae; Murinae;
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43027 a 22119 c 22734 g 41572 t 1858 others
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O.6%; Score 21; DB 2; Length 131310;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 21; Conservative 0; Mismatches 0; Indels 0
  8: gap of unknown length
5: contig of 7227 bp in length
5: gap of unknown length
5: contig of 8920 bp in length
5: gap of unknown length
5: gap of unknown length
6: gap of unknown length
7: contig of 6486 bp in length
7: gap of unknown length
8: contig of 13886 bp in length
8: contig of 13894 bp in length
7: gap of unknown length
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/db_xref="taxon:3880"
/clone="mth2-13e5"
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HTG; HTGS_PHASE1.
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miner,G., Miner,2., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N., Ordeo,R., Newtson,S., Oguh,M., Okwuonu,G., Organye,N., Ovitedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Paul,L., Oulles,M., Ron,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherrs,S., Scott,G., Shen,H., Shoshtari,N., Sisson,I., Sodergren,E., Sonalke,T., Shen,H., Staniey,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tangy,H., Tansey,J., Taylor,C., Vera, V., Villalon,D., Vinson,R., Wangy,G., Warlliams,G., Walliamson,A., Washington,C., Watlington,S., Wulliams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Waishinston
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* NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morley, K.C.
Direct Submission
Submitted (08-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 135458)
Worley, K.C.
Direct Submission
Direct Submission
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Center clone name: GHZH-20-387J16
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 108275 bases at least Q30
Consensus quality: 113987 bases at least Q30
Consensus quality: 117413 bases at least Q20
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1752: gap of unknown length
2894: contig of 1142 bp in length
2994: gap of unknown length
4051: contig of 1057 bp in length
4151: gap of unknown length
6042: contig of 1891 bp in length
7419: contig of 1277 bp in length
7419: contig of 1277 bp in length
7519: gap of unknown length
7519: gap of unknown length
8897: contig of 1278 bp in length
1167: contig of 2570 bp in length
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Contact: hgsc-help@bcm.tmc.edu
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On Nov 8, 2000 this sequence version replaced gi:9795184.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL: Sw: SWISSPROT: Tr:, TREMBL: WP: WORNPEP: Information on the WORNPEP database can be found at heart sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 mapping Group. Further information can be found at http://www.sanger.ac.uk/HGPC/hr20

This sequence is the entire insert of clone RP4-606P22 The true left end of clone RP5-1140M3 is at 113895 in this sequence. The regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclones and the assembly was confirmed by the group of Pieter de Jong. For first than the subclone or more than one MI3 subclone; and the first fairs and accessions and repeats all regions were either double-stranded or sealure over the Jong-ED2 is from the first of the proper of the first of the group of Pieter de Jong. For the first of the proper of the
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//clone="P24-606P22"
//clone="1912"
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//clone=110="RPC1-4"
//mote="1018"
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note="Lime2 repeat: matches 5737. .5949 of consensus"
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/note="AluJo repeat: matches 42. .302 of consensus"
11416. .11571
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564. .8897
note="match: STS: Em:HSPF05F12"
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/note="LiMC/D repeat: matches 5399. .5522 of 8911. .9038
/note="64 copies 2 mer at 71% conserved" 9317. .9514
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11463. 11570
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http://www.chori.org/bacpac/home.htm
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/db_xref="taxon:9606"
/chromosome="20"
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Catarrhini; Hominidae; Homo.
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1 (bases 1 to 137723)
Steward.C.
Direct Submission
Submitted (105-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CBIO 15A, UK. E-mail enquiries; humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
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          13. gap of unknown length
25. contig of 2929 bp in length
25. contig of 3884 bp in length
26. gap of unknown length
27. contig of 3684 bp in length
28. gap of unknown length
28. gap of unknown length
29. contig of 4762 bp in length
29. contig of 4882 bp in length
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29. contig of 2283 bp in length
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29. contig of 2283 bp in length
29. contig of 10371 bp in length
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29. contig of 10373 bp in length
29. contig of 10373 bp in length
29. contig of 1033 bp in length
29. gap of unknown length
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29. gap of unknown length
29. contig of 10373 bp in length
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20. contig of 2833 bp in length
20. contig of 2833 bp in length
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/db_xref="taxon:10116"
/clone="CH230-387J16"
40755 a 25518 C 24639 g 41919 t
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AL034551.17 GI:11125134
HTG; KIAA0581; phospholipase; PLCB1.
human.
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TITLE
JOURNAL
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/note="MIR repeat: matches 21. .148 of consensus"
23832 .24499
23832 .24499
Anote="Match: GSS: Em:AQ029286
match: .25027
Anote="Links repeat: matches 5792. .6050 of consensus"
25067 .25131
/note="Links repeat: matches 6088 .6152 of consensus"
25132 .25456
Anote="Links repeat: matches 5701 .6152 of consensus"
25449 .2539
Anote="Links repeat: matches 5701 .6152 of consensus"
25449 .2539
Anote="Links repeat: matches 5701 .6152 of consensus"
2549 .2539
   // / 10521. / 10521. / 10521. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. / 10522. 
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Anote-"MIR repeat: matches 40. .262 of consensus" 31542. 31542. 31542.
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note="MIR repeat: matches 148. .260 of consensus"
12786. .23092
note="AluSx repeat: matches 1. .305 of consensus"
13093. .23229
mer atatat 67% conserved"
copies 6
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7.note=""Later and the state and stat
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC
clone:Oll102_DO9

Published Only in Database (2001)
2 (bases 1 to 138931)
2 sasaki,T., Matsumoto,T. and Yamamoto,K.

Direct Submission
Submitted (08-AUG-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kannondal
Agrobiological Libraki 305-8602, Japan
(E-mail:tasasakienlas affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaes; Oryza.
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Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
clone:011126_D09.
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OJ1126_D09, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
AP004023
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Pred. No. 27;
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/note="match: GSS: Em:AQ103099"
                                                                                           32523, .33151
/note="match: GSS: Em:AQ540822"
32533, .33003
                                                                Em: AQ785577"
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                                 32447. .32919
/note="match: GSS:
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The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. daps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers

irree | 1. 138931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRI 05-JUN-2002
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Submitted (19-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Submitted (13-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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AC110620
HZC10620.3 GI:21326423
                                                                                                                                                                                                                                                                                            /organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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Center code: WUGSC
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1 (bases 1 to 142234)
Sulston,J.E. and Waterston,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 138931;
                                                                                                                                                                                                                                                                                                                                                                                                      566 others
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Trani,L. and Kozlowicz,A.
The sequence of Homo sapiens BAC clone RP11-68317
Unpublished (2001)
3 (bases 1 to 142234)
Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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Pred. No. 27;
Mismatches C
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Genome Res. 8 (11), 1097-1108 (1998)
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30336 c 30692 g 37874 t
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Pred. No.
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100.0%; Pre
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4 (bases 1 to 142234)
Waterston, R.H.
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Waterston, R.
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Best Local Similarity 100.0
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AC110620
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Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                   NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 511-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphisms have been identified between AC084367 and AC110620.
Data from AC084367 was used to finish this clone, AC110620.
Location/Qualifiers
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1. .142234
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
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/rpt_family="AT_rich"
176. 400
/rpt_family="L1"
402. 630
/rpt_family="MER1_type"
654. 987
/rpt_family="L1"
1043. 1198
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'rpt_family="MER1_type"
437. .1578
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/clone_lib="RPCI-11"
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2007. . 2511
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581. .1876
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2874. .2975
/rpt_family="L1"
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/rpt_family="AT_rich"
10934. 11245
/rpt_family="Atu"
11881. 12615
/rpt_family="ERV1"
/rpt_family="BRV1"
/rpt_family="AT_rich"
/rpt=family="AT_rich"
/rpt_family="AT_rich"
/rpt=family="AT_rich"
/rpt=family="AT_rich"
/rpt=family="AT_rich"
/rpt=family="AT_rich"
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/rpt_family="GC_rich"

21376. 21471

/rpt_family="G-rich"

/rpt_family="G-rich"
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25123. .25244
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23500. .23629
/rpt_family="MER1_type"
23629. .23656
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33657. 239040
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/rpt_family="MER1_type"
24306. .24743
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'rpt_family="GC_rich"
1189. .21244
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/rpt_family="GC_rich"
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/rpt_family="Ll"
/rpt_family="MalR"
/rpt_family="Rall"
/rpt_family="Rall"
/rpt_family="Rall"
/rpt_family="Rall"
/rpt_family="Rall"
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5244. 6154
7rpt_family="L1"
6235. 6603
7rpt_family="L1"
6609. 6785
7rpt_family="ERVL"
6812. 7007
7rpt_family="ERVL"
7706. 7196
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23950. .2401
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10257. .10545
/rpt_family="Alu"
10810. .10837
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24762. 2/02
                                             /rpt_fanily="11"
/rpt_fanily="11"
/rpt_fanily="Alu"
4300. 4724
4300. 4724
4725. 5018
//rpt_fanily="11"
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/rpt_family="MIR"
25288. .25995
2976. .3321
/rpt_family="Alu"
3573. .3986
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Ruzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,

Ruzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,

Barbaria, J., Benton, J., Bulange, K., Blankenburg, K., Bondin, D.,

Bouck, J., Bowde, S., Barteva, M., Brown, E., Brown, M., Bryant, N.P.,

Bouck, J., Bowde, S., Barteva, M., Brown, E., Brown, M., Bryant, N.P.,

Bouch, J., Bowde, S., Barteva, M., Cavazos, S.R., Checko, J., Chavez, D.,

Carron, T.F., Carter, M., Cavazos, S.R., Checko, J., Chavez, D.,

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Carron, T.F., Davis, C., Davy-Carroll, L., Dederich, D. A.,

Davila, M.E., Delgado, O., Denn, A.L., Didn, Y., Didn, H.H.,

Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,

Earnhart, C., Edgar, D., Edwards, C., C., Eladj, C., Eladj, C., Protter, P., Frantz, P.,

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Ranis, A., Gao, J., Garcia, A., Garner, T., Garza, N., Glils, B.,

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Li, J., Li, Z., Lichtarge, O., Lidu, C., Liu, M., Loulseged, H.,

Lozado, R.J., Lichtarge, O., Lidu, C., Liu, M., Loulseged, H.,

Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Martindale, A., Martinez, E.,

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Moser, M., Necerson, E., Wwokenko, S., Oguh, M., Okwuon, G.,

Nguyen, N., Nickerson, E., Wwokenko, S., Oguh, M., Sisson, I.,

Rives, M., Rojas, A., Rojubokan, I., Robie, M., Tang, H.,

Scherer, S., Socott, G., Shen, H., Taborsh, Tangelisa, R., Tangelis, R., Tangelisa, R., Tangelisa, R., Tangelisa, R., Tangelis, R., Tangelis, R., Tangelis, R., Tangel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150055 bp DNA linear HTG 17-JUL-2002 Rattus norvegicus clone CH230-190K14, *** SEQUENCING IN PROGRESS Ax., 69 unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Pred. No. 27;
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27530 . 27528
/rpt_family="MER1_type"
25996. .26326
/rpt_family="Alu"
26327. .26352
                                                                                                                                                                                                                                                                                         /rpt_family="Alu"
27633. .27772
/rpt_family="L1"
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Best Local Similarity 100.0
Matches 21; Conservative
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Rattus norvegicus
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Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wieczyk, R., Wooden, S., Worley, K., Wu, Y., Wu, Y., Zhou, J., Zorrilla, S., Nelson, D., Neinstock, G. and Gibbs, R.

Neinstock, G. and Gibbs, R.

Direct Submission

AL Unpublished

SE (bases 1 to 150055)

Noley, K.C.

Direct Submission

AL Submitted (27-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Noley, K.C.

Direct Submission

AL Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 13, 2002 this sequence version replaced gi:18846337.

Center: Baylor College of Medicine

Center: Center code: BCM

Center: Daylor College of Medicine
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NOTE: This is a "working draft' sequence. It currently consists of 69 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Runny,D.W., Adams,C., Adio-Oduola,B., All-osman,F.R., Allen,C.,

Alabrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,

Barbaria,J., Benton,J. Bimage,K., Blankenburg,K., Bonnin,D.,

Bundy,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,

Carroon,T.F., Carter,M., Cavazos,S.R., Chackon,M.C.,

Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,

Chen,G., Chen,R., Chen,Z., Chowdhry,I., Duton,R.R.,

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Gabisi,A., Geo,J., Garner,H., Hauts,P., Hale,S., Hamilton,K.,

Harris,C., Harris,K., Hart,M., Harlay,P., Hammadez,J.,

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Harris,C., Harris,K., Hart,M., Harlay,P., Markin,C., Jackson,L.E.,

Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudh,S.,

Jang,Y., Li,L., Lichtage,O., Lieu,C., Liu,J., Liu,M., Martin,E.E.,

Massey,E., Mawhiney,E., McLeed,M., Martindale,A., Martinca,E.,

Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Moyen,M.,

Nayuen,N., Nickerson,E., Workenkoo,J., Newtson,N., Nguyen,N., Nguyen,N., Nayuen,N., Nayus,P., Nathor,S., Savery,G.,

Sodergen,B., Sonalker,P., Panerisa,A., Tamerisa,K., Tang,H.,

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Sutton,A., Syatek,A., Papukokan,I., Rolfed,B., Tommas,S.,

Sudmani,K., Vasquez,L., Tanker,R., Wooden,S., Worlley,R.,

Walliams,G., Williamson,A., Wileson,R., Wooden,S., Worley,R.,

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Walliams,G., Williamson,A., Wileson,R., Wooden,S., Woolley,R.,

Walliams,G., Williamson,A., Wileson,R., Wooden,S., Woolley,R.,

Direct Submission

Milliams,G., Williams,G.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                     0.6%; Score 21; DB 2; Length 150055; 100.0%; Pred. No. 27; 0; Indels 0
81753: gap of unknown length
81926: contig of 2173 bp in length
84026: gap of unknown length
86352: contig of 2326 bp in length
86452: gap of unknown length
89388: contig of 3486 bp in length
90038: gap of unknown length
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Rattus norvegicus.
Rattus norvegicus
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Rattus norvegicus clone CH230-302H2, *** SEQUENCING IN PROGRESS
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HTG: HTGS.PHASE1.
Rattus norvegicus.
Adammalia; Schordata; Craniata; Vertebrata; Euteleostomi;
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Submitted (16-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Pluston, TX 77030, USA
3 (bases 1 to 155859)
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NOTE: This is a 'working draft' sequence. It currently consists of 62 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Worley, K.C. Submission
Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor plaza, Houston, TX 77030, USA
On Jul 19, 2002 this sequence version replaced gi:20806243.
                                                                                                                                                                                                                     Center project name: GYLF
Center clone name: CH30-302H2
Center clone name: CH30-302H2
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.999329
Consensus quality: 105802 bases at least 040
Consensus quality: 112657 bases at least 020
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: project Information
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20901
20901
22706
23834
23834
23934
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Gaps

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LOCUS

RESULT 29 AC015953

ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

AUTHORS TITLE JOURNAL REFERENCE AUTHORS

REFERENCE

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05 4204: gap of contig of 2283 bp in length 08 6587: contig of 2283 bp in length 08 6587: contig of 1750 bp in length 100 bp pp 1781: contig of 1750 bp in length 08 11781: contig of 3344 bp in length 08 11881: gap of 100 bp 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114102 114201: gap of 100 bp 114202 134807: contig of 20606 bp in length 134808 134907: gap of 100 bp 100 bp 134908 155904: contig of 20997 bp in length. Location/Qualiflers
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: 3153 bp in length
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81 bp in length
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5045 bp in length
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38012: contig of 3485 bp in length
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6082 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4386: contig of 8181 bp in length 6: gap of 100 bp
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/clone_lib="RPCI-11 Human Male BAC"
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26029: contig of 3327 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8438. 11781
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14451. 19102
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19203. 22602
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26130. .29282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of
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vector_side:right"
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34428 34527: gap of
34528 38012: conti
38013 38112: gap of
38113 43120: conti
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64386: rorr
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43221 49302: cont
49303 49402: gap of
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71513 71612:
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State 155904)
Baldwin, "D. Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, "J. Barna, M., Beckerly, E., Booulalavki, L., Booukhgalter, B.,
Baldwin, "J. Castle, A., Colangelo, M., Collins, S., Collymore, A.,
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Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Direct Submission
Submitted (17-Nov-1999) Whitehead Institute/MIT Center for Genome
No Jun 28, 2000 this sequence version replaced gi:7382672.
All repeats were identified using Repeatwasker:
Smit, A.F.A., & Green, P. (1996-1999)
http://ftp.genome.washington.edu/RW/Repeatwasker.html
                                                                                                                                                                                                                    AC015953 155904 bp DNA linear HTG 28-JUN-2000 HOMO Sapiens chromosome 18 clone RPll-7M5 map 18, WORKING DRAFT SEQUENCE, 23 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 155904)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 18, clone RP11-7M5
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact project Information
Center project Information
Center project name: 1263
Center clone name: 7_M_S
Center clone name: 7_M_S
Center clone name: 7_M_S
Sequencing vector: M13; M7815; 100% of reads
Centerity: Dye-terminator: Big Dye; 93% of reads
Chemistry: Dye-terminator: Big Dye; 93% of reads
Chemistry: Dye-terminator: Big Dye; 93% of reads
Consensus quality: 144110 bases at least Q40
Consensus quality: 144110 bases at least Q20
Consensus quality: 149726 bases at least Q20
Consensus quality: 152136 bases at least Q20
Insert size: 153704; sum-of-contigs
Quality coverage: 4.0 in Q20 bases;
Consists of 23 contigs. The true order of the piaces
** is not known and their order in this sequence record is
** is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary, Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                AC015953
AC015953.4 GI:8783308
HTG: HTGS_PHASE1; HTGS_DRAFT.
HOMO: Sapiens.
Db 75430 TTTTTTTTTTTTTATCTAGT 75450
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TITLE JOURNAL

COMMENT

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Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Mai, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neat, D., Newtson, N., Nguyen, A., Nguyen, N., Ovidoo, R., Payton, B., Perey, J., Perez, I., Peters, L., Pickens, R., Prims, E., Payton, B., Peery, J., Perez, I., Peters, L., Pickens, R., Prims, E., Polito, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, R., Thomas, K., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, B., Vinson, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Wulliams, G., Williamson, A., Wilchen, R., Washington, C., Watlington, S., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "vorking draft' sequence. It currently

* consists of 63 contigs. The true order of the pleces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Worley, A.C.

Direct Submission

Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 11, 2002 this sequence version replaced g1:19224398.

Center: Genome Center

Center: Baylor College of Medicine

Center: Center: College of Medicine

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Direct Submission
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Of Molecular and Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 157759)
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Center clone name: CH230-14017
Center clone name: CH230-14017
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 105056 bases at least Q40
Consensus quality: 110211 bases at least Q20
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Adio-Oduola, B., Ali-osman, D., Banks, T., Barbaria, J., Benton, J., Bireva, M., Brown, E., Brown, M., Bryant, N.D., Bundy, C., Burerli, R.L., Byrd, N.C., Carron, T.F., Carrer, M., Cavazos, S.R., Chacko, J., Chavez, D., Cax, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Douthwaite, K.J., Earnbart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Garrell, J.H., Guevara, W., Ganrer, T., Garza, N., Gall, R., Gorrell, J.H., Guevara, W., Havlak, P., Hawes, A., Hennandez, J., Howard, S., Huber, J., Hawes, A., Hennandez, J., Jacobson, B., Jia, T., Johnson, R., Jolivet, S., Joudah, S., Karlsson, B., Alle, S., Huber, J., Hulyk, S., Hume, J., Johnson, R., Jacobson, B., Jacobson, B., Jacobson, B., Lucher, R., Lucier, R., Luna, R., Lucier, R., Lucier, R., Luna, R., Lucier, R., Luna, R., Lucier, R., Luna, R., Lucier, R., Lucier, R., Luna, R., Lucier, R., Lucier
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contig of 1154 bp in length

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contig of 146 bp in length

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contig of 1643 bp in length

gap of unknown length

contig of 1680 bp in length

contig of 1887 bp in length

contig of 1887 bp in length

contig of 1889 bp in length

contig of 1843 bp in length

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Anderson, S., Baldwin, J., Barna, N., Battlen, V., Beda, F.,

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Submitted (05-APR-2000) Whitehead Institute/MIT Center for Genome Submitted (05-APR-2000) Whitehead Institute/MIT Center for Genome Submitted (05-APR-2000) Whitehead Institute/MIT Center for Genome Nessearch, 320 Charles Street, Cambridge, MA 02141, USA

On May 22, 2000 this sequence version replaced gi:7417882.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158158 bp DNA linear HTG 22-MAY-2000 Homo sapiens chromosome 8 clone RP11-194B7 map 8, WORKING DRAFT ACCES. 11 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. (pases 1 to 158158)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo, sapiens chromosome 8, clone RP11-19487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21; DB 2; Length 157759;
Pred. No. 27;
0; Mismatches 0; Indels 0:
85869: contig of 2980 bp in length 85669: gap of unknown length 89739: contig of 3770 bp in length 99239: contig of 2890 bp in length 92829: gap of unknown length 92829: gap of unknown length 92846: contig of 2117 bp in length 95646: gap of unknown length 97784: gap of unknown length 97784: gap of unknown length 100890: contig of 3166 bp in length 100390: contig of 3166 bp in length 100390: gap of unknown length 104065: gap of unknown length 10635: contig of 2975 bp in length 106455: gap of unknown length 106455: contig of 2290 bp in length 11548: contig of 4149 bp in length 115697: contig of 4149 bp in length 115697: contig of 4149 bp in length
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HTG; HTGS_PHASE1; HTGS_DRAFT.
HOMO sapiens.
HOMO sapiens
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100.0%; Pred
0; N
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Best Local Similarity 100.
Matches 21; Conservative
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Homo sapiens.
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                                                    Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                         web site: http://www-seq.wi.mit.edu
web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Conter project information
Center clone name: 1944_B_7
Center clone name: 1944_B_7
Sequencing vector: M13: M77815; 100% of reads
Sequencing vector: M13: M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 152650 bases at least Q40
Consensus quality: 155710 bases at least Q30
Consensus quality: 155710 bases at least Q20
Insert size: 160000; agarose-fp
Insert size: 160000; agarose-fp
Consensus quality: 0.0000; agarose-fp
Consensus quality: 0.0000; agarose-fp
Consensus quality coverage: 5.0 in Q20 bases; sum-of-contigs
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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|Clone_lb="RPCI-11 Human Male BAC"
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|/note="assembly_fragment"
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/note="assembly_fragment"
2804. .4714
/note="assembly_fragment"
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/db_xref="taxon:9606"
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Direct Submission

Direct Submission

Submitted (01-02T-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Bircan, B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, Brown, A., Camarata, J., Campoplano, A., Chang, J., Chararo, B., Choepel, Y., Colangello, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Landerase, R., Landers, T., Landerasares, R., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Norman, C.H., O'Connor, T., O'Connell, P., O'Neil, D., Oliver, J., Peterson, R., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
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Homo sapiens chromosome 18, clone RP11-7K9, complete seguence.
ACO11155
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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1 (bases 1 to 158371)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 18, clone RP11-7K9
2 (bases 1 to 158371)
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Direct Submission

N. Bubmitted (16-OCT-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 158371)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen N., Brown, A., Camarata, J., Campopiano, A., Chang, J., Gook, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Govette, M., Galagan, J., Gand-Pierre, N., Hanges, B., Horton, L., Hullne, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lander, E., Manch, L., Mador, J., Marquis, N., Manchs, L., Mihova, T., McKernan, K., Major, J., Marquis, N., Mencus, L., Mihova, T., McKernan, K., Major, J., Marquis, N., Mencus, L., Mihova, T., Norman, C.H., O'Connor, T., O'Donnell, P., Mardin, J., Noylor, J., Rogan, J., Respack, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuber, S., Schuer, S., Schuber, S., Schuer, S., Schuber, S., Schuer, S., Schuber, S., Schuber, J., Zimner, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wuller, A., and Zody, M., Santos, B., Waller, A., and Zody, M., Santos, B., Stange-There, M., and Zody, M., Santos, B., Stange-There, M., and Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (17-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 17, 2002 this sequence version replaced gi:16152312.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/dosg/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 53 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                       Durest, Authorisation
Submitted (02-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                     Direct Submission Submitted (29-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: Plasmid;
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 114920 bases at least Q40
Consensus quality: 120930 bases at least Q20
Consensus quality: 124914 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2: contig of 1072 bp in length
2: gap of unknown length
5: gap of unknown length
6: contig of 1384 bp in length
6: contig of 1380 bp in length
6: contig of 1513 bp in length
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9: gap of unknown length
9: contig of 1059 bp in length
9: contig of 1059 bp in length
9: contig of 1131 bp in length
9: contig of 1131 bp in length
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contig of 1319 b
gap of unknown l
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Rattus norvegicus clone CH230-253D15, *** SEQUENCING IN PROGRESS
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Length 160083;

/organism~"Rattus norvegicus"

Location/Qualifiers

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11 MARLU AC091357 AC091357 A** SEQUENCING IN PROGRESS ***, AC091357 ó Eukaryota, Métazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; ö 0; Indels 0.6%; Score 21; DB 2; 100.0%; Pred. No. 27; tive 0; Mismatches Db 60031 TTTTTTTTTTTTATCTAGT 60011 AC091357.4 GI:21953953 HTG; HTGS_PHASE1. 581 TTTTTTTTTTTTTATCTAGT 601 Similarity 100.( Norway rat. Query Match Best Local Simil Matches 21; C VERSION KEYWORDS SOURCE ORGANISM DEFINITION TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS REFERENCE AUTHORS RESULT 34 AC091357 ACCESSION δ

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 77 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Gaps

RESULT 35 AP001802/c LOCUS DEFINITION

ORGANISM

ACCESSION VERSION KEYWORDS SOURCE JOURNAL REFERENCE

TITLE

AUTHORS

AUTHORS REFERENCE

TITLE JOURNAL

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39548. 71742.
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71843. 99207.
//octe="assembly_fragment"
99308. 117912.
//octe="assembly_fragment"
118033. 134993.
//octe="assembly_fragment"
139809. 139809
//octe="assembly_fragment clone_end:SP6 vector_side:right"
139900. 145501
//octe="assembly_fragment clone_end:Ty vector_side:left"
//octe="assembly_fragment clone_end:Ty vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168763 bp DNA linear HTG 10-JUL-2002
Rattus norvegicus clone CH230-7M2, *** SEQUENCING IN PROGRESS ***,
70 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                               117933 117932: contig of 2/365 bp in length 99208 99307: gap of 100 bp 117933 117932: contig of 18625 bp in length 117933 118032: gap of 100 bp 118032: gap of 100 bp 118032: gap of 100 bp 118033 134394: gap of 100 bp 134394 13499: gap of 100 bp 139990 139980: gap of 100 bp 139990 139990 145501: contig of 5512 bp in length 139990 145501: contig of 5512 bp in length 150057: 150156: gap of 100 bp 155057 150156: gap of 100 bp 155057 150156: gap of 100 bp 155057 150156: gap of 100 bp 165057 150156: gap of 100 bp 165097 150156: gap of 165097 150156: gap of 100 bp 165007 150156: gap of 100 bp 165
1 39447: contig of 39447 bp in length
39448 39547: gap of 100 bp
39548 71742: contig of 32195 bp in length
71743 71842: gap of 100 bp
71843 99207: contig of 27365 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1000 others
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27;
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0.6%; Score 21; DB
Best Local Similarity 100.0%; Pred. No. 27;
Matches 21; Conservative 0; Mismatches
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/note="assembly_fragment"
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                    EURATYCTA, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bass 1 to 15569)
S Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Hongosapiens 165,699 genomic DNA of 11q

Published only in Database (200)
E thattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Hongosapiens 165699
S Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fullyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission

Numatited (14-APR-2000) Masamira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

Lis-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, VRL:http://hpp.gsc.riken.go.jp/, On Aug 9, 2000 this sequence version replaced gi:8117473.

Center: RIKEN Genomic Sciences Center(GSC)
Contact: hattori@gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp/
Center rode: RIKEN
Web site: http://hpp.gsc.riken.go.jp/
Center project Information
Center project Information
                                                                                                                             AP001802 165699 bp DNA linear HTG 08-AUG-2000 HOMO Sapiens chromosome 11 clone RP11-100J10 map 11q, WORKING DRAFT SEQUENCE, 11 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: PCR products; 100% of reads chemistry: Dye-terminator ET-amersham; 100% of reads chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 162162 bases at least 040 consensus quality: 163565 bases at least 030 consensus quality: 163565 bases at least 030 consensus quality: 164699; sum-of-contigs (unsert size: 164699; sum-of-contigs (unlity coverage: 11.49x in 020 bases; sum-of-contigs
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Homo sapiens DNA, clone:RP11-100J10.
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Center clone name: RP11-100J10
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CE I (Dassel 1 to 168763)

Muzny, D.M., Admaratunge, H.C., AreJ.R., Ayele, M., Banks, T.,
Alsbrooks, S. L., Amaratunge, H.C., AreJ.R., Ayele, M., Banks, T.,
Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Burch, P., Burkett, C., Burtaell, K.L., Byrant, N.P.,
Barbaria, J., Burkett, C., Burch, E., Brown, B., Brown, C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Cox, C., Coyle, M.D., Dathorne, S. R., David, R.,
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Barnhart, C., Edgardo, O., Penn, A.L., Ding, Y., Duh, H.H.,
Douthwaite, K.J., Draper, H., Duyan-Rocha, S., Durbin, K.J.,
Barnhart, C., Edgardo, D., Edwards, C., Eladi, C., Bordic, R.,
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Lu, X., Ludgeson, R., Hogues, M., Hollows, J., C.,
Lu, J., Lu, X., Ludges, M., Martindale, A., Martinez, E.,
Massey, E., Mawhiney, E., Maltchell, T., Mohabbat, K., Morgan, M., Marsey, M., Ren, Y.,
Nguyen, N., Naclo, N., Newfson, N., Warden, G., Mane, G., Mane, G., Mane, G., Mane, G., Martine, E., Pull, L.L., Quiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojuboka, I., Rolfe, M., Stone, H.,
Sodergien, E., Sonakke, P., Tabote, Y., Stone, H., Shocker, M., Svatek, A., Tabot, T., Telffod, B., Thomas, N., Tanesy, J., Taylor, C., Taylor, T., Telffod, B., Thomas, N., Tanesy, J., Taylor, C., Yers, V., Villalon, D., Villans, N., Weinstook, S., Warthoore,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission

Direct Submission

Submitted (10-701-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On 511 9, 2002 this sequence varsion replaced gi:17941975.

Center: Baylor College of Medicine
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
Contact: hgsc.help@bcm.tmc.edu
Center project name: GCKQ
Center project name: GCKQ
Center project name: CRQ
Center clone name: CR230-7M2
Center clone name: Tatistics
Sequencing vector: Plasmid;
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2 (bases 1 to 168763)
Worley, K.C.
                                                                       (bases 1 to 168763)
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 70 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as Thus of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                     1194: contig of 1194 bp in leng 1294: gap of unknown length 4034: contig of 1079 bp in leng 2473: contig of 1079 bp in length 4034: contig of 1561 bp in length 4034: gap of unknown length length 5583: gap of unknown length 10390: contig of 1340 bp in length 7013: contig of 1430 bp in length 874: gap of unknown length 10390: contig of 1661 bp in length 10390: gap of unknown length 1040: gap of unknown length 1040: gap of unknown length 1242: contig of 1852 bp in length 1420: contig of 1852 bp in length 1430: gap of unknown length 1430: gap of unknown length 1430: gap of unknown length 1430: contig of 1185 bp in length 1541: contig of 1363 bp in length 1591: gap of unknown length 175: gap
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NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved
Hattori, M., Ishil, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission
Submitted (09-MAR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Kitasato Uniy., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@gsc.riken.go.jp,
URL:http://hqp.gsc.riken.go.jp/, Tel:81-42-778-9923,
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Contact: hattori@gsc.riken.go.jp/
Contact: pattori@gsc.riken.go.jp/
Contact project Information
Center project name: Humbrafil8
Center clone name: RP11-68317
Center project name: RP11-68317
Center project name: RP11-68317
Center project name: RP11-68317
Center project name: RP11-68317
Contact project name: RP11-89310
Consensus quality: 159730 bases at least Q40
Consensus quality: 159730 bases at least Q40
Consensus quality: 16878 bases at least Q30
Consensus quality: 16878 bases at least Q30
Consensus quality: 168302 bases at least Q30
Consensus quality: 169302 bases at least Q20
Insert size: 169596; sum-of-contigs
Quality coverage: 5.19x in Q20 bases; sum-of-contigs
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 171196)

Hattori,M., Ishi,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Matanabe,H. and Sakaki,Y.

Published Only in DataBase (2000)

2 (bases 1 to 171196)
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HOMO sapiens DNA, clone:RP11-68317.
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Hattori, M. Ishli,K., Toyoda,A., Taylor,T.D., Hong. Hondo.

Hattori,M. Tayda,T., Totodi,Y., Watanabe,H. and Sakaki,Y.

Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Homo sapiens genomic DNA

L. Published Only in DataBase (1999)

2. (bases 1 to 171853)

2. (bases 1 to 171853)

3. Hattori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,

Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission

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Tel:81-45-503-9111, Past.81-45-503-9170)

On Mar 16, 2001 this sequence version replaced gi:10130050.
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Machine Aria 199991

AC126420.

AC1
                                                                 171853 bp DNA linear PRI 06-MAR-2001
HOMO sapiens genomic DNA, chromosome 11q, clone:RP11-839D17,
AP000880
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Mus musculus clone RP23-153M4, WORKING DRAFT SEQUENCE, 30 ordered
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Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
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Homo sapiens
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199178 118993: contig of 9816 bp in length 118994 19033: gap of 100 bp 128220 128319: gap of 100 bp 128320 128320 136575: contig of 9126 bp in length 136320 136675: contig of 9126 bp in length 13676 136675: contig of 100 bp 136676 136677: contig of 7713 bp in length 14489 14588: gap of 100 bp 14489 150077: contig of 5489 bp in length 150078 150177: gap of 100 bp 156099 156777: contig of 5489 bp in length 156099 161857: contig of 4959 bp in length 156799 161857: contig of 4959 bp in length 16589 161957: gap of 100 bp 161857: contig of 3422 bp in length 16580 165779: contig of 3422 bp in length 16580 165879: contig of 100 bp 16580 165879: contig of 100 bp 16580 165879: contig of 100 bp 16581 16581 165879: contig of 100 bp 168414 168413: gap of 100 bp 168415 169534; gap of 100 bp 168415 1695
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74381 74460: gap of 100 bp 74481 74461: gap of 100 bp 74481 77561: gap of 100 bp 77462 77561: gap of 100 bp 77562 89014: contig of 11453 bp in length 77562 89014: contig of 11453 bp in length 89015 89114: gap of 100 bp 100 bp 1000867 100086: contig of 1072 bp in length 100887 100986: gap of 100 bp 116991 117990: gap of 100 bp in length 115991 117990: gap of 100 bp in length 115504 15503: contig of 18413 bp in length 115504 15503: contig of 18413 bp in length 115504 15503: contig of 100 bp in length 15504 157463: contig of 100 bp in length 17464 177453: gap of 100 bp in length 17464 177454: contig of 482 bp in length.
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                                                                                                                                                     gap of 100 bp 5
51: contig of 2129 bp in length
                                                                                                                                                                                                       0 bp
259 bp in length
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30: contig of 1555 bp in length
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/db_xref="taxon:10090"
/clone="Rp23-153M4"
/clone=lb="RPCI-23 Female Mouse BAC"
1. 2956
/note="assembly_fragment
                                                                                                                                                                                                                                                         100 bp
       58789: gap of 100 bp
61160: contig of 2371
61260: gap of 100 bp
63311: contig of 2051
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72725: contig of 2115
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/note="assembly_fragment"
4230. _5714
/note="assembly_fragment"
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6176, 48108
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note="assembly_fragment"
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note="assembly_fragment"
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/note="assembly_fragment"
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70510: cont
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McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Mulphy, T., Naylor, J., Naylor, J., Norbu, C., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., Pulch, R., Stange, T., Ratca, R., Rase, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Tarvers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Labek, L., Zimmer, A. and Zody, M.

Submitted (Ob-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

Conter: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 2957 3056: app of 100 bp

* 3057 4129: contig of 2956 bp in length
4130 4239: gap of 100 bp

* 4230 5715 5814: gap of 100 bp

* 7319 7418: gap of 100 bp

* 7419 8623: contig of 1504 bp in length

* 8624 1015: contig of 1205 bp in length

* 8623: contig of 1205 bp in length

* 8624 1015: contig of 1205 bp in length

* 8624 1015: contig of 1205 bp in length

* 8724 1015: contig of 1205 bp in length
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Center clone name: L53_M_4
Center clone name: 153_M_4
Sequencing vector: Plasmid: no. 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Censensus quality: 162284 bases at least Q40
Censensus quality: 171255 bases at least Q30
Censensus quality: 171255 bases at least Q20
Insert size: 183000; agarose-fp
Insert size: 172345; sum-of-centigs
Quality coverage: 4.8 in Q20 bases; sum-of-centigs
Quality coverage: 5.1 in Q20 bases; sum-of-centigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
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Web site: http://www-seq.wi.mit.edu
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52640: contig of
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14823: cont
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Homo sapiens clone RP11-44J17, WORKING DRAFT SEQUENCE, 7 unordered
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
                                                                                                                               Gaps
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AC009420.3 GI:14150911
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
HOMO Sapiens.
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                                                                        0.6%; Score 21; DB 5
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iive 0; Mismatches
48001 a 42063 c 41121 g 45849
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                                                                           Query Match 0.6%
Best Local Similarity 100.0
Matches 21; Conservative
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AC009420
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KEYWORDS
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Homo sapiens genomic DNA.

Leatorilshed only in DataBase (2000)

E (Dases 1 to 177034)

E (Sassing A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission

E Submitted (04-Add-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

I T-22 Suehiro-chou,Tsurum! *Ku, Yokohama, Ranagawa 230-0045, Japan 17-22 Suehiro-chou,Tsurum! *Ku, Yokohama, Ranagawa 230-0045, Japan Tel:81-445-503-9111, Fassill-445-503-9170)

I Docation/Qualifiers
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HOMO Sapiens genomic DNA, chromosome 11q, clone:RP11-159N11, complete sequences.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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O.6%; Score 21; DB 2; Length 175245;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 21; Conservative 0; Mismatches 0; Indels 0
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Homo sapiens
                    66023. .68151

/note="assembly_fragment"

68252. .70510

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70611. .72725

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72826. .74380

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77562. .89014

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56023. .68151

    177034
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    /db_xref="taxon:9606"
    /chromosome="11"

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Mus musculus clone RP23-382N7, WORKING DRAFT SEQUENCE, 14 ordered
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-382N7
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
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               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
not known and their order in this sequence record is
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53222 53321; gap of 100 bp
53322 54413; contig of 1092 bp in length
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AC109179.2 GI:20336065
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus.
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Anderson.S., marra.N., Basteinny, Boqualavkiy, D., Bounkalter, B., Gooka, Gooden, C., Cooka, Cooke, D., Cooke,
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AP001934
INDEAD DNA linear HTG 30-MAY-2000
DNAFT SEQUENCE, 36 unordered pieces.
AP001934.
AP001934.2 GI:8117581
AP001934.2 GI:8117581
HTG; HTGS_PHAREI; HTGS_DRAFT.
HTG; HTGS_PHAREI; HTGS_DRAFT.
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EUKaryord: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
All (bases 1 to 179281)
EUSiyana, A., Yada, T., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
HOMO sapiens
Hattori,M., Ishi,K., Totoki,Y., Watanabe, H. and Sakaki,Y.
Direct Submission
AL Euliyama, A., Yada, T., Totoki,Y., Watanabe, H. and Sakaki,Y.
Direct Submission
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                                                                                                                                                                              Length 179025;
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16532 bp in length
15685 bp in length
14893 bp in length
13572 bp in length
5960 bp in length
                                                                      1306 others
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Contact: hattori@gsc.riken.go.jp/
Contact: project Information
Center project name: Humbraft18
Center clone name: RP11-711G5
                                                                                                                                                                          Query Match 0.6%; Score 21; DB 2; Best Local Similarity 100.0%; Pred. No. 27; Matches 21; Conservative 0; Mismatches
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vector_side:right" 56670 a 32505 c 32335 g 56209 t
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AP001934
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**NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be preserved.

1 1404 11503: gap of 11403 bp in length 11504 11503: gap of 1100 bp 111604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 11604 116
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7016- assembly_fragment.
3861. 45758
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4417	* 14/019 * 147119	4849	000	996	3158 3168	326	3491	5501	5665	5821 5831	5055	5065 5264	5274	5442	5562	5674 5684	* 168236 * 168336	9966	7093	7267	7277	7386	7541	7702	7814 7824	러근				reature I	sc_leature s	eature 4	misc_feature 6	misc_feature 7	misc_feature 9	misc_feature 9	misc_feature 1	misc_feature 1	misc_feature 1

Length 179281;

DB 2; 27;

Score 21; Pred. No.

0.6%; 8

Query Match Best Local Similarity us-09-782-874-1.oli.rge

AC083994 LOCUS

REFERENCE

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* arbitrary Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 2630 229; app of 100 bp 2730 2903: contig of 174 bp in length 2504 3002; app of 100 bp 2730 2904; contig of 174 bp in length 4170 4269; app of 100 bp 2730 2904; contig of 100 bp 2730 2905: contig of 1231 bp in length 2005: contig of 7231 bp in length 2005: contig of 7231 bp in length 2005: contig of 7231 bp in length 2005: contig of 100 bp 2005: contig of 2005 bp in length 2005: contig of 2006 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vector_side:right"
34004 c 34091 g 55706 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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1. .181265
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCOSSY 181265 bp DNA linear HTG 15-JAN-2001 HOMO Sapiens clone RP11-222H22, WORKING DRAFT SEQUENCE, 13
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                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 181265) Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-222H22
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: sequence_submissions@genome.wi.mit.edu
Contact project Information
Center project Information
Center project name: 212,#22
Center clone name: 222,#22
Sequencing vector: Plasmid; name; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 175722 bases at least Q30
Consensus quality: 178722 bases at least Q30
Consensus quality: 179651 bases at least Q20
Insert size: 189000; agarose-fp
Insert size: 180065; sum-of-contigs
Quality coverage: 5.4 in Q20 bases; sum-of-contigs
Quality coverage: 5.7 in Q20 bases; sum-of-contigs
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     ö
     Indels
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Web site: http://www-seq.wi.mit.edu
0; Mismatches
                                                                                                                                                                                                                                                                                           AC083994
AC083994.2 GI:12229379
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                         Db 94307 GGAATATGGTCAGGTGTTTGT 94327
                                               QY 2329 GGAATATGGTCAGGTGTTTGT 2349
Conservative
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
21;
                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
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JOURNAL
Matches
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COMMENT

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Gaps

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1200 others

LOCUS DEFINITION

RESULT 45 AC113269

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS TITLE JOURNAL REFERENCE

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   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALETOR, Linton, L., Nubbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barran, N., Bastlen, V., Boquslawkiy, L., Boukhgalter, B., Entren, S., Linton, L., Nubbaum, C., Lander, J., Charato, B., Charato, B., Charato, S., Brand, S., Bastlen, V., Boquslawkiy, L., Boukhgalter, B., Erron, S., Choppell, Y., Collangolo, M., Clampoplano, A., Clangroblano, A., Clangroblano, A., Charato, B., Choopell, Y., Collangolo, M., Clangoplano, J., Cangoplano, S., Dadago, S., Faro, S., Faro, S., Farreir, P., Fitzhiqh, W., Gasp, D., Galsgan, J., Gardyna, S., Godd, S., Faro, S., Farreir, P., Fitzhiqh, W., Gasp, D., Galsgan, J., Gardyna, S., Godd, S., Faro, S., Farreir, P., Fitzhiqh, W., Gasp, D., Galsgan, J., Gardyna, S., Gardyna, S., Godd, S., Gardyna, J., Levine, M., Chang, J., Marchar, C., Manather, C., Macharae, M., Kells, C., Lancoque, K., Lamazares, N., Horton, L., Marchay, C., Macharae, M., Marchay, T., Naylor, J., Marchay, C., McCarth, M., McKerna, K., Malder, N., Marchay, C., McCarth, M., McKerna, K., Malder, Y., Naylor, J., Marchay, C., McCarth, M., Roy, A., Santos, R., Schauer, S., Schauer, S., Schauer, J., Robert, M., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Robertson, S., Spencer, B., Stange-Thomann, V., Stojanovic, M., Stranss, M., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wiwan, D., Ye, W.J., Yassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wiwan, D., Ye, W.J., Yassillev, H., Allen, N., Allenn, M., Anderson, S., Brown, L., Chongoplano, R., Changolano, A., Changolano, A., Chang, J., Characto, B., Brown, L., Changer, E., All, A., Allen, N., Anderson, S., Barrei, B., Linton, L., Walman, M., Characto, B., Gard, E., Marchi, M., Characto, B., Gard, P., Chongell, Y., Collangelo, M., Collins, S., Collymore, R., Chock, P., Chongell, Y., Collangelo, M., Collins, S., Collymore, R., Chock, P., Chongell, Y., Collongolo, M., Collins, S., Characto, S., Berreir, B., Hagos, B., Lebotzeky, M., Marchy, M., Marchy, M., Marchy, M., Marchy, M., Marchy, M., Marchy
                                                                                                                                                                                                                              AC113269 183951 bp DNA linear HTG 06-JUN-2002 Mus musculus clone RP23-372F2, WORKING DRAFT SEQUENCE, 13 ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 183951)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-372F2
                                                                                                                                                                                                                                                                                                                                 AC113269
AC113269.3 GI:21327574
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
                                         QY 1941 AATCAGACAACATAAAGTTAG 1961
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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TITLE JOURNAL

REFERENCE AUTHORS

TITLE JOURNAL

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Center: Whitehead Institute/ MIT Center for Genome Research
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 6, 2002 this sequence version replaced gi:21313780.
All repeats were identified using RepeatMasKer:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                               Center project name: 120332
Center clone name: 372_F_2
Centering vector: Plasmid: na; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 181016 bases at least Q40
Consensus quality: 182175 bases at least Q20
Insert size: 182000; agarose-fp
Insert size: 182751; sum-of-contigs
Quality coverage: 7.9 in Q20 bases; sum-of-contigs
Quality coverage: 7.9 in Q20 bases; sum-of-contigs
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3550 35749; gap o.
3570 55284: contig of 19535 ~r
55285 55384: gap of 100 bp
55385 74290: contig of 18906 bp in length
74291 74390; gap of 100 bp
74291 98334: contig of 23944 bp in length
                                                                                                                                                                                                                       127343 127442: gap of 100 bp 127443 148645: contig of 21203 bp in length 148646 148745: gap of 100 bp 100 bp 148746 183951: contig of 35206 bp in length. Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304: gap of 100 bp 35649: contig of 10345 bp in length 49: gap of 100 bp 55284: contig of 19535 bp in length
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8861 10331: contig of 1471 bp in length

10332 10431: gap of 100 bp

10432 11525: contig of 109 bp in length

11526 11625: gap of 109 bp

11626 13553: contig of 1928 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13554 13653: gap of 100 bp 13554 2393; contig of 6740 bp in length 20494 20493: gap of 100 bp 20494 25204: contig of 4711 bp in length
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1. .8760
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PRI 26-JAN-2002
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1 (bases 1 to 185148)

1 (bases 1 to 185148)

Sauly.R.v., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Phelps,R.A., Raymond,C. and Haugen,E.D. Direct Submissined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 185148)
Kaul, R.K., Olson, M.V., Raymond, C., Clendenning, J. and Haugen, E.D.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (26-JAN-2002) Genome Center, University of Washington,
Box 35145, Seattle, WA 98195, USA
On Jan 26, 2002 this sequence version replaced gi:15668078.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (19-SEP-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA

3 (bases 1 to 185148)

Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nocypota
Homo sapiens chromosome 1 clone RP11-361K17, complete sequence.
AC096641 AL445987
AC096641.2 GI:18376908
HTG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 183951;
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Center Code: UWGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1221 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.genome.washington.edu
Contact: uwgchtge@u washington.edu
Drafting Center: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: chr-1
center clone name: RP11.361K17 (sc0678)
--------- Summary Statistics
Sequencing vector: plasmid; 50% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.6%; Score 21; DB 2; Best Local Similarity 100.0%; Pred. No. 26; Matches 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            vector_side:right"
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                                                                                                                                                                                                                                                                                                                                                                                                           clone_end:T7
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misc_feature
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VERSION
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REFERENCE
AUTHORS
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AC096641
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AUTHORS
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This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mi3 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                  This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.

Base-by base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
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Sequencing vector: plasmid; L08752; 50% of reads Chemistry: Dye-terminator ET; 80% of reads Assembly program: Phrains of big Dye; 20% of reads Assembly program: Phrains version 0.990319 Consensus quality: 184740 bases at least Q40 Consensus quality: 185096 bases at least Q30 Consensus quality: 1851046 bases at least Q20 Insert size: 186166; sum-of-contigs Quality coverage: 8.4x in Q20 bases; sum-of-contigs
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misc_feature

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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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source FEATURES

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* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "vorking draft' sequence. It currently

* consists of 66 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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Contact: hgsc-help@bcm.tmc.edu
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Rattus norvegicus clone CH230-7B13, *** SEQUENCING IN PROGRESS ***,
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Submitted (30-7010-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Rattus norvegicus
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Query Match
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Contact: sequence_submissions@genome.wi.mit.edu

DD 97976 TCAGGAAAGTGAAGGACAAAG 97956

Muneeler, J., Wai, X., Wyman, D., Ye, W.J. and Zody, M.

Direct Submission

Submitted (24-AuG-1999) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 19329)

Barra, M. Bastlen, V. Boguslavkiy, L. Boukhgalter, B. Brown, A.,

Canarata, J. Campopiano, A., Choepel, Y., Colangelo, M., Collins, S.,

Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,

Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Galagan, J.,

Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N.,

Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R.,

Jones, C., Karatas, A., LaRocque, K., Lancaraes, F., Landers, T.,

Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P.,

Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McGran, C. H.,

O'Connor, T., O'Donnell, P., O'Nell, D., Ollver, J., Peterson, K.,

Rieback, M., Raylor, J., Naylen, C., Robu, C., Retta, R.,

Rieback, M., Raylor, J., Naylen, S., Schupback, R., Seaman, S., Severy, P.,

Sougnes, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,

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Wilson, B., Wu, X., Wyman, D., Yassillev, H., Viel, R., Vo, A.,

Wilson, B., Wu, X., Wyman, D., Yassillev, H., Viel, R., Vo, A.,

Milson, B., Wu, X., Wyman, D., Yasyillev, H., Viel, R., Viel, R., Submitted (15-DEC-2000) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:

Sumit, A.F. A. & Green, P. (1996-1997) S Birran, B. Linton, L. Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Balman, V., Beckerly, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colagelo, M., Collins, S., Collymore, A., Castle, A., Cerny, J., Colagelo, M., Collins, S., Collymore, A., Cooke, P., Devarellano, K., Depayre, E., Devon, K., Dewar K., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, P., FitzHugh, W., Forrest, C., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGrnan, R., McLaughlin, J., Mohla, M., Morris, W., Morrow, J., Mychalecky, J., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stanger, Thomann, N., Stojanovic, N., Stojanovic, N., Stojanovic, M., Vassiliev, H., Vo, A., Wagner, A., Phinger, J., Wheeler, J., Whwell, Levil, L., Vassiliev, H., Vo, A., Wagner, A., Pricott, E., Milla, M. X., Myman, D., Ye, W.J. and Zody, M., Vo, A., Wagner, A., AC009466 193279 bp DNA linear PRI 15-DEC-2000 Homo sapiens chromosome 11, clone RP11-87N22, complete sequence. AC009466 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 193279)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 11, clone RP11-87N22 Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu AC009466.17 GI:11321807 Homo sapiens RESULT 49 AC009466 LOCUS DEFINITION ACCESSION VERSION KEYWORDS ORGANISM REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL SOURCE COMMENT

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1319. 13349

770F. family="L2"

complement(14968. 15042)

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770F. family="MR"
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Streen, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldavin, J., Barna, N., Bastren, V., Bastren, V., Bastren, V., Bastren, V., Bastren, V., Barket, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dlaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Grand-liere, N., Grand, G., Hagos, B., Haedroid, M., Grand, L., Hagos, B., Haedroid, M., Garats, R., Horber, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehocky, J., Helin, J., McCann, P., McGernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., Misconnal, P., Morrow, J., Murphy, T., Maylor, J., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Wurphy, T., Maylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., Ollvar, T.M., Ollver, J., Peterson, K., Pierre, N., Stange, Thomann, N., Stojanovic, N., Severy, P., Spencer, B., Stange, Thomann, N., Stojanovic, N., Severy, P., Spencer, B., Vasailiev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Voll, M., Lamer, M., Lander, J., All Mison, B., Wu, X., Wyman, D., Ye, Whither, M., Voll, R., Wilson, B., Willer, M., Wilson, M., Mison, M., Mayman, D., Yon, M., Wilson, B., May, M., Wilson, M., Mison, B., May, M., Mayman, M., Sandon, M., Zimmer, A. and Zoddy, M., Mison, B., May, M., Mayman, M., Sandon, M., Zimmer, A. and Zoddy, M., Mison, M., Myman, D., Myman, M., Mayman, M.
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Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 020781)
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5 Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, M., Bastien, V., Bloom, T., Boyuslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Hulme, M., Illev, I., Johnson, R., Jones, C., Kanat, A., Karles, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLenn, C., Macdonald, P., Major, J., Milova, T., Minova, T., Minova, T., Minova, T., Minova, T., Minova, T., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C., Peterson, K., Phunkhang, P., Pletre, N., Raymond, C., Retta, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, V., Stojanovic, N., Talamas, J., Peterson, M., Viel, R., Vo, A., Wilson, M., Wi
                                                                                                                                                                                                                                                                                                                 Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 202781)

Birren,B., Nusbaum,C. and Lander,B.

Mus musculus, clone RP23-15417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ...... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
musculus clone RP23-15417, *** SEQUENCING IN PROGRESS ***,
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------- Project Information
Center project name: L8049
Center clone name: 154_L_
                                                                                                AC055817 -
AC055817.5 GI:22123678
HTG: HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
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KEYWORDS
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Gaps
NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Tomato RNA-directe	Tomato RNA-directe	Tomato RNA-directe	Potato calmodulin	RACE PCR primer, G	RACE PCR primer, G	Tomato RNA-directe	Tomato RNA-directe	RACE PCR primer. G
QI QI	AAD04370			AAT18078	AAD04371	AAD04373			
DB	22	23	23	17	22	22	23	23	22
% Query Match Length DB ID	3731			906	25	25	25	25	25
% Query Match	100.0	100.0	93.7	0.8	0.7	0.7	0.7	0.7	0
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New nucleic acid molecules encoding polypeptides with RNA-directed RNA polymerase enzymatic activity, useful in modulating gene expression in plants, humans and animals, as well as in plant cell/tissue cultures or
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Sequence 3731 BP; 1064 A; 669 C; 849 G; 1149 T; 0 other;

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The sequence represents a crown encount. The niveral creation comprises the nucleic acid and protein of the invention. The protein of the invention can catalyse in vitro transcription can be either primed by RNA or DNA carealyse in vitro transcription can be either primed by RNA or DNA coligonucleotides or be unprimed. The protein may have cytostatic or virucide activities. The sequences of the invention may be used in gene therapy or as an RNA directed RNA synthesis inhibitor. The RGRP CDNA sequence and a template nucleic acid molecule derived from a nucleic acid molecule which causes a disease are useful for treating a disease caused by the undesired expression or overexpression of a nucleic acid molecule in a human, rat or mouse, by administering the molecules. This system can be used in the preparation of a pharmaceutical composition and for inhibiting expression of any desired gene by transferring the RRP system to organisms that either lack a comparable mechanism or do not sufficiently expression of any desired gene by transferring the rinhibitor to the protein are useful for inhibiting RNA directed RNA synthesis and for ensuring stable heterologous, gene expression in the control of gene expression as primers for amplification of nucleic acid molecules and as tools for the detection of expression of the CDNA molecules and as therapeutic agent for the mulans and animals and virus infersion of indesired gene expression in humans and animals and for inhumance and virus infersion of indesired gene expression of the antibody is useful for invention is an inferior. The control of cancer and virus infersion of indesired gene expression of the antibody is useful for invention and animals and animals and animals and animals and animals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid molecule encoding a polypeptide having the enzymatic activity of RNA-directed RNA polymerase, for modulating gene expression and treating cancer and virus infection in human and animals
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence represents a cDNA encoding the tomato RNA-directed RNA
                                                                                            Tomato; RGRP; RNA-directed RNA polymerase; in vitro transcription; cytostatic; virucide; RNA synthesis inhibitor; antibody; immunogen; transgenic plant; transgenic animal; cancer; viral infection; immunoprecipitation; immunolocalisation; ss; gene therapy.
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                                                    Tomato RNA-directed RNA polymerase (RdRP) cDNA
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                                                        GTIGTGATAATAAATTTGGTTGTGCTTCAGTTTCAGTCACTGCTGGGTAGTTTTTAT
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QY	28	TCCAAATGGAAGAACAATGATGGGATGTTTGGATGAATCCAGAACCTTGGAATATGGTCA 234
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VO dd	2341	GGTGTTTGTTCAGTTTACTGGTGCTGGACATGGAGAGTTTTCTGACGATTTACATCCATT 2400 
ò	40	TAATAACAGCAGATCCACCAAGAAATTTTATTTTTTTTTT
7 A	40	TARTARAGAGCAGATCCACCAACAGTAATTTCATTCTGAAGGGAAATGTGGTTGTTGCAAAAAAAA
QY	2461	AAATCCATGCTTGCATCCTGGTGATATTCGTGTTTTAAAGGCTGTAAATGTTCGAGCGC
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Oy	2521	GCACCACATGGTAGATTGTGTTGTATTCCCTCAGAAAGGAAAAAGACCTCATCCGAAT
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3 8	י נ	AIGITCIGGGAGIGGAITTIGGAGGGGGGATAICTACITIGTIGGGGGATCAAGACAIGAI 204
ογ	64	CCCGCCAAGGCAAGTCCAGCCGATGGAATATCCTCCAGCACCCAGCATACAGTTGGACCA 270
QQ	2641	CGCCAAGGCAAGTCCAGCCGATGGAATATCCTCCAGCACCCCAGCATACAGTTGGAC
δλ	2701	IGTCACAATTGAGGAAGTTGAAGAGTACTTCACCAACTATATTGTGAATGACA
q ₀	2701	TCACAATTGAGGAAGTTGAAGAGTACTTCACCAACTATATTGTGAATGACAGTT
QY	2761	GGAATCATAGCAAATGCCCATGTCGTATTTGCAGACAGAGAACCTGATATGGCCATG
qa	2761	SCCCATGTCGTATTTGCAGACAGAGAACCTGATATGGCCATGA
QY	2821	ATCCATGCAAAAAACTTGCTGAGCTCTTTTCAATTGCAGTGGACTTTCCAAAGAC
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ÓΫ	2881	TTCCCGCTGAAATACCATCTCAGTTGCGCCCTAAAGAATACCCAGACTTCATGGA
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Qy	2941	GACAAGACCAGCTATATCTCAGAAAGAGTTATTGGAAAGCTTTTCAGGAAAGT
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ΟY	3121	TATGACAAGCTGGGTAATTTAATGGACTACTATGGCATAAAAA
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                                                                 TCCCTGGTGTTTTATGACCAGCTAATCCAGATTAAGAAGGACAAAGCACGTAACAGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                 Tomato RNA-directed RNA polymerase (RdRP) cDNA from clone HF.
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This sequence represents a cDNA encoding the tomato RNA-directed RNA polymerase (RdRP/HF) of the invention. The invention comprises the nucleic acid and protein sequences of RdRP. The protein of the invention can catalyse in vitro transcription of short single stranded RNAs into can catalyse in vitro transcription of short single stranded RNAs into CDNA molecules, this transcription can be either primed by RNA or DNA oligonuclectides or be unprimed. The protein may have cytostation or virucide activities. The sequences of the invention may be used in gene therapy or as an RNA directed RNA synthesis inhibitor. The RdRP cDNA sequence and a template nucleic acid molecule which causes a disease are useful for treating a disease acid molecule which causes a disease are useful for treating a disease acid molecule which causes a disease are useful for treating a disease caused by the undesired expression or overexpression of a nucleic acid molecule in a human, rat or mouse, by administering the molecules. This system can be used in the preparation of any desired gene by transferring the system to organisms that either lack a comparable mechanism or do not sufficiently express their own RdRP. An antibody or an antagonist or inhibitor to the protein are useful for inhibiting RNA directed RNA synthesis and for menuing stable heterologus, gene expression in transgenic organisms. The sequence is useful for inhibiting to the control of gene expression, as primers for amplification of nucleic acid molecules and as thoraptericagened gene expression in humans and animals. The control of sequences are useful for infection in humans and animals and the antibody is useful for infection in humans and animals and the antibody is useful for infection or immunoprecipitation or immunological and the antibody is useful for infection in humans and animals and the antibody is useful for the indexer from the wild type RdRP sequence shown in the Pacellication but was created by the information shown in table 1.
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                                                                                                                                                                                                                                                                                             New nucleic acid molecule encoding a polypeptide having the enzymatic activity of RNA-directed RNA polymerase, for modulating gene expression and treating cancer and virus infection in human and animals -
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                                                                                                                                                                                                         Sanger
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                                                                                                                                    (WASS/) WASSENEGGER M.
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          CTCCAGCACCCAGCATACAGTTGGACCATGATGTCACAATTGAGGAAGTTGAAGAGTACT
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potato calmodulin
            Controlling growth and development of potato plants can be achieve by increasing or decreasing the expression of a gene encoding calmodulin. Transpente potato plants carrying sense nucleic acid constructs of p-PCM-1, a CDNA clone of potato calmodulin, exhibit increased shoot and tuber growth yet plants carrying antisense nucleic acid constructs exhibit decreased shoot and tuber growth.
ATGTAATAGGGTGTGATCATAAGAAAACTGTTATGCATTGTTGACTACCTTTTGTCTTTA
                                            3633 AAACTGCATGAAGCTGCAACATATATGCAGTACTCTAAGAAACAGATGTACAGCTAAGTA
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0.8%; Score 30; DB 17; Lengum ...
Pred. No. 0.00031; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 906 BP; 254 A; 151 C; 219 G; 282 T; 0 other;
                                                                                         Transgenic potato plants with increased stem and contain nucleic acid construct pPCM-1 comprising coding sequence in the sense direction
                                                                                                                                                                                                                                                                 Potato; calmodulin; gene expression; shoot; development; antisense; increase; decrease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takezawa D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAAGTACTAATATGTATGTGATTTGAGTTT 3716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/product= Calmodulin,
                                                                                                                                                                                                                                                                                                     Solanum tuberosum (Isolate p-PCM-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Columns 7-8; 14pp; English.
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                         BP,
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Conservative 0;
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                                                                                                                                                             078/c
AAT18078 standard; cDNA; 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Han T, Poovatah BW,
                                                                                                                                                                                                                                                                                                                                                                                                                                93US-0100874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-0100874
                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                     81..530
/*tag=
                                                                                                                                                                                                                                            Potato calmodulin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-159687/16.
P-PSDB; AAR81571.
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Best Local Similarity
Matches 30; Conserv
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                                                                                                                                                                                              AAT18078;
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                      3573
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3573
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Sanger HL;

Schiebel W,

97US-0811583. 97US-0811583

RIEDEL

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New nucleic acid molecules encoding polypeptides with RNA-directed RNA polymerase enzymatic activity, useful in modulating gene expression in plants, numans and animals, as well as in plant cell/tissue cultures or
                                                                                                                                                                                                                                                                                             Wassenegger M, Riedel L,
                                               Sycopersicon esculentum.
                                                                                                                                                                                                                                       (WASS/) WASSENEGGER M.
         PCR primer; RACE; ss.
                                                                                                                                                                                                                                                                                                                             WPI; 2001-289830/30.
                                                                                                                                                           05-MAR-1997;
                                                                                                                                                                                               05-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is RACE (rapid amplification of 5'-cDNA ends) PCR gene specific reverse (GSP) primer, GSP400, used to amplify a cDNA encoding tomato C-protein having RNA-directed RNA polymerase (RARP) activity. This protein is capable of RNA-directed RNA synthesis, thus using RNA as a template for synthesising complementary RNA molecules. RARP nucleic acid is useful for modulating gene expression in plants, humans and animals. This may lead to various physiological, developmental and/or morphological changes. Transgenic plants containing RARP nucleic acid is especially useful in plant cell or tissue cultures and in plant breeding. RARP is useful in gene therapy, particularly for treating a disease that is caused by the undesirable expression or overexpression of
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                                                                                                                                                                   Tomato; gene therapy; RNA-directed RNA polymerase; RdRP; gene expression; transgenic plant; tissue culture; plant breeding; therapy; C-protein; PCR primer; RACE; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tomato; gene therapy; RNA-directed RNA polymerase; RdRP; gene expression; transgenic plant; tissue culture; plant breeding; therapy; C-protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid molecules encoding polypeptides with RNA-directed RNA polymerase enzymatic activity, useful in modulating gene expression in plants, humans and animals, as well as in plant cell/tissue cultures or
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RACE PCR primer, GSP1200 to amplify tomato RdRP cDNA.
                                                                                                                             RACE PCR primer, GSP400 to amplify tomato RdRP cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sanger HL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25 BP; 10 A; 4 C; 7 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schiebel W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Column 20; 31pp; English.
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                 AAD04371 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD04373 standard; DNA; 25
                                                                                           (first entry)
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25; Conservative
                                                                                                                                                                                                                                             Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Riedel
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RIEDEL L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-289830/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wassenegger M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plants, humans
plant breeding
                                                                                                                                                                                                                                                                                 US6218142-B1.
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                                                                                           04-JUL-2001
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                                                         AAD04371;
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(RIED/)
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ID AAD0437
XX
XX
XX
DF 04-JUL
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KW TOMATO
KW TAMS9
AAD04371/c
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The present sequence is RACE (rapid amplification of 5'-cDNA ends) PCR gene specific reverse (GSP) primer, GSP1200, used to amplify a cDNA encoding tomato crprotein having RNA-directed RNA polymerase (RRRP) activity. This protein is capable of RNA-directed RNA synthesis, thus using RNA as a template for synthesising complementary RNA molecules. RARP nucleic acid is useful for modulating gene expression in plants, humans and animals. This may lead to various physiological, developmental and/or morphological changes. Transgenic plants containing RARP nucleic acid is especially useful in plant cell or tissue cultures and in plant breeding. RARP is useful in plant cell or tissue cultures and in plant disease that is caused by the undesirable expression or overexpression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tomato, RdRP, RNA-directed RNA polymerase; in vitro transcription; oytostatic, virucide; RNA synthesis inhibitor; antibody; immunogen; transgenic plant; transgenic animal; cancer; viral infection; RACE; immunoprecipitation; immunolocalisation; PCR primer; GSP400;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tomato RNA-directed RNA polymerase (RdRP) GSP400 PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
0.093;
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25 BP; 4 A; 5 C; 10 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.7%; Score 25; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 25; Conservative 0; Mismatches
                                                Example 3; Column 20; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2659 GCCGATGGAATATCCTCCAGCACCC 2683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 GCCGATGGAATATCCTCCAGCACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
AAS17838/c
ID AAS17838 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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plant breeding
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Sanger HL;

Wassenegger M, Riedel L, Schiebel W,

WPI; 2001-595798/67.

(WASS/) WASSENEGGER M. (RIED/) RIEDEL L.

08-FEB-2001; 2001US-0782874

Lycopersicon esculentum.

US2001023067-A1

97US-0811583

05-MAR-1997;

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This sequence represents the tomato RNA-directed RNA polymerase (RdRP) specific PCR primer (SS4400 used to to obtain the 5' and of the CDNA molecule using the rapid amplification of CDNA ends (RACE) technique. The invention comprises the nucleic acid and protein sequences of RdRP, the invention comprises the nucleic acid and protein sequences of RdRP, short single stranded RNAs into DNA molecules, this transcription of either primed by RNA or DNA molecules, this transcription of short single stranded RNAs into DNA molecules, this transcription of either primed by RNA or DNA molecules, this transcription can be invention may be used in gene therapy or as an RNA directed RNA synthesis inhibitor. The RGRP CDNA sequence and a template nucleic acid molecule which causes a disease are useful for treating a disease caused by the undesired expression or overexpression of a nucleic acid molecule in a human, rat or mouse, by administering the molecules. This system to ne used in the preparation of a pharmaceutical composition and for inhibiting expression of any desired gene by transferring the RdRP system to organisms that either case, a comparable mechanism or do not sufficiently express their own RdRP. An antibody or an antagonist or inhibition to the protein are netting the part of inhibiting man directed RNA synthesis and for sensions of the preparation of the principle of the princ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heterologous, gene expression in transgenic organisms. The sequence is useful for probes and/or for the control of gene expression, as primers for amplification of nucleic acid molecules and as tools for the detection of expression of the CDNA molecules. Additionally, nucleotide and protein sequences are useful for suppression of undesired gene expression in humans and animals. The RARP is useful as a therapeutic agent for the control of cancer and virus infection in humans and animals and the antibody is useful for immunopercupitation or immunoleculisation of the protein, identification of polypeptides interacting with it and screening expression libraries.
                                                                                                                                                                                                                                                                                                                                                    New nucleic acid molecule encoding a polypeptide having the enzymatic activity of RNA-directed RNA polymerase, for modulating gene expression and treating cancer and virus infection in human and animals -
                                                                                                                                                                                                                   Schiebel W, Sanger HL;
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                                  97US-0811583.
                                                                                                                                                                                                               Wassenegger M, Riedel L,
                                                                                                         WASS/) WASSENEGGER M.
RIED/) RIEDEL L.
                                                                                                                                                                                                                                                                                   WPI; 2001-595798/67
                                  05-MAR-1997;
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Gaps
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0.7%; Score 25; DB 23; Length 25; 100.0%; Pred. No. 0.093; lve 0; Mismatches 0; Indels
   Similarity 100.08; Pred. No. ...
                                                               1838 CCATCTGCTTTCCAGATTCGTTATG 1862
                                                                                  25 CCATCTGCTTTCCAGATTCGTTATG 1
Query Match 0.79
Best Local Similarity 100.(
Matches 25; Conservative
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Tomato, RGRP; RNA-directed RNA polymerase; in vitro transcription; eytostatic; virucide; RNA synthesis inhibitor; antibody; immunogen; transgenic plant; transgenic animal; cancer; viral infection; RACE; immunoprecipitation; immunolocalisation; PCR primer; GSP1200;
                                                                                                                                            Tomato RNA-directed RNA polymerase (RdRP) GSP1200 PCR primer.
RESULT 8
AAS17840/c
ID AAS17840 standard; DNA; 25 BP.
                                                                                                           08-MAY-2002 (first entry)
                                                                                                                                                                                                                                                        yene therapy; ss
                                                                       AAS17840;
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This sequence represents the tomato RNA-directed RNA polymerase (RdRP) specific PCR primer GSP1200 used to to obtain the 5' end of the cDNA obtain the 5' end of the cDNA specific PCR primer GSP1200 used to to obtain the 5' end of the cDNA obtain the 5' end of the cDNA modecules (RACE) technique. The invention comprises the nucleic acid and protein sequences of RdRP, the protein of the invention can catalyse in vitro transcription of Short single stranded RNAs into DNA molecules, this transcription of a cither primed by RNA or DNA oligonacledides or be unprimed. The protein may have cytostatic or virucide activities. The sequences of the cither primed by RNA or DNA oligonacledides or be unprimed. The protein may have cytostatic or virucide activities. The sequences of the cither primed by RNA or DNA sequence and a template nucleic acid molecule derived from a nucleic acid molecule which causes a disease are useful for treating a disease caused by the undesired expression or overexpression of a nucleic acid molecule in a human, rat or mouse, by administering the molecules. This system can be used in the preparation of a pharmaccutical composition and for inhibiting expression of any desired gene by transferring the RNAP system to organisms that either lack a comparable mechanism or do not sufficiently express their own RRPP. An antibody or an antagonist or inhibitor to the protein are useful for inhibiting RNA directed RNA synthesis and for ensuring stable of a ramplification of nucleic acid molecules and as tools for the control of cancer and virus infection in humans and animals. The RAPP is useful as a therapeutic agent for the control of cancer and virus infection in humans and animals. The RAPP is useful as a therapeutic amimals and the antibody is useful for immunolocalisation of the protein, identification of interacting with it and screening expression libraries.
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100.0%; Pred. No. 0.093;
Live 0; Mismatches 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 11; 34pp; English.
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ID AAD04372 standard; DNA; 25 BP.
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Matches 25; Conservative
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EX PX PX P
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05-MAR-1997;
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 20-SEP-2001.
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ABL64204/c
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                                                                                                                                                                                                                                                                                                                              The present sequence is RACE (rapid amplification of 5'-cDNA ends) PCR ence specific reverse (GSP) primer, GSP470, used to amplify a CDNA encoding tomato C-protein having RNA-directed RNA polymerase (RdRP) activity. This protein is capable of RNA-directed RNA synthesis, thus using RNA as a template for synthesising complementary RNA molecules. RdRP nucleic acid is useful for modulating gene expression in plants, humans and animals. This may lead to various physiological, developmental and/or morphological changes. Transgenic plants containing RdRP nucleic acid is sepecially useful in plant call of tissue cultures and in plant breeding. RdRP is useful in gene therapy, particularly for treating a disease that is caused by the undesirable expression or overexpression of
         Tomato; gene therapy; RNA-directed RNA polymerase; RdRP; gene expression;
transgenic plant; tissue culture; plant breeding; therapy; C-protein;
PCR primer; RACE; ss.
                                                                                                                                                                                                                                                   New nucleic acid molecules encoding polypeptides with RNA-directed RNA polymerase enzymatic activity, useful in modulating gene expression in plants, humans and animals, as well as in plant cell/tissue cultures or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tomato RNA-directed RNA polymerase (RdRP) GSP420 PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 24; DB 22; Length 25;
Pred. No. 0.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                         Sanger HL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 25 BP; 9 A; 9 C; 4 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                        Schiebel W,
                                                                                                                                                                                                                                                                                                           Example 3; Column 20; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1879 IGIGGGIGITGAICCGGAIICAIC 1902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 TGTGGGTGTTGATCCGGATTCATC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.08;
                                                                                                                          97US-0811583
                                                                                                                                                97US-0811583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS17839 standard; DNA; 25
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                                                                                                                                                                                                        Riedel L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24; Conservative
                                                      Lycopersicon esculentum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lycopersicon esculentum.
                                                                                                                                                                      (WASS/) WASSENEGGER M. (RIED/) RIEDEL L.
                                                                                                                                                                                                                              WPI; 2001-289830/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy; ss
                                                                                                                                                                                                        Wassenegger M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2001023067-A1
                                                                                                                                                                                                                                                                                     plant breeding
                                                                                                                       05-MAR-1997;
                                                                                                                                                3-MAR-1997;
                                                                            JS6218142-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAY-2002
                                                                                                  17-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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This sequence represents the tomato RNA-directed RNA polymerase (RdRP) specific PCR primer (SSA20 used to to obtain the 5' end of the cDNA colecule using the rapid amplification of CDNA ends (RACE) technique. The invention comprises the nucleic acid and protein sequences of RdRP, the invention can catalyse in vitro transcription of Short single stranded RNAs into DNA molecules, this transcription can be either primed by RNA or DNA oligonucleotides or be unprimed. The protein may have cytostatic or virucide activities. The sequences of the invention may be used in gene therapy or as an RNA directed RNA synthesis inhibitor. The RdRP CDNA sequence and a template nucleic acid molecule derived from a nucleic acid molecule which chauses a disease are useful for treating administering a disease caused by the undesired expression or overexpression of a nucleic acid molecule in a human, rat or mouse, by administering the molecules. This system can be used in the preparation of a pharmaceutical composition and for inhibiting expression of any desired gene by transferring the RdRP system to organisms that either lack. An antibody or an antagonist or inhibitor to the protein are useful for inhibiting RNA directed RNA synthesis and for ensuring stable useful for inhibiting RNA directed RNA synthesis and for ensuring stable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid molecule encoding a polypeptide having the enzymatic activity of RNA-directed RNA polymerase, for modulating gene expression and treating cancer and virus infection in human and animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heterologous, gene expression in transgenic organisms. The sequence is useful for probes and/or for the control of gene expression, as primers for amplification of nucleic acid molecules and as tools for the detection of expression of the cDNA molecules, Additionally, nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and protein sequences are useful for suppression of undesired gene expression in humans and animals. The RdRP is useful as a therapeutic agent for the control of cancer and virus infection in humans and animals and the antibody is useful for immunoprecipitation or immunolocalisation of the protein, identification of polypeptides interacting with it and screening expression libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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00.0%; Pred. No. 0.3;
ve 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                      Sanger HL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25 BP; 9 A; 9 C; 4 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                      Schiebel W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1879 TGTGGGTGTTGATCCGGATTCATC 1902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 11; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 TGTGGGTGTTGATCCGGATTCATC 1
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08-FEB-2001; 2001US-0782874.
                                                                                   97US-0811583
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                                                                                                                                                                                                                                                                                                                      Riedel
                                                                                                                                                                            (WASS/) WASSENEGGER M.
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-595798/67.
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                                                                                                                                                                                                                             (RIED/) RIEDEL
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to CDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host calls comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigen
                                                                                                                                                                                                             cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; lifertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss.
activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell carcinoma, infiltrating ductal cancer infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                Score 20; DB 24; Length 407; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human ovarian antigen HCORB20 cDNA, SEQ ID NO:1175.
                                                                                                                                                                                                                                                                                                                         Sequence 407 BP; 120 A; 98 C; 92 G; 97 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                          0.5%; Scur
100.0%; Pred
0; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1916 TIGAGAAGAGCATGICGAA 1935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      384 TIGAGAAAGAGCAIGICGAA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABQ55295 standard; cDNA; 786
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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ABQ55295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŝ
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01-NOV-2000; 2000US-245084P
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18-SEP-2000;
18-SEP-2000;
18-SEP-2000;
                                                                Homo sapiens.
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Soppet DR,
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treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmeorinoea), endocrine disorders, infertions (e.g., chlamwdia, HIV, toxoplasmosis, and toxic shock syndrome, ovarian cysts, and dysmeorinoea), inflammatory conditions (e.g., mastitis, oophoritis and againtis), immune disorders (e.g., congenital and acquired toxic shock syndrome, ophoritis, systemic lupus erythematosus), blood-related disorders (e.g., congenital and acquired immunodeficiencies, neurological disorders, gastrointestinal disorders and uninary system disorders. Ovarian antigen polypeptides and polymuleorides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polymuleorides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the contine may be used as food additives or to prepare antibodies contined to the present contined to the energy contined and phenotyping. The present contined to the present contined and phenotyping of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Non-typeable Haemophilus influenzae strain 3224A BASB205 DNA #7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 20; DB 24; Length 786; Pred. No. 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 786 BP; 184 A; 198 C; 190 G; 198 T; 16 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1916 TTGAGAAGGGCATGTCGAA 1935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 TTGAGAAAGAGCATGTCGAA 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASB205
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AAD38196/c
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The invention relates to non-typeable Haemophilus influenzae BASB205 polypeptides and polynucleotides. Sequences of the invention are used to treat non-typeable H. influenzae infections. They are also used as components of vaccines useful for treating infections preferably bacterial infections such as otitis media, pneumonia, sinusitis, nosocomial infections, invasive diseases, chronic otitis media with hearing loss, fluid accumulation in the middle ear, auditive nerve damage, delayed speech learning, infections of the upper respiratory tract and inflammation of the middle ear. The present sequence is non-typeable H. influenzae strain 3224A BASB205 DNA upstream region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human nucleic acid sequences from pancreatic tumors, and
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Pred. No. 32;
0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                  24; Length 1000;
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                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                Sequence 1000 BP; 288 A; 151 C; 256 G; 305 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                               O.5%; Score 20; DB Similarity 100.0%; Pred. No. 32; Ob. Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-621386/54.
P-PSDB; AAY73986, AAY73987, AAY73988
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             2414 TCCACCAACAGTAATTTCAT 2433
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Best Local Similarity 100.0
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Best Local Simi
Matches 20;
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WO200055199-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence encodes the TATA-binding protein (TBP) binding protein, designated TIP49, of the invention TIP49 and its associated nucleic acids and antibodies are useful in investigation of the process of DNA transcription control by TBP in vivo, and in detection of the blocking of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         TBP-binding protein with DNA helicase and ATPase activities - gene encoding it, and antibodies recognising it.
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Pred. No. 32;
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                                                                                                                                                                      TIP49; TATA binding protein; TBP binding protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.5%; Scc. 100.0%; Pred. No. c. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         Kishimoto T, Makino Y, Niwa S, Tamura T;
                                                                AAX18199 standard; cDNA to mRNA; 1730 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; Page 43-45; 64pp; Japanese,
                                                                                                                                                                                                                                                                                                                                                 (SUME ) SUMITOMO ELECTRIC IND CO
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                                                                                                                                                                                      DNA transcription control; ss.
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                                                                                                                                                                                                                                                                                             98WO-JP02836.
                                                                                                                     (first entry)
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                                                                                                                                              TIP49 coding sequence #2.
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                                     RESULT 15
AAX18199
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The invention relate to the isolation of genes AAC59215-C59261 encoding 47 human secreted proteins AAB27794-B27840. The genes can be used to generate fusion proteins by linking to the gene for the human immunoglobulin G Fc portion for increasing the stability of the fusion protein as compared to the human protein only. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and outber cancers of the adrenal gland, bone, bone marrow, breast, and other cancers of the adrenal gland, bone, bone marrow, breast, and other cancers of the adrenal gland, bone, bone condities, (c) candiovascular discons, allergies, autoimmune thyroiditis, diabetes mellitus, crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative collitis; (c) cardiovascular discorders such as myocardial ischaemias; (d) epilepsy; and (f) infections diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human regulatory molecule; HRM-1; cytostatic activity; immune modulator; transcription factor; enhancer; cell proliferation stimulation; cancer; treatment; microarray; detection; diagnosis; cell.proliferation disease; leukemia; lymphoma; myeloma; adenocarcinoma; sarcoma; bladder; bone; brain; lung; liver; ovary; skin; teratocarcinoma; immune response; allergy; asthma; diabetes; multiple sclerosis; Grave's disease; myasthenia gravis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition
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                                                                                                                                                                                                                                                                                                                                   Rosen CA, Ruben SM, Komatsoulis G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 343; 433pp; English.
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                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                   99US-0138598.
09-MAR-2000; 2000WO-US06014.
                                                                                    99US-0124095.
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Best Local Similarity 100.
Matches 20; Conservative
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                                                                                    12-MAR-1999;
                                                                                                                            11-JUN-1999;
03-DEC-1999;
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The present invention describes a complex (1) comprising a TIP49 family member and STAP1 (Skpl(a cyclin A-interacting protein)-associated ratio. Also described are: (1) a transcription regulatory complex comprising TIP48 and/or TIP49 and three or more proteins or polypeptides; (2) identifying an agent active against cancer cells that polypeptides; (2) identifying an agent active against cancer cells that with a test compound and measuring TIP49 ensymatic or ligand binding activity; and (3) an anti-cancer agent, preferably an anti-proliferative agent, particularly a nucleic acid or antibody identified by the method of (2). (1) has cytostatic activity, and can be used in transcription regulation. (1) can be used for screening new agents for the treatment arms.
                                                                                                                               Complex containing a TIP48 or a TIP49 family member and various other proteins is useful to screen for new agents to treat cancers that do not express \rm cMyc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.5%; Score 20; DB 24; Length 1750;
100.0%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1750 BP; 476 A; 403 C; 484 G; 387 T; 0 other;
(NOVS ) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIP49 from the present invention.
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                                                                                                                                                                                                                  Example 8; Fig 4; 34pp; English.
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2000US-0186350.
2000US-0189874.
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2000US-0214886.
2000US-0215135.
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2000US-0205515.
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                                         Gstaiger MGC, Krek W;
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                                                                               WPI; 2002-049448/
P-PSDB; ABB04982.
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
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18-APR-2000;
19-MAY-2000;
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28-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel human regulatory molecules (HRM) which have cytostatic activity and act as immune modulators, transcription factors or enhancers. The HRMS can be used to stimulate cell proliferation. Antagonists and agonists of the proteins of the invention can be used to treat cancer. The encoding nucleic acids can be used in microarrays to detect polynucleotides (and their expression levels) that encode HRMs in a biological sample. The HRMs and microarrays can be used diagnose, treat or prevent cell proliferation diseases especially cancer, e.g. leukemia, lymphoma, myeloma, adenocarcinoma, sarcoma, cancer of e.g. bladder, bone, brain, lung, liver, ovarry, skin, etc, teratocarcinoma, or to treat or prevent immune responses e.g. allergies, asthma, diabetes, multiple sclerosis, Grave's disease or myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, STAP1; Skp2; cyclin A-interacting protein; TIP48; TIP49;
Skp2-associated protein one; anti-cancer; anti-proliferative; cancer; cytostatic; transcription regulation; non-cMyc expressing cancer; ss.
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100.0%; Pred. No. 32;
iive 0; Mismatches 0; Indels (
                                                                                                                                                                                                 Guegler KJ, Hillman JL, Lal P;
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                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page 70-71; 76pp; English.
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/product= "TIP49"
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                                                                                                                                                                                                                                                                                                                    New human regulatory molecules
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hes 20; Conservative
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P-PSDB; AAW93945.
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Shah P, Yue H;
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    WO9915658-A2
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                                         01-APR-1999
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Matches
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17-NOV-2000; 2000US-0249215. 17-NOV-2000; 2000US-0249216. 17-NOV-2000; 2000US-0249217. 17-NOV-2000; 2000US-0249218. 17-NOV-2000; 2000US-0249245. 2000US-0241826. 2000US-0246417. 2000US-0246476. 2000US-0246476. 2000US-0246477. 2000US-0246477. 2000US-0246523. 2000US-0246524. 2000US-0246526. 2000US-0246526. 2000US-0246526. 2000US-0246527. 2000US-0246526. 2000US-0246526. 2000US-0246526. 2000US-0246527. 2000US-0246509. 2000US-0246509. 2000US-0246619. 2000US-0246619. 2000US-0246619. 2000US-0246619. 2000US-0246619. 2000US-0246619. 2000US-0246619. 17-NOV-2000; 2 17-NOV-2000; 2 17-NOV-2000; 2 17-NOV-2000; 2 17-NOV-2000; 2 01-DEC-2000; 2 05-DEC-2000; 2 05-DEC-2000; 2 05-DEC-2000; 2 06-DEC-2000; 2 06-DEC-2000; 2 

(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 27160; 3071pp + Sequence Listing; English.

AMK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or delactions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting

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the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases. especially cancers and cancer metastases of haematopoietic actived cells. AAK64703 to AAK87649 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK854942 to AAK874950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tomato; gene therapy; RNA-directed RNA polymerase; RdRP; gene expression;
transgenic plant; tissue culture; plant breeding; therapy; C-protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid molecules encoding polypeptides with RNA-directed RNA polymerase enzymatic activity, useful in modulating gene expression in plants, humans and animals, as well as in plant cell/tissue cultures or
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                                                                                                                                                                            DB 22; Length 38653;
                                                                                                                                         Sequence 38653 BP; 10472 A; 7264 C; 8237 G; 12680 T; 0 other;
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR primer; ss.
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Length 34;

DB 22;

Score 19;

0.58;

Query Match

Sequence 34 BP; 8 A; 15 C; 4 G; 7 T; 0 other;

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This sequence represents the tomato RNA-directed RNA polymerase (RdRP) specific PCR primer P127Baml used to clone the full length RdRP CDNA molecule of the invention. The invention comprises the nucleic acid and protein sequences of RdRP, the protein of the invention can catalyse in vitro transcription of short single stranded RNAs into DNA molecules, this transcription of short single stranded RNAs into DNA molecules, this transcription of about single stranded RNAs into DNA molecules, The sequences of the invention may be used in gene therapy or as an RNA directed RNA synthesis inhibitor. The RdRP CDNA sequence and a template nucleic acid molecule derived from a nucleic acid molecule which causes a disease are useful for treating a disease caused by the undesired expression or overexpression of a nucleic acid molecule which causes preparation of a pharmaceutical composition and for inhibiting expression of any desired gene by transferring the RdRP system to corganisms that either lack a comparable mechanism or do not sufficiently express their own RdRP. An antibody or an attagonist or inhibitor to the protein are useful for inhibiting RNA directed RNA synthesis and for protein are useful for inhibiting RNA directed RNA synthesis and for protein are useful for inhibiting RNA directed RNA synthesis and for protein are useful for inhibiting RNA directed RNA synthesis and for protein are properties.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ensuring stable heterologous, gene expression in transgenic organisms. The sequence is useful for probes and/or for the control of gene expression, as primers for amplification of nucleic acid molecules and as tools for the detection of expression of the CDNA molecules. Additionally, nucleotide and protein sequences are useful for is useful as a therapeutic agent for the control of cancer and virus insueful as a therapeutic agent for the control of cancer and virus infection in humans and animals. The RdRP insueful in humans and animals and the antibody is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid molecule encoding a polypeptide having the enzymatic activity of RNA-directed RNA polymerase, for modulating gene expressic and treating cancer and virus infection in human and animals
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   Tomato, RGRP; RNA-directed RNA polymerase; in vitro transcription; oytostatic, virucide; RNA synthesis inhibitor; antibody; immunogen; transgenic plant; transgenic animal; cancer; viral infection; RACE; immunoprecipitation; immunolocalisation; PCR primer; P127Baml;
                                      ö
                                                                                                                                                                                                                                                                                                                                                                          Tomato RNA-directed RNA polymerase (RdRP) P127Baml PCR primer.
                                   Indels
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0
                Pred. No. 95;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Page 12; 34pp; English.
100.08; PLY
0;
                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-FEB-2001; 2001US-0782874.
                                                                                 51
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                                                                                                                                                                                                                                       AAS17841 standard; DNA; 34
                                                                                                                                                                                                                                                                                                                                  (first entry)
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                Best Local Similarity 100.
Matches 19; Conservative
                                                                                   33 ACTCATCACTCCCCTCAAG
                                                                                                                            16 ACTCATCACTCCCCTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lycopersicon esculentum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Riedel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-595798/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2001023067-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIEDEL
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                                                                                                                                                                                                                                                                                    AAS17841;
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(RIED/)
                                                                                                                                                                                              RESULT 21
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BP

95

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'264/c
ABN67264 standard; DNA; 327
 113 ATGTCTTTTCTGATGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                           ABN67264/
                                                                          This invention describes a nucleic acid (I) with differential expression between tumour and normal cells and which has cytostatic activity. (I) work as modulators of Ras activity by inducing expression of tumour suppressor genes. (I), and polypeptides encoded by them, are useful as targets for diagnosis or therapy and in screening to determine the particularly for diagnosis and treatment of tumors, especially by modulating expression of (I) by gene therapy, antisanse RNA or ribozyme modulating expression of (I) by gene therapy, antisanse RNA or ribozyme polypeptides (by administration of the polypeptide or its activator, antication of many class II tumour suppressor genes (i.e. genes that are not primary targets for tumour-initiating mutations).

Chilaly 2. Aghlasize for tumour-initiating mutations).

Challely 2. Aghlasize for tumour-initiating mutations.
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immunoprecipitation or immunolocalisation of the protein, identification of polypeptides interacting with it and screening expression libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids differentially expressed between tumor and normal cells, useful for diagnosis or therapy of tumors and for screening active
                                                                                    Gaps
                                                                                                                                                                                                                                                                                          Differential transcription; human; rat; tumour cell; cytostatic; Ras modulator; Class II tumour suppressor gene; gene therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B, Schaefer R, Zuber J, Tchernitsa O;
Schmitz A, Sers C;
                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.5%; Score 19; DB 22; Length 255; 100.0%; Pred. No. 99; 1.ive 0; Mismatches 0; Indels
                                                          Length 34;
                                                                                                                                                                                                                                                                       Rat differential transcription-associated cDNA SEQ ID 412.
                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fragments described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 255 BP; 98 A; 47 C; 59 G; 51 T; 0 other;
                                                           23;
                                    Sequence 34 BP; 8 A; 15 C; 4 G; 7 T; 0 other;
                                                          DB 95;
                                                          Score 19; DB 2
Pred. No. 95;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (META-) METAGEN GES GENOMFORSCHUNG MBH.
                                                 0.5%; Scur.
100.0%; Pre
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                                                                                                                                                                     RESULT 22
AAH81903/c
ID AAH81903 standard; DNA; 255 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                               31-JAN-2000; 2000DE-1004102.
                                                                                                                       16 ACTCATCACTCCCCTCAAG 34
                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-2001; 2001WO-EP01003
                                                                                                            33 ACTCATCACTCCCCTCAAG 51
                                                                                                                                                                                                                                              (first entry)
                                                         Query Match 0.55
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosenthal A, Hinzmann B
Grips M, Hellriegel M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-483415/52.
                                                                                                                                                                                                                                                                                                                                                         WO200157058-A2.
                                                                                                                                                                                                                                              21-SEP-2001
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SS X 8
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus galactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5843 sequences (51), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN6604-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                           Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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100.0%; Pred. No. 99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 327 BP; 99 A; 57 C; 74 G; 97 T; 0 other;
                                                                                                                               Streptococcus polynucleotide SEQ ID NO 2441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Masignani V, Margarit Ros YI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Page 3395; 4525pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-OCT-2001; 2001WO-GB04789
                                                                   (first entry)
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(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                 Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-352536/38.
P-PSDB; ABP26633.
                                                                                                                                                                                                                                                                                                                                                                                                 WO200234771-A2.
                                                               01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     relford J,
Tettelin H;
ABN67264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local 9
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Gaps

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1758 ATGICTITICIGATGGAAT 1776

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19; Conservative

Best_Local Similarity Matches 19; Conserv

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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to growth in call offerentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis; immunostimulatory peptide; T cell epitope; stimulate; interferon-gamma; IFN-gamma; production; vaccine; tuberculin skin test; ds.
vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Partial DNA clone AciI#1-426 encoding immunostimulatory peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 7495; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.5%; Score 19; DB 22; Length 452; 100.0%; Pred. No. 18+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 452 BP; 213 A; 53 C; 77 G; 104 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104/c
AAT49104 standard; DNA; 456 BP.
                                                                                                                                                                                                                                                                                                                                                                                       Drmanac RT
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                                                                                                                                                                                                                              26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                      28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.5%
Best Local Similarity 100.(
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-514838/56.
P-PSDB; AA007504.
                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                    Tang YT, Liu C,
                                                                                                                                        WO200164835-A2
                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9700067-A1
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                                                                                                                                                                                07-SEP-2001
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0
                                                                                                                                                                                                                                                 Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
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red. No. 99;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 369 BP; 72 A; 76 C; 83 G; 138 T; 0 other;
                                                                                                                                                                                                        Human secreted protein 5' EST, SEQ ID NO: 35472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID 35472; 71pp + CD-ROM; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pr
tive 0;
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                                                                     AAC31397 standard; cDNA; 369 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0122487.
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                                                                                                                                                             (first entry)
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nes 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                 EP1033401-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-1999;
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                                                                                                                AAC31397;
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                       RESULT 24
AAC31397/c
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single exon nucleic acid probes for analyzing gene expression in human brains -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer; ss.
                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
                                                                                                                                                                                                                            claim 1; SEQ ID NO 7457; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.5%; Score 19; DB 22; Length 461;
00.0%; Pred. No. 1e+02;
ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human brain expressed single exon probe SEQ ID NO: 7329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 461 BP; 162 A; 78 C; 101 G; 120 T; 0 other;
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                                                                                  Rank
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100.0%; Pre
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                                          (MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                  Chen W,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          647
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27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          629 TCATATGAAAATATATGGC
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                                                                                  Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-483446/52.
                                                                                                                          WPI; 2001-483447/52.
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21-SEP-2000;
27-SEP-2000;
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26-MAY-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between vaccinated and infected subjects) and as immunoassay reagents for detecting specific antibodies. An advantage of these peptides is that they stimulate production of IFN-gamma (critical for a protective immuno response to M. tuberculosis) by CD4-positive T cells. The protein encoded by this sequence has amino acid similarity to a dipeptide transport protein.
                                                                                                                                                                                                                                                                                                                                                   AAT49100-175 are DNA sequences isolated from Mycobacterium tuberculosis, which encode partial sequences of immunostimulatory peptides. Each of the clones encode at least one immunostimulatory T cell epitope. The clones were identified by testing over 300 fusion clones (alkaline phosphatase-M. tuberculosis peptide fusions) for their ability to stimulate interferon (IRN)-gamma production. By clones were initially designated to have some ability to stimulate IRN-gamma production, of which 76 are shown in AAT49100-175. These sequences can be used to obtain the full length M. tuberculosis genes and corresponding proteins using standard techniques. The peptides are useful in vaccines, as reagents in an improved tuberculin skin test (especially using peptides different from those used in vaccines so as to allow differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                               New immuno:stimulatory peptide(s) of Mycobacterium tuberculosis useful in vaccines, diagnostic skin test, immunoassay and gene isolation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               % Match 0.5%; Score 19; DB 18; Length 456; Local Similarity 100.0%; Pred. No. 1e+02; les 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human foetal liver single exon nucleic acid probe #7457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 456 BP; 63 A; 121 C; 165 G; 98 T; 9 other;
                                                                                                                                                                                                                                                                                                                 Claim 1; Page 34; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABA59152 standard; DNA; 461 BP
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26-MAY-2000; 2000US-0207456.
30-UUN-2000; 2000US-0608409.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-023659.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296 ACAGCAGATCCACCAACAG 278
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                      96WO-US10375
                                                            95US-0000254
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                      14-JUN-1996;
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                                                            15-JUN-1995;
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RESULT 27 ABA59152/c

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The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                         Probe #7587 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon probe from lung SEQ ID No 7914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.5%; Score 19; DB 22; Length 461; Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                            microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 461 BP; 162 A; 78 C; 101 G; 120 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W, Rank DR;
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ABSO7923/c
ID ABSO7923 standard; DNA; 461 BP.
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2000US-0207456.
2000US-0608408.
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2000US-0234687.
2000US-0236359.
2000GB-0024263.
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ID AAI38901 standard; DNA; 461
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                                               56 TCATATGAAAATATATGGC
                        629 TCATATGAAAATATATGGC
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                                                                                                                                                                                                                                                                                                                                     genetic disorder; ss.
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                Probe;
                                                                                                                         RESULT 30
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                                The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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Example 4; SEQ ID NO: 7329; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human bone marrow expressed single exon probe SEQ ID NO: 7663.
                                                                                                                                                                                                                            Score 19; DB 22; Length 461;
Pred. No. 1e+02;
0: Mismatches 0; Indels
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                                                                                                                                                                                         Sequence 461 BP; 162 A; 78 C; 101 G; 120 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    analyzing gene expression in human bone marrow
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100.0%; Pre
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26-MX-2000; 2000US-0207456.
30-UNN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
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                                                                                                                                                                                                                                                                                                          629 TCATATGAAAATATATGGC 647
                                                                                                                                                                                                                                                                                                                                 AAK33106 standard; DNA; 461
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                                                                                                                                                                                                                            Query Match 0.5 Best Local Similarity 100. Matches 19; Conservative
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Best Local Similarity
Matches 19; Conserva
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                                                                                                                                                        invention.
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AAK33106/c

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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12887 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising can a collection of detectably labeled nucleic acids derived from human lung many in a baseled nucleic acids from eukaryote lung mRNA, to a single exon probe, a labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, the above mentioned microarray; assigning exons in several that above mentioned microarray assigning exons to a single exon probe, comprising (a) identifying exons from genomic sequence by the method in the above mentioned microarray; assigning exons in several classus and/or cell types using hybridisation to a single exon probe, comprising (a) identifying exons from genomic sequence by the method classus and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of the exons should be assigned to a single gene; a petide composition of the exons in the tissues and/or cell types using hybridisation to a single exon expression analysis, and for identifying exons in a gene; particularly cush as asthma, lung cancer, chronic obstructive pulmonary disease (COPP), interstitial lung disease (ILD), familial idopathic pulmonary alveolar proteinosis, karagenes suddences, guilmonary dysplasia, primary cilaray equence is a single exon pulmonary and hy
Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tubercous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histlocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary histlocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary histlocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary displasia; pulmonary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spatially-addressable set of single exon nucleic acid probes, used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      measure gene expression in human lung samples -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 7914; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penn SG, Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-2000; 2000US-180312P.
26-MAY-2000; 2000US-207456P.
30-UUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0532366.
21-SEP-2000; 2000US-23468PP.
27-SEP-2000; 2000US-235359P.
                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-114183/15.
                                                                                                                                                                                                                                                                                  WO200186003-A2.
                                                                                                                                                                                                                                       Homo sapiens.
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probe of the invention

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AAB63122 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                                                                                                                                                                                          Human breast cancer associated antigen nucleotide sequence SEQ ID NO:180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014
                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 757;
                                                                                                                     Length 461;
                                                                                    78 C; 10. 0.5%; Score 19; DB 24; Lengua. ... Pred. No. 1e+02; 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; breast cancer; gastric cancer; prostate cancer; cancer associated antigen; cytostatic; cancer vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 757 BP; 146 A; 232 C; 244 G; 132 T; 3 other;
                                                                                    Sequence 461 BP; 162 A; 78 C; 101 G; 120 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 0.5%; Score 19; DB 22; Local Similarity 100.0%; Pred. No. 1e+02; nes 19; Conservative 0; Mismatches 0;
                                                                                                                     Ouery Match 0.5%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 1e+Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 50; Page 332; 799pp; English.
                                                                                                                                                                                                                                                                                                         AAF22601 standard; cDNA; 757 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LUDW-) LUDWIG INST CANCER RES.
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                                                                                                                                                                                       629 TCATATGAAAATATATGGC 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAY-2000; 2000WO-US14749.
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                                                                                                                                                                                                           56 TCATATGAAATATATGGC 38
                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-025274/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-DEC-2000
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                                                                                                                                                                                                                                                                                                                                             AAF22601;
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Matches
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                                                                                                                                                                                                                                                                                              AAF22601/
   SSSSSS
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990S-0139458

990S-0139460

990S-0139460

990S-0139461

990S-0139461

990S-0139461

990S-0139463

990S-0139463

990S-0139463

990S-0139463

990S-013963

990S-014083

990S-014083

990S-0142976

990S-01429763

990S-01429763

990S-0144331

990S-0144332

990S-0144332

990S-0144332

990S-0144332

990S-0144332

990S-0144332

990S-0144332

990S-0144332

990S-0144332

990S-0145085

990S-0145085

990S-0145089

990S-0145193

990S-0145193

990S-0145193

990S-0145193

990S-0145193

990S-0147319

990S-0147319

990S-0147319

990S-0147319

990S-0147319

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990S-0147319

990S-0147319

990S-0147318
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02 - AUG - 1999;
02 - AUG - 1999;
03 - AUG - 1999;
04 - AUG - 1999;
04 - AUG - 1999;
05 - AUG - 1999;
                                                                                                                                                                         Hybridisation assay, genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                           Arabidopsis thaliana DNA fragment SEQ ID NO: 21334.
                                                    AAC38539 standard; DNA; 783 BP
                                                                                                                                                                                                                                                                                                                                                           990S-0121825.
990S-0123180.
990S-0123788.
990S-0123786.
990S-01277462.
990S-01277462.
990S-0127462.
990S-0128714.
990S-0128714.
990S-0130077.
990S-0131486.
990S-0131486.
990S-0131486.
990S-0131486.
990S-0131488.
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990S-0131488.
990S-0131883.
990S-0131883.
990S-0131892.
990S-0131892.
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990S-0131892.
990S-0131892.
990S-0131893.
990S-0131894.
990S-0131894.
990S-0131894.
990S-0131894.
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                                                                                                                 (first entry)
                                                                                                                                                                                                                                      Arabidopsis thaliana
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23 - APR - 1999;
28 - APR - 1999;
28 - APR - 1999;
30 - APR - 1999;
40 - APR - 1999;
65 - MAY - 1999;
66 - MAY - 1999;
66 - MAY - 1999;
67 - APR - 1999;
68 - APR - 1999;
69 - APR - 1999;
69 - APR - 1999;
60 - APR - 1999;
61 - APR - 1999;
62 - APR - 1999;
63 - APR - 1999;
64 - APR - 1999;
66 - APR - 1999;
67 - APR - 1999;
68 - APR - 1999;
68 - APR - 1999;
69 - APR - 1999;
61 - APR - 1999;
62 - APR - 1999;
63 - APR - 1999;
64 - APR - 1999;
66 - APR - 1999;
67 - APR - 1999;
68 - A
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                                                                                                                 17-0CT-2000
                                                                                   AAC38539;
                        RESULT 33
                                        AAC38539
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                                                                                                                                                                                                                                                                                                                                   The invention relates to novel genes (AAI93926-AAI97963) expressed in human neuroblastoma. The nucleic acids are applicable as a probe or primer in diagnosing the prognosis of human neuroblastoma, malignancy and susceptibility indicators or tumour markers for anti-cancer agents. The gene information for diagnosing prognosis is related to factors similar to that for N-myc and TrkA genes.
                                                   Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss.
                                                                                                                                                                                                                                                          Nucleic acids originating in gene expressed in human neuroblastoma, useful as probe or primer in diagnosing prognosis of human neuroblastoma, malignancy and susceptibility indicator or tumour marker for anti-cancer agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

0.5%; Score 19; DB 22; Length 889;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels
                               Human neuroblastoma expressed polynucleotide SEQ ID NO 259.
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 889 BP; 240 A; 157 C; 142 G; 317 T; 33 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse pheromone receptor VR10 coding sequence.
                                                                                                                                                                                                                                                                                                                 Claim 1; Page 230-231; 2979pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX05849 standard; cDNA; 1296 BP
                                                                                                                                                                                (CHIB-) CHIBA PREFECTURE.
(HISM ) HISAMITSU PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 627 TTTCATATGAAAATATATG 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             533 TTTCATATGAAAATATATG 551
                                                                                                                                       02-MAR-2001; 2001WO-JP01629.
                                                                                                                                                           07-MAR-2000; 2000JP-0159195
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         (first entry)
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                                                                                                                                                                                                                                      WPI; 2001-565584/63.
                                                                                            WO200166719-A1.
                                                                                                                                                                                                                 Nakagawara A;
                                                                         Homo sapiens
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         13-NOV-2001
                                                                                                                  13-SEP-2001,
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AAX05849
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1e+02;
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Pred. No. 1e+0
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2094 TCTTGCATGATTCTTTGAA 2112
                                               990S-0150566
990S-0150884.
990S-0151065.
990S-0151066.
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990S-0159638
990S-015984.
990S-0160767.
990S-0160768
990S-0160768
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99US-0151930.
99US-0152363.
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99US-0153758.
99US-0154018.
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99US-0154779.
99US-0155139.
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99US-0155659.
99US-0156458.
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99US-0157117.
99US-0157753.
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99US-0158029.
99US-0158232.
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99US-0159329.
99US-0159330.
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99US-0160989.
99US-0161404.
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99US-0159293
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99US-0162142
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Best Local Similarity 100...
Best Local 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             990S-01
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                20-AUG-1999;
23-AUG-1999;
25-AUG-1999;
26-AUG-1999;
27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
                                                                                                              25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
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AAI94184;

RESULT 34
AAI94184
ID AAI94
XX
AC AAI94

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The present sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number and the clone it was derived from are given in the descriptor line.

The invention relates to 31 novel genes and their fragments (nucleic acid sequences: AAA61260-A61293; amino acid sequences AAB12301-B12371) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 31 polynucleotides, based on which tissues they are most highly expressed in and include products for the diagnosis or treatment of cancer; tumours, AIDS, autofumune disorders, allergy, cardiovascular disorders, viral, bacterial and fungal infection. The genes are used to generate fusion for increasing stability of the fused protein as compared to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to polynucleotide sequences encoding mammalian pheromone receptor polypeptides. The polypeptides are expressed in murine and rat vomeronasal organ. The products can be used for modifying pheromone activity, e.g. for decreasing pheromone receptor mediated signal transduction. They can be used for controlling fertility and behaviour in vertebrates and invertebrates. Compositions comprising the polypeptides are particularly useful in e.g. controlling fertility in livestock and controlling reproduction in rodents or insects by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated pheromone receptor polypeptides - used to develop products for controlling fertility and behaviour in vertebrates and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor; signal transduction; fertility; behaviour;
                                                                                                                                                                                                                                                                                                                                      DB 21; Length 1405; 1e+02;
                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                      Sequence 1405 BP; 410 A; 264 C; 312 G; 412 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse pheromone receptor VR11 coding sequence.
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.00.0%; Pred. No. 1e4
.ve 0; Mismatches
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100.0%; Pic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX05850 standard; cDNA; 1521
                                                                                                                                                                                                                                                                                                                                                                                                       2300 ATGGGATGTTTGGATGAAT 2318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Buck L, Dulac C, Herrada G,
                                                                                                                                                                                                                                                                                                                                                                                                                                       822 ATGGGATGTTTGGATGAAT 840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-095684/08.
P-PSDB; AAW94911.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX05850;
                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
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                                                                                                                                                                                           The invention relates to polynucleotide sequences encoding mammalian pheromone receptor polypeptides. The polypeptides are expressed in murine and rat vomeronasal organ. The products can be used for modifying pheromone activity, e.g. for decreasing pheromone receptor mediated behaviour in vertebrates and invertebrates. Compositions comprising the polypeptides are particularly useful in e.g. controlling fertility and polypeptides are particularly useful in e.g. controlling fertility in interrupting the normal behaviours of rodents or insects by interrupting the normal behaviours of rodents or insects that result in mouse pheromone receptor VRIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                               New isolated pheromone receptor polypeptides - used to develop products for controlling fertility and behaviour in vertebrates and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human secreted proteins useful for diagnosing, preventing, treating and ameliorating a medical condition e.g. cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted protein; fusion protein; gene therapy;
protein therapy; diagnosis; tissue; cancer; tumour; AIDS;
autoimmune disorder; allergy; cardiovascular; viral; bacterial;
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Pred. No. 1e+02;
0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1296 BP; 414 A; 229 C; 238 G; 415 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein gene 30 clone HYBAR26,
                   Matsunami H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fungal infection; immunosuppressive; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruben SM, Rosen CA, Ebner R,
SE, Carter KC, Komatsoulis G;
                                                                                                                                                             Claim 23; Page 183; 308pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 0.5%; Scc
Local Similarity 100.0%; Pries 19; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA61289 standard; DNA; 1405 BP
                   Herrada G,
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                                              WPI; 1999-095684/08
                 Dulac C,
                                                               P-PSDB; AAW94910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200029422-A1.
                                                                                                                                 invertebrates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39-NOV-1999;
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               Buck
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AAA61289
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Gaps

Wed Nov

AAX05810 standard; cDNA; 2732 BP.

AAX05810

(first entry)

04-MAY-1999

AAX05810;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophilar. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
interrupting the normal behaviours of rodents or insects that result reproduction. The present sequence represents the coding sequence of mouse pheromone receptor VR11.
                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster expressed polynucleotide SEQ ID NO 20840.
                                                                                                                                                                                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                    Score 19; DB 20; Length 1521; Pred. No. 1e+02; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19; DB 23; Length 2606;
Pred. No. 1e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 20840; 21pp + Sequence Listing; English.
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                                                         Sequence 1521 BP; 489 A; 264 C; 288 G; 480 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myers EW;
                                                                                                                                                                                                                                                      ABL08786 standard; cDNA; 2606 BP
                                                                                    0.5%; Scilarity 100.0%; P
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                                                                                                                                                2806 TGATATGGCCATGAGTGAT 2824
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11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                             pharmaceutical; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ABB57737-ABB72072).
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                                                                                   Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PEKE ) PE CORP NY.
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Best Local
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888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated pheromone receptor polypeptides - used to develop products for controlling fertility and behaviour in vertebrates and
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                                                                                                  transduction; fertility; behaviour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2732;
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7. 1e+02;
0; Indels
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                                                                        Mouse pheromone receptor VR10 encoding cDNA
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Pred. No.
                                                                                                              reproduction; rodent; insect; mouse; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 18; Page 99-101; 308pp; English.
                                                                                                                                                                 Location/Qualifiers
80..1378
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100.0%; Pre
0;
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                                                                                                  receptor; signal
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Best Local Similarity
Matches 19; Conserva
                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAW94910.
                                                                                                                                                                                                                                                                                                                                                                                                                                               invertebrates
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                                                                                                  Pheromone
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                                                                                                                                         Mus sp.
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Matches
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Mus sp.

Key

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The present sequence encodes a heat stable DNA polymerase from the present sequence encodes a heat stable DNA polymerase from has an extremely high heat stability and can catalyse reactions at 70-90 degrees celsius. High molecular weight DNA was isolated from the bacteria, and screened with probes based on the polymerase genes of P. furiosus and Thermococus littoralis to isolate the present sequence. Host cells transformed with DNA encoding the present polymerase are used to produce recombinant DNA which is useful for nucleic acid amplification, including direct, reversed polymerase chain reaction (PCR) on double-stranded matrices and PCR on matrices having secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antidiaterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human musculoskeletal system related polynucleotide SEQ ID NO 2690.
                                                                                                                                                                                                                                                                                                                                                                         Heat stable DNA polymerase from Pyrococcus species - and related DNA, vectors and transformed cells, useful in nucleic acid amplification reactions performed at temperatures high enough to denature secondary structures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     structures that block the process at conventional elongation
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100.0%; Pred. No. 1e+02;
tive 0; Mismatches 0
/*tag= a
/product= DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Pages 37-41; 80pp; French.
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Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                         Querellou J;
                                                                                                                                                                                                                                                                                                             WPI; 1998-101062/09.
P-PSDB; AAW60719.
                                                            WO9801567-A2
                                                                                                                                            10-JUL-1997;
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                                                                                                                                                                                                                                                                       Cambon MA,
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AAL36325
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                                                   Pheromone receptor; signal transduction; fertility; behaviour; reproduction; rodent; insect; mouse; ss.
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Pred. No. 1e+02;
0; Mismatches 0; Indels (
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           Mouse pheromone receptor VR11 encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matsunami H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 18; Page 102-105; 308pp; English.
                                                                                                                                                       Location/Qualifiers
81..1604
/*tag= a
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1547..3862
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                                                                                                                                                                                                                                                                                                                                                                                                               (HARD ) HARVARD COLLEGE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heat stable DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invertebrates
                                                                                                                                                                                                                                                                                                                            30-JUN-1998;
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Query Match

Local

Matches

δ g Pyrococcus

Key

AAV36034;

AAV36034/C

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Gaps

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0; Indels

Length 4446;

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20000S-017906S.
20000S-018662B.
20000S-0186564.
20000S-0186350.
20000S-019874.
20000S-0198123.
20000S-0198123.
20000S-0205515.
20000S-0205515.
                                                                                                                                                                  20000S-0215135
2000US-0215135
2000US-021647
2000US-0217487
2000US-0217496
2000US-0220963
2000US-0220963
2000US-0220963
2000US-0220963
2000US-0220963
2000US-022553
2000US-022553
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20000S-0231414
20000S-0232081
20000S-023239
20000S-023239
20000S-023239
20000S-023240
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           31-JAN-2000)
24-FEB-2000)
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28-FEB-2000)
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28-JUL-2000)
29-JUL-2000)
29-JUL-2000)
20-JUL-2000)
20-JU
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20000S - 0237037 20000S - 0237038 20000S - 0237040 20000S - 0237040 20000S - 0241786 20000S - 02411826 20000S - 02411826 20000S - 02411826 20000S - 0244617 20000S - 0244617 20000S - 0244617 20000S - 0244617 20000S - 0246617 20000S - 0246617 20000S - 0246613 20000S - 0246526 20000S - 0246526 20000S - 0246521 20000S - 0249218 20000S - 024928 20000S - 024928 20000S - 024928 20000S - 025188 2000S - 025188 200S - 025188 200S - 025188 2000S - 025188 2000S - 025188 2000S - 025188 2000 022-0CT-20000 022-0CT-20000 022-0CT-20000 023-0CT-20000 023-0CT-20000 024-0CT-20000 025-0CT-20000 026-0CT-20000 027-0CT-20000 027-0CT-20000 028-0CT-20000 029-0CT-20000 039-0CT-20000 039-0CT-20000 049-0CT-20000 059-0CT-20000 069-0CT-20000 079-0CT-20000 079-0CT-20000 079-0CT-20000 079-0CT-20000 079-0C 05-JAN-2001; 

S (HUMA-) HUMAN GENOME SCI INC Rosen CA, Barash SC,

WPI; 2001-451937/48.

Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including

us-09-782-874-1.oli.rng

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AAC75998;
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                                                      The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, of strointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple, sclerosis, theumatoid arthritis and ulcerative colitis;
                                                                                                                                                                                                           (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                                                                 parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated polypeptide, used to treat or prognose a disorder characterized by expression of a hCAAP e.g. cancer, is encoded by an isolated nucleic acid comprising an NA Group 3 or 4 molecule -
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; small cell lung cancer; therapy; hCAAP; nucleic acid; NA; melanoma; cancer; colon; breast; head; neck; transitional cancer; leimyosarcoma; synovial sarcoma; cytostatic; ds.
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musculoskeletal cancers and also for testing and detection e.g.
                                    Example 2; SEQ ID NO 2690; 781pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                         Length 4656;
                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                 Sequence 4656 BP; 1461 A; 810 C; 804 G; 1581 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human small cell lung cancer associated gene, KIAA0963.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gure AO,
                                                                                                                                                                                                                                                                                                                                      Score 19; DB 22;
Pred. No. 1e+02;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57; Page 105-107; 152pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jager D,
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ID AAD11120 standard; DNA; 4877 BP.
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100.0%;
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Best Local Similarity 100.C
Matches 19; Conservative
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The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with small cell lung cancer. The molecules provided by the invention can be used in the diagnosis, monitoring, research or treatment of conditions characterised by the expression of one or more cancer associated antigens. The polypeptide is used to treat a disorder characterised by expression of a hcAAP, and determine regression, progression or onset of a condition characterised by expression of an abnormal amount of a protein encoded by a nucleic acid (NA) Group I molecule. The disorders are small and non-small cell lung cancer, melanoma, colon, breast, head and neck, or transitional cancer, leimyosarcoma or synovial sarcoma. The present sequence is a small cell lung cancer associated gene designated as NY-SCLC-11, encoding human KIAA0963 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ORFX ORF1553 polynucleotide sequence SEQ ID NO:3105.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC75998 standard; cDNA; 4924 BP
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02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-WAR-2000; 2000US-0540763.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-FEB-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-602362/57.
P-PSDB; AAB41789.
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which represent the human ORFX open reading frames 1 to 3161. The ORFX
sequences have activities such as: cytostatic; hepatotropic; vulnerary;
attipsoriatic; antiparkinsonian; nootropic; neuroprotective;
costeopathic; anticonvulsant; antiarthritic; immunosuppressant;
immunostimulant; cardiant; thrombolytic; coaquiant; vasotropic;
antidiabetic; hypotensive; dermatological; immunosuppressive;
antidiabetic; hypotensive; dermatological; immunosuppressive
antidiabetic; hypotensive; dermatological; immunosuppressive;
antidiabetic; hypotensive; dermatological; immunodeficiency carbe therapy
the presence of or predisposition to, or preventing or treating
pathological conditions associated with an ORFX-associated disorder. The
nucleic acids can be used to express ORFX proteins in gene therapy
vectors. The proteins and nucleic acids may be used to treat cancers,
proliferative disorders, neurodegenerative disorders, osteoarthritis,
graft vs host disease, cardavoascular disease, diabetes mallitus,
hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
nocturnal haemoglobinuria, antiinflammatory disease; to enhance
coagulation; to inhibit thrombosis; and as a contraceptive.
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Pred. No. 1e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4924 BP; 892 A; 1694 C; 1572 G; 765 T; 1 other;
neurodegenerative disorders and cardiovascular disease
                                        Page 2323-2326; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.08; Pr
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ID ABL30262 standard; DNA; 5415 BP.
XX
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2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid
genes from Drosophila and
interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100. es 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmaceutical; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-656860/75.
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11-JUL-2000;
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                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL0176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shrimp white spot Bacilliform virus; WSBV; diagnosis; viral infection; antiviral agent; gene expression; antisense construct; transgenic viral resistant shrimp; ds.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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1.1e+02;
hes 0;
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(THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C
(SINO-) SINOGENOMAX CO LTD.
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                                                                                                                                                                                                                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.1
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.5%; Score 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       He M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Figure 3; 626pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.50,
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pham L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH62719 standard; DNA; 18234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3562 ATATATATATATGTAATA 3580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5286 ATATATATATGTAATA 5268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38-NOV-2000; 2000WO-US28888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99CN-0124717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-355877/37.
                                                                                                                                                                                                     sequences (ABL01840
(ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
es 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAG84939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200138351-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH62719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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us-09-782-874-1.oli.rng

Query Match

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Best Loca Matches

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The present sequence is reverse PCR primer, P127BGL, used to amplify a ctDNA encoding tomato C-protein having RNA-directed RNA polymerase (RdRP) activity. This primer contains BgIII site to enhance the clouing efficiency. This primer contains partial states of RNA-directed RNA synthesis, thus using RNA as a template for synthesising complementary RNA molecules. RdRP nucleic acid is useful for modulating gene expression in plants, humans and animals. This may lead to various physiological, developmental and/or morphological changes. Transgenic plants containing RdRP nucleic acid is sepecially useful in plant cell or tissue cultures and in plant breeding. RdRP is useful in gene therapy, particularly for treating a disease that is caused by the undesirable expression or overexpression of
                                                                                                                                                                    !/ Iomato; gene therapy; RNA-directed RNA polymerase; RdRP; gene expression;
transgenic plant; tissue culture; plant breeding; therapy; C-protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid molecules encoding polypeptides with RNA-directed RNA polymerase enzymatic activity, useful in modulating gene expression in plants, humans and animals, as well as in plant cell/tissue cultures or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tomato; RdRP; RNA-directed RNA polymerase; in vitro transcription; cytostatic; virucide; RNA synthesis inhibitor; antibody; immunogen; transgenic plant; transgenic animal; cancer; viral infection; RACE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fomato RNA-directed RNA polymerase (RdRP) P127Bgl PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                             primer, P127BGL to amplify tomato RdRP cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sanger HL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
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.3e+02;
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100.0%; Pred. No.
ative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schiebel W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Column 21; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS17843 standard; DNA; 35 BP.
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                                                                                                                                                                                                                                                                                                                                                                            97US-0811583
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    AAD04376 standard; DNA; 35
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                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAY-2002 (first entry)
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                              PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (RIED/) RIEDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plants, humans
plant breeding
                                                                                                                                                                                                                                                                                                                                                                            05-MAR-1997;
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                                                                                                                             Reverse PCR
                                                                                                                                                                                                                                                                                                                                    17-APR-2001.
                                                                                   04-JUL-2001
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AAS17843/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention provides the primary nucleotide sequence of the WSBV genome AAM6289), predicted transcript sequences (AAM6289), predicted transcript sequences (AAM6289), and encoded proteins (AAM62910-AAG85051) and oligonucleotide sequences (AAM62840-63160) suitable for use as primers or probes. The nucleic acid molecules and proteins of the invention are useful for diagnosis and monitoring viral infection, in screens for antiviral agents and for monitoring viral gene expression or activity during a treatment regimen. The nucleic acid molecules are also useful as antisense constructs to control viral gene expression in infected cells and tissues and to create transgenic viral resistant shrimp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primary nucleotide sequence of the shrimp white spot Bacilliform virus (WSBV), useful for producing viral polypeptides that can be used to screen for agents that are useful for treating WSBV infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                   Shrimp white spot Bacilliform virus; WSBV; diagnosis; viral infection; antiviral agent; gene expression; antisense construct; transgenic viral resistant shrimp; ds.
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                           Length 18234;
                                                                                                                                                                                                                                                                                                                                                                                           Shrimp white spot Bacilliform virus (WSBV) genomic sequence.
Sequence 18234 BP; 5373 A; 4270 C; 3810 G; 4781 T; 0 other;
                     DB 22; Le.,
1.10+02;
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PENY-) PE CORP NY.
(THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.
(SINO-) SINOGENOMAX CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.5%; Score 19; DB 22; I
100.0%; Pred. No. 1.1e+02;
11ve 0; Mismatches 0;
                            0.5%; Scor.
100.0%; Pred. No. 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 He M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Figure 2; 625pp; English.
                                                                                                                                                                                                                                                                     AAH62689 standard; DNA; 305107 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pham L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4662 ATTCAATTTGGCATTGGAT 4680
                                                                                                                        554 ATTCAATTTGGCATTGGAT 572
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                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      White spot syndrome virus.
                                                           Local Similarity 100.
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Yang F, He J,

Χu Χ,

WO200138351-A2

31-MAY-2001

11-SEP-2001

AAH62689;

RESULT 47 4AH62689

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24-NOV-1999;

WPI; 2001-355877/37.

Local Similarity es 19; Conserv

Best Loca Matches

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RESULT 48 AAD04376/c

Query Match

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Gaps

.; 0

Primer base sequence used to illustrate primer selection method

Primer; optimum sequence; differential display; ss.

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Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents the tomato RNA-directed RNA polymerase (RdRP) specific PCR primer P127Bg1 used to clone the full length RdRP cDNA molecule of the invention. The invention comprises the nucleic acid and protein sequences of RdRP, the protein of the invention can catalyse in vitro transcription of short single stranded RNAs into DNA molecules, this transcription can be either primed by RNA or DNA oligonuclectides or be unprimed. The protein may have cytostatic or virucide activities. The sequences of the invention may be used in gene therapy or as an RNA directed RNA synthesis inhibitor. The RdRP cDNA sequence and a template nucleic acid molecule derived from a nucleic acid molecule which causes a disease are useful for treating a disease caused by the undesired expression or overexpression of a nucleic acid molecule in a human, rat or mouse, by administering the molecules. This system can be used in the preparation of any desired gene by transferring the RdRP system to expression of any desired gene by transferring the RdRP system to cryanisms that either lack a comparable mechanism or of nutbitor to the protein are useful for inhibiting RNA directed RNA synthesis and for protein are useful for inhibiting RNA directed RNA synthesis and for the protein are useful for inhibiting RNA directed RNA synthesis and for the protein are useful for inhibiting RNA directed RNA synthesis and for the protein are useful for inhibiting RNA directed RNA synthesis and for the protein are useful for inhibiting RNA directed RNA synthesis and for the protein are useful for inhibiting RNA directed RNA synthesis and for the protein are useful for inhibiting RNA directed RNA synthesis and for the protein are useful for inhibiting RNA directed RNA synthesis and for the protein are useful for inhibiting RNA directed RNA directed RNA synthesis and for any and a second and a se
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ensuring stable heterologous, gene expression in transgenic organisms. The sequence is useful for probes and/or for the control of gene expression, as primers for amplification of nucleic acid molecules and as tools for the detection of expression of the cDNA molecules. Additionally, nucleotide and protein sequences are useful for suppression of undesired gene expression in humans and animals. The RdRP is useful as a therapeutic agent for the control of cancer and virus infection in humans and animals and the antibody is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunolocalisation of the protein, identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid molecule encoding a polypeptide having the enzymatic activity of RNA-directed RNA polymerase, for modulating gene expression and treating cancer and virus infection in human and animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of polypeptides interacting with it and screening expression libraries.
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immunoprecipitation; immunolocalisation; PCR primer; P127Bgl;
gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 35
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Pred. No. 3e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sanger HL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schiebel W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Page 12; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.5%,
100.0%; Pre
                                                                                                                                                                                                                                                                                              08-FEB-2001; 2001US-0782874.
                                                                                                                                                                                                                                                                                                                                                             97US-0811583.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.5
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                 Lycopersicon esculentum
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                                                                                                                                                                                                                                                                                                                                                                                                                            WASSENEGGER M.
RIEDEL L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               munoprecipitation
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                                                                                                                                                             US2001023067-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wassenegger M,
                                                                                                                                                                                                                                                                                                                                                             05-MAR-1997;
                                                                                                                                                                                                                               20-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                               (WASS/) V
(RIED/) I
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This invention relates to a method for selecting the sequence of a primer. The method comprises obtaining an optimum sequence for differential display from an expression gene data base, and using the base sequences most frequently expressed as the primer candidates in the order of frequency. The optimum primer group characterised by the use of genetic algorithm from the primer candidates is selected. The method is used for selecting a primer sequence quickly. The present sequence represents a primer used in an illustration of the method of the

Selection of primer base for optimizing primer selection comprises obtaining an optimum sequence for differential display from an expression gene data base -

Disclosure; Fig 9; 13pp; Japanese.

(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN

WPI; 2001-046077/06.

99JP-0088410 99JP-0088410

30-MAR-1999; 30-MAR-1999;

07-NOV-2000

JP2000308487-A.

Synthetic.

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5, 2002, 23:52:42
5 ATTGAAGAAATTTTTTT 22
                                                                Search completed: November
Job time : 1690 secs
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AAF29312 standard; DNA; 48 BP

(first entry)

18-APR-2001

AAF29312;

RESULT 50
AAF29312
ID AAF29
XX
AC AAF29
XX
DT 18-AP

3615 GACTACCTTTGTCTTTA 3632

35 GACTACCTTTTGTCTTTA 18

g ολ

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Gaps

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0.5%; Score 18; DB 22; 100.0%; Pred. No. 3e+02; iive 0; Mismatches 0

571 ATTGAAGAAATTTTTT 588

Local Similarity 100. les 18; Conservative

Sequence 48 BP; 18 A; 2 C; 5 G; 23 T; 0 other;

nvention

Length 48; Indels

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5, 2002, 23:26:27; Search time 142 Seconds (without alignments) 8057.824 Million cell updates/sec
                                                                                                                                                                                   US-09-782-874-1
3731
1 GAAATATTCTTTACTTACTT.....AGTTTCATCTTTCTTAAA 3731
                                                                                                                                                                                                                                                                                                                                                                                                882724
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                      441362 segs, 153338381 residues
                                                                         OM nucleic - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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length: 2000000000
                                                                                                               November
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                                                                                                                                                                                       Title:
Perfect score:
Sequence:
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Maximum DB seq
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                                                                                                               Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*

Post-processing: Listing first 50 summaries

Issued_Patents_NA:*

Database :

## SUMMARIES

Description	Sequence 1, Appli	H		ý	'n	54	54	,	'n	ω̈	'n	δ	20	20	15	34	1	m	m	m	35	45	328	'n	Sequence 3, Appli	4, App.	Sequence 3, Appli
1	1 1	-08-100-	1-583-	-08-811-583-	-08-811-	-933-750C	-09-234-61	-811-583-	-08-990-85	-07-732-242C-	-13	-08-811-58	-09-058-389A-	11-781-20	5-1	1-638-34	US-09-134-001C-1922	08-383-750-	US-08-352-678-3	-98960-	US-08-454-720A-35	4	-09-620-41	-11	-08-348-14	US-08-348-143-4	US-08-571-785-3
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99-192-435 99-192-435 99-192-435 99-192-435 99-192-435 99-192-435 99-192-345 99-192-345 99-192-345 99-192-345 99-483-35 99-483-35 99-483-35 99-483-35 99-483-35 99-483-35 99-166-35 99-166-35 99-166-35	US-09-188-930-36 US-08-671-525B-7 US-08-672-109B-7 US-08-842-045-7
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Sequence 1, Application US/08811583

Patent No. 6218142

GENERAL INFORMATION:
APPLICANT: Wassenegger, Michael
APPLICANT: Riedel, Leonhard
APPLICANT: Schiebel, Winfried
APPLICANT: Schiebe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IDM PC compatible

CORRATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/811,583

FILING DATE: 05-MAR-1997

CLASSIFCATION: 336

ATCRNEY/AGBNT INFORMATION:

NAME: Haley, James F.

REGISTRATION NUMBER: WG-1

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-596-9000

TELEFAX: 212-596-9000

TELEFAX: 212-596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CIIY: New York
STATE: New York
ZIOTIRY: USA
ZIP: 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 3731 base pairs
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STRANDEDNESS: single
TOPOLOGY: linear
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ORIGINAL SOURCE:
ORGANISM: Tomato
RESULT 1
US-08-811-583-1
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1860 2100 1320 1380 1380 1440 1500 1560 1620 1680 1680 1740 1800 1080 **AGATGAAGTTCTCGAACAGAAGCAAAAGGAAGCTGTAGATCAGCTTGATGCTATCTTGCA** TCTCAAGGGTAGACCACCTCCAAAATCTCCGTCCATCACTTTAGATGATGGGTTGGTGA TCTCAAGGGTAGACAACCTCCAAAATCTCCGTCCATCACTTTAGATGGGTTGGTGTA TGGTGGATATAAAGGTGTTGTGGGTGTTGATCCGGATTCATCAATGAAGTTGTCTTTGAG ATATCAGCCTTGTTATCTTAATCGTCAACTGATTACGCTCTTGTCTACACTTGGAGTGAA GGTTCCCAATGTCCAGCCTCCGGAAGGAATTTCAATTCCCTACAAGATTTTGTTCAAAAT CTATATAAAGGAGTGCTGTTATGATCCCGTGAGGTGGCTCACTGAGCAGTATGATGGTA AGTGTGGATGTTTGCATCAAGACCTGGCCTTACTGCAAATGATATAAGAGCTTGGATGGG TICCICCAGAGAGITITGAGIGITCITAGGCAIGAGATIGAAGITATICCCGATGIAAA GGTTCATGGAACCAGCTATGTCTTTTCTGATGGAATTGGTAAAATATCTGGTGACTTTGC TAGTICITIGGIACAGCAIGGAIGCAIACCIGGGCCAGCAITAAAIGICIACIITIICCG ATTAGTTGATCCTCGAAGGAGAAATGTGGCATGCATTGAGCATGCCTTAGAGAAACTGTA TGTAAGAAGGGTCCTAGTAACACCATGCAAAGTTTATTTTTGGTGGTCCAGAGGTTAATGT TICCAATCGGGTICICCGCAAITAITCIGAAGACATAGATAACITICTICGIGIITICITI TGTTGATGAGGAGTGGGAGAAACTGTATTCTACAGACTTATTACCAAAAGCAAGTACTGG **AATTGGTGATAAAAATTTGAATTTCTTGCATTTTCATCGAGCCAGTTGCGGGATAATTC** TAGTICTTTGGTACAGCATGGATGCATACCTGGGCCAGCATTAAATGTCTACTTTTTCCG 1261 1321 1381 1441 1441 1501 1561 1621 1681 1741 1801 1801 1861 1861 1921 1921 1981 2041 1081 1201 1201 1261 1381 1561 1621 1681 1741 1981 1021 1141 1321 1501 1021 1081 1141 961 961

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	2161 TCTCAAGCAATGCTAAACTGTGGTTATAAGCCTGATGCTGAGCCCTTTCTTT	2220
oy.	2221 GTTGCAAACCTCCGCGCATCCAAGTTGCTCGATTTGCGGACTAGATCAAGAATATTTAT	2280 2280
, d	2281 TCCAAATGGAAGAACAATGATGGGATGTTGGATGAATCCAGAACCTTGGAATATGGTCA 	2340
oy do	2341 GGTGTTTGTTCAGTTTACTGGTGCTGGACATGGAGAGTTTTCTGACGATTTACATCCATT	2400
o do	2401 TAATAACAGCAGATCCACCAACAGTAATTTCATTCTGAAGGAAATGTGGTTGTTGCAAA 	2460
ob ob	2461 AAATCCATGCATCCTGGTGATATTCGTGTTTTAAAGGCTGTAAATGTTCGAGCGCT [	2520 2520
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č da	2581 ATGTTCTGGGAGTGATTTGGATGGGGATATCTACTTTGTTTG	2640
75 GG	2641 CCCGCCAAGGCAAGTCCAGCCGATGGAATATCCTCCAGCACCAGCATACAGTTGGACCA	2700
oy du	2701 TGATGTCACAATTGAGGAAGTTGAAGAGTACTTCACCAACTATATTGTGAATGACAGTTT 	2760
70 dg	2761 GGGAATCATAGCAAATGCCCATGTCGTATTTGCAGACAGA	2820 2820
o do	2821 TGATCCATGCAAAAACTTGCTGAGCTCTTTTCAATTGCAGTGGACTTTCCAAAGACTGG 	2880 2880
7, d	2881 IGTICCGGIGAAATACCATCICAGTTGCGCCCTAAAGAATACCCAGACTTCATGGATAA	2940
o d	2941 GCCGGACAAGACCAGCTATATCTCAGAAAGAGTTATTGGAAAGCTTTTCAGGAAAGTGAA 	3000
oy a	3001 GGACAAAGCACCTCAGGCTATCGCGACCTTCACAAGAGATGTTGCAAGAGATCT GCAAGAGATCT 11111111111111111111111111111111111	3060
2y 3	3061 AIATGATGCTGATATGGAAGTTGATGGATTTGAAGATTACATTGACGAAGCTTTTGACTA 	3120 3120
(*)	3121 CAAAACTGAATATGACAAGCTGGGTAATTTAATGGACTACTATGGCATAAAAAGAGA	3180

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3421 TCCCTGGTGTGTTTATGACCAGCTAATCCAGATTAAGAAGGACAAAGCACGTAACAGGCC 3480
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                                                                                                       3241 IGCIGAGGCCATTAGTGTTGCTGTGAGGGCCTTGAGGAAGGAGGCAAGAGCCTGGTTCAA 3300
                                                                                                                                                                             3301 GAGGCGTAATGATATAGATGACATGTTACCAAAGGCTTCGGCTTGGTACCACGTTACATA 3360
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                                                                                                                                                                                                                                                                                                                                                                                                                   3601 IGTTATGCATTGTTGACTACCTTTTGTCTTTAAAACTGCATGAAGCTGCAACATATATGC 3660
3121 CAAAACTGAATATGACAACAAGCTGGGTAATTTAATGGACTACTATGGCATAAAAAAGAGA 3180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3541 TICCAGTCGAGCGTTAAGCTGATATATATATGTAATAGGGTGTGTGATCATAAGAAAC 3600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: POOVAIGH, B. W.
APPLICANT: Takezawa, D.
APPLICANT: Takezawa, D.
APPLICANT: Han, T. J.
APPLICANT: M. G. H.
TITLE OF INVENTION: Control of Growth and Development of
TITLE OF INVENTION: Potato Plants
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,874
FILING DATE: JULY 30, 1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Smith, DeAnn F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Harness, Dickey & Pierce STREET: P.O. Box 828 CITY: Bloomfield Hills STATE: MI COUNTRY: USA ZIP: 48303 COMPUTER READALLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08100874; Patent No. 5498533; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3721 TTTCTTCTAAA 3731
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US-08-100-874-1/c
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NUCLEIC ACID MOLECULES ENCODING
POLYPEPTIDES HAVING THE ENZYMATIC ACTIVITY OF AN
RNA-DIRECTED RNA POLYMERASE (RdRP)
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                                                                           Query Match 0.7%; Score 25; DB 4; Length 25; Best Local Similarity 100.0%; Pred. No. 0.01; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,583
FILING DATE: 05-MAR-1997
CLASSIFICATION: 536
ATTONEY/AGENT INFORMATION:
NAME: HALLEY, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MPG-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.7%; Score 25; DB 4; Best Local Similarity 100.0%; Pred. No. 0.01; Matches 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
ADDRESSEE: 1251 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                     1838 CCATCTGCTTTCCAGATTCGTTATG 1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 1000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2659 GCCGATGGAATATCCTCCAGCACCC 2683
                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Wassenegger, Michael
APPLICANT: Riedel, Leonhard
APPLICANT: Schiebel, Winfried
APPLICANT: Sanger, Heinz
TITLE OF INVENTION: NUCLEIC ACID N
TITLE OF INVENTION: POLYPEPIDES;
TITLE OF INVENTION: RNA-DIRECTED I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
                                                                                                                                                                                                 25 CCATCTGCTTTCCAGATTCGTTATG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 GCCGATGGAATATCCTCCAGCACCC 1
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US-08-811-583-5/C
; Sequence 5, Application US/08811583
; Patent No. 6218142
; GENERAL INFORMATION:
APPLICANT: Wassenegger, Michael
                                                                                                                                                                                                                                                                                                           US-08-811-583-6/c
; Sequence 6, Application US/08811583
; Patent No. 6218142
          DESCRIPTION: /desc = "primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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            ;
US-08-811-583-4
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                                                                                                                                                                                                                                                                                            RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAVING THE ENZYMATIC ACTIVITY OF AN RNA POLYMERASE (RGRP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 30; DB 1; Length 906;
Pred. No. 3.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: ....
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: INW PC COMPATIBLE
OPERATING SYSTEM: PC-DOS_MS-DOS
SOTTWARE: PATENTE Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/811,583
FILING DATE: 05-MAR-1997
CLASSIFICATION: 536
ATTORREY AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INC. 62181423
GENERAL INCRMATION:
GENERAL INCRMATION:
APPLICANT: Wassenegger, Michael
APPLICANT: Schiebl, Winfried
APPLICANT: SCHIEBLES: 13
COURESPONDRICE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
COUNTRY: ITSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3687 TAAGTACTAATATGTATGTGATTTGAGTTT 3716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 TAAGTACTAATATGTATGTGATTTGAGTTT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        other nucleic acid
REFERENCE/DOCKET NUMBER: 755:
TELECOMONICATION INFORMATION:
TELEPHONE: (313) 641-1600
TELEFAX: (313) 641-0270
TELEPHONE: 387637 HARNESS UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
IENGTH: 906 base pairs
TYPE: NUCLEAC acid
STRANNEDNESS: both
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                 ORGANISM: Solanum tuberosum INDIVIDUAL ISOLAȚE: p-PCM-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.89
Best Local Similarity 100./
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                        CDS
81..530
                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-08-811-583-4/c
                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
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US-08-100-874-1
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Length 1750;
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Sequence 54, Application US/09234613
Patent No. 6133973
APPLICANT: Lal, Preeti
APPLICANT: Ball, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
IITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSE: ALICYTE Pharmaceuticals, Inc.
STREET: 314 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: TEASTEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
APPLICATION NUMBER: SAFICATION SAFICATION NUMBER: FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BILINGS, LUCY J.
RECESTRATION NUMBER: 36,749
REFERENCEY/DOCKET NUMBER: PF-0356 US
TELEPHONE: 415-85-0555
TELEPHONE: 415-85-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.5%; Score 20; Best Local Similarity 100.0%; Pred. No. Matches 20; Conservative 0; Mismatci
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PRICR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1750 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: HMCINOT01
CLONE: 9476
US-08-933-750C-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1916 TIGAGAAGAGCAIGICGAA 1935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1355 TTGAGAAGAGCATGTCGAA 1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM COMPUTED OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Win
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
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APPLICANT: Riedel, Leonhard
APPLICANT: Schiebel, Winfried
APPLICANT: Schiebel, Winfried
APPLICANT: Schiebel, Winfried
APPLICANT: Schiebel, Winfried
APPLICANT: Sanger, Heinz
TITLE OF INVENTION: NOLYPEPTIDES HAVING THE ENZYMATIC ACTIVITY OF AN TITLE OF INVENTION: RNA-DIRECTED RNA POLYMERASE (RdRP)
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.6%; Score 24; DB 4; Length 25; Best Local Similarity 100.0%; Pred. No. 0.033; Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURREWY APPLICATION DATA:

APPLICATION NUMBER: US/08/811,583

FILING DATE: 05-MAR-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Haley, James F.

REGISTRATION NUMBER: MFG-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 12-596-9000

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 base pairs

TYPE: NUCLEIC acid

STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KESULT 6

US-08-933-750C-54

Sequence 54, Application US/08933750C

Patent No. 5932442

GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: We, Henry
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: WILL C.
TITLE OF SEQUENCES: 98

CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear MOLECULE TYPE: other nucleic acid ; DESCRIPTION: /desc = "primer" US-08-811-583-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1879 TGTGGGTGTTGATCCGGATTCATC 1902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 TGTGGGTGTTGATCCGGATTCATC 1
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                              CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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Gaps

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Gaps

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RESULT 9
US-08-990-823-5/c
US-08-990-823-5/c
US-08-990-823-5/c
| Sequence 5, Application US/08990823D
| Patent No. 6228371
| GENERAL INFORMATION:
| APPLICANT: Namo, Francis
| TITLE OF INVENTION: immunostimulatory Peptides
| TILE REFERENCE: 49086
| CURRENT APPLICATION NUMBER: US/08/990,823D
| CURRENT APPLICATION NUMBER: US/96/10375
| EARLIER APPLICATION NUMBER: 60/000,254
| EARLIER FILING DATE: 1995-06-15
| NUMBER OF SEQ ID NOS: 113
| SOFTWARE: PatentIN Ver. 2.0
| SEQ ID NO 5
| TENTIFE PATENTIAL OF THE 
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   4; Length 34;
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Sequence B, Application US/07732242C

Patent No. 5/98399

GENERAL INFORMATION:
APPLICANT: UOCUMI, Takeshi, Masaki, Haruhiko;
APPLICANT: Maeda, Michihisa; Yoneta, Yasuo;
TITLE OF INVENTION: Gene of Urease
NUMBER OF SECURNCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSE: Frishauf, Holtz, Goodman & Woodward, P.C.
STREET: 600 Third Avenue
CITY: New York
STREET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 Inch, 0.72mb
COMPUTER: IBM PC COMPATIBLE (NEC PC-9801 RX)
OPERATING SYSTEM: MS DOS
SOFTWARE: ASCII FORM
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/732,242C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ore 19; DB 4;
red. No. 12;
Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: Modified base
; OTHER INFORMATION: n represents a or g or c or
US-08-990-823-5
0.5%; Score 19; DB 4
100.0%; Pred. No. 11;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 19;
Pred. No.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JPN 2-210178
FILING DATE: 10-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match

Best Local Similarity 100.0%; P. Matches 19; Conservative 0;
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                                                                                                                                                          16 ACTCATCACTCCCCTCAAG 34
                                                                                                                          33 ACTCATCACTCCCCTCAAG 51
Query Match
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RY: USA
10016-2088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
US-07-732-242C-8/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
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Patent No. 6218142
GENERAL INFORMATION:
APPLICANT: Masseneger, Michael
APPLICANT: Riedel, Leonhard
APPLICANT: Schiebel, Winfried
APPLICANT: Schiebel, Winfried
APPLICANT: Schoel, Leonhard
APPLICANT: Schoel, MUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: POLYPEPTIDES HAVING THE ENZYMATIC ACTIVITY OF AN TITLE OF INVENTION: RNA-DIRECTED RNA POLYMERASE (RGRP)
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.5%; Score 20; DB 3; Length 1750; Best Local Similarity 100.0%; Pred. No. 4.1; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,583
FILING DATE: 05-MAR-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSEE: FISH 6 NEAVE
F: 1251 Avenue of the Americas
New York
New York
                                                                   PF-0356 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESCRIPTION: /desc = "primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUBBER: 27,794
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
   NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1916 TIGAGAAAGAGCAIGICGAA 1935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1355 TTGAGAAAGAGCATGTCGAA 1374
                                                             REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855 -0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 54:
                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
IENGTH: 1750 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: HMCINOT01
CLONE: 9476
US-09-234-613-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HPORMATION FOR STATICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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STREET: 125
CITY: New Y
STATE: New
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-811-583-7
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Gaps

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RESULT 13
US-09-058-389A-20/C
Sequence 20, Application US/09058389A
Sequence 20, Application US/09058389A
Patent No. 6130065
GENERAL INFORMATION:
APPLICANT: Eatl, Judith A.
APPLICANT: Eatl, Judith A.
APPLICANT: Patel, Divyen
ITILE OF INVENTION: (NBWER)-INSENSITIVE, BOULLIBRAITYE, NUCLEOSIDE TRANSPORT
TITLE OF INVENTION: USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
STREET: 411 Hackensack
STREET: 411 Hackensack
STREET: How Jersey
COUNTRY: USA
ADDRESSEE: David A. Jackson, Esq.
STREET: Float
CITY: Hackensack
STREET: Float
STREET: Float
CITY: New Jersey
COUNTRY: USA
MEDIUM TPE: Floapy disk
COMPUTER: IBM PC COMPATION:
REDICATION: NUMBER: US/09/058,389A
TILING STEATION: 800
CLEASIFICATION: WUMBER: 26,742
RESIDATION: WUMBER: 26,742
RESIDATION: NUMBER: 26,742
RESIDATION: NUMBER: 1340-1-013N
TELEPONMUNICATION: INPORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                  COMPUTER READABLE FORM:
MEDIUM TYPE: Elpopy disk
COMPUTER IBM PC compatible
COMPUTER: IBM PC compatible
CONFUREN: BEN PC compatible
CORRENT APPLICATION DATA:
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/811,583
FILING DATE: 05-MAR-1997
CLASSIFICATION: 536
ATTORNEY/AGREY INFORMATION:
NAME: Haley, James: 27,794
REGISTATION NUMBER: 27,794
REGISTATION NUMBER: 27,794
REGISTATION NUMBER: 27,794
REGISTATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 9:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
ILENGTH: 35 base pairs
TTELECOMMUNICATION
STRANDENESS: slingle
STRANDENESS: slingle
TTELECOMMUNICATION OF STRANDENESS: Slingle
STRANDENESS: Slingle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No.
Matches 18; Conservative 0; Mismatci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3615 GACTACCTTTTGTCTTTA 3632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 GACTACCTTTTGTCTTTA 18
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-811-583-9
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US-05-13-133A-3/C
US-05-13-133A-3/C
Sequence 3, Application US/09813133A
Sequence 3, Application US/09813133A
Sequence 3, Application US/09813133A
Sequence 3, Application Selection Selecti
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Patent No. 6218142

GENERAL INFORMATION:
APPLICANT: Wassenegger, Michael
APPLICANT: Riedel, Leonhard
APPLICANT: Schlebel, Winfried
APPLICANT: NAN-TICE AND MOLECULES ENCODING
TITLE OF INVENTION: POLYPEPTIDES HAVING THE ENZYMATIC ACTIVITY OF AN TITLE OF INVENTION: NAN-DIRECTED RNA POLYMERASE (RGRP)
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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100.0%; Pred. No. 15;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.5%; Score 19; DB 1; Length 6131; Best Local Similarity 100.0%; Pred. No. 14; Matches 19; Conservative 0; Mismatches 0; Indels
                                                       REGISTRATION NUMBER: 17081
REFERENCE/DOCKET NUMBER: 910532/HG
TELECOMMUNICATION INFORMATION:
TELEFPHONE: (212)972-1400
TELEFRA: (212)972-1400
TELEFRA: 236268
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 6131 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic) US-07-732-242C-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2524 GACTGGTTTCACCTTTTTC 2506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     627 ITTCATATGAAAATATATG 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               922 GACTGGTTTCACCTTTTTC 940
       ATTORNEY/AGENT INFORMATION:
NAME: Goodman, Herbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.5
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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New York
                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 3
LENGTH: 55827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-811-583-9/c
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Sequence 345, Application US/09641638

Fatent No. 643264

GENERAL INFORMATION:
APPLICANT:
Bulmenfeld, Marta
APPLICANT:
Chumakov, IIya
APPLICANT:
COHEN, Annick
ITILE OF INVENTION:
BILLE OF INVENTION:
BILLE OF INVENTION:
CURRENT FILING DATE:
CURRENT APPLICATION NUMBER:
CURRENT FILING DATE:
1999-00-07
PRIOR PELING DATE:
1999-00-07
PRIOR APPLICATION NUMBER:
CONTACT OF SEQ ID NOS:
1304
SOFTWARE:
PRIOR PELING DATE:
1999-02-12
NUMBER OF SEQ ID NOS:
1304
SOFTWARE:
CEG ID NOS:
CEG ID NO 345
LEGG ID NOS:
CEG ID NO 345
LEGG ID NOS:
CEG ID NO 345
LEGG ID NOS:
CEG ID NO 345
CEG ID NO 345
CEG ID NO 345
CEG ID NO 345
CEG ID NOS:
CEG ID NO 345
CEG ID NO 345
CEG ID NOS:
CEG ID NO 345
CEG ID NO 345
CEG ID NOS:
CEG ID N
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                             Gaps
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                             Indels
                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: BREAST SPECIFIC GENES AND PROTEINS NUMBER OF SEQUENCES: 30
COMPUTER READABLE FORM:
MEDIUM YPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18; DB 5;
Pred. No. 40;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF LANCE PATENCE.

SOFTHARE: Patence.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/08295

TOTAL DATE: 30-JUN-1995
                                                                                                                                                                                                                                                                           Sequence 15, Application PC/TUS9508295 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.5%; Scc.
100.0%; Pre
0; )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US95-08295-15
                                                                                   2068 GGAAGCIGIAGAICAGCT 2085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2989 CAGGAAAGTGAAGGACAA 3006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 30-JUN-1995
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 481 base pairs
TYPE: nucleic acid
                                                                                                                       427 GGAAGCTGTAGATCAGCT 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 CAGGAAAGTGAAGGACAA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.5%
Best Local Similarity 100.(
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: allele
LOCATION: 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 16
US-09-641-638-345/c
                                                                                                                                                                                                                            RESULT 15
PCT-US95-08295-15
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APPLICANT: Crawford, Charles R.
APPLICANT: Crawford, Charles R.
APPLICANT: Crawford, Charles R.
APPLICANT: Crawford, Charles R.
APPLICANT: Patel, Divyen
TITLE OF INVENTION: (NBMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
TITLE OF INVENTION: USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                           DB 3; Length 461; 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZUP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PER PC compatible
OPERATUG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/611,781
FILING DATE:
                                                                                                                                                                                                                                                                                                                                       Query Match 0.5%; Score 18; DB Best Local Similarity 100.0%; Pred, No. 40; Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) MOLECULE TYPE: other nucleic acid
) DESCRIPTION: /desc = "intron 10(5')"
US-09-058-389A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "intron 10(5')"
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.5%; Score 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/09611781 Patent No. 6423829 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 461 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2068 GGAAGCTGTAGATCAGCT 2085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      427 GGAAGCTGTAGATCAGCT 410
                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
  201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                         linear
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US-09-611-781-20/C
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Birkenbach, Mark
APPLICANT: Kieff, Elliott
TITLE OF INVENTION: EPSTEIN BARR VIRUS INDUCED GENES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
STREET: Asston
STATE: MA
                                                          COMPUTER READABLE FORM:

MEDIUW TYPE: FIDPPY disk
COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,750
FILING DATE: Herewith
CLASSIFICATION: 436
ATTONNEY/AGENT INFORMATION:
NAME: FOX, Samuel, L.
REGISTRATION NUMBER: 30,353
REFRENCE/DOCKET NUMBER: 0627.3300001
TELEPRAX: (202) 371-2600
TELEFRAX: (202) 371-2500
INFORMATION FOR ESD ID NO: 3:
SEQUENCE CARRACTERISTICS:
LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDBNESS: both
TYPE: TILEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: MA
ZID: 02210
CONMTRY: USA
ZID: 02210
COMPUTER: ELADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/352,678
FILING DATE: 30-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.5%; Score 18;
nilarity 100.0%; Pred. No.
Conservative 0; Mismatc
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APPLICATION NUMBER: US 07/980,518
FILING DATE: 25-NOV-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 19
US-08-352-678-3/c
'Sequence 3, Application US/08352678
'Patent No. 604331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: B080:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1382 GTTGATGAGGAGTGGGAG 1399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     540 GTTGATGAGGAGTGGGAG 523
                         ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
34..1116
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Best Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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; LOCATION:
US-08-383-750-3
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Patent No. 6380370
GENERAL INFORMATION:
DENORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/065,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR PLING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1922
LENGTH: 1440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
          NAME/KEY: misc_binding

LOCATION: 481.500

OTHER INFORMATION: 12-854-64.misl, potential

NAME/KEY: misc_binding

LOCATION: 502.521

OTHER INFORMATION: 12-854-64.mis2, potential complement

NAME/KEY: primer_bind

LOCATION: 438.457

OTHER INFORMATION: upstream amplification primer

NAME/KEY: primer_bind

LOCATION: 942..962

OTHER INFORMATION: downstream amplification primer

NAME/KEY: misc_binding

LOCATION: 489..513

OTHER INFORMATION: 12-854-64 potential probe

US-09-641-638-345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ore 18; DB 4; Length 1440;
red. No. 42;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match

0.5%; Score 18; DB 4; Length 1001;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 0; Indels
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; Patent No. 5744301
; GENERAL INFORMATION:
APPLICANT: Blikenbach, Mark
APPLICANT: Kleff, Elliot
; TITLE OF INVENTION: Epstein Barr Virus Induced Genes
; VUMBER OF SEQUENCES: 8
; CORESPONDENCES: 8
; CORESPONDENCE ADDRESS:
; STREET: 1100 New York Avenue, N.W.,
; STREET: Suite 600
; STREET: D.C.
OTHER INFORMATION: 12-854-64 : polymorphic base A or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 0.5%; Score 18; Best Local Similarity 100.0%; Pred. No. Matches 18; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-1922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3562 ATATATATATGTAAT 3579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 ATATATATATATGTAAT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          603 TCGTCCATATGGTCAAAA 620
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US-09-134-001C-1922
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US-08-383-750-3/c
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Gaps
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US-09-323-672A-45/C
US-09-323-672A-45/C
Sequence 45, Application US/09323872A
Patent No. 6395539
GENERAL INFORMATION
TILLE OF INVENTION: Compositions and Methods for Bioremediation
FILLE REFERENCE: OHIO-03640
CURRENT APPLICATION NUMBER: US/09/323,872A
CURRENT FILING DATE: 2001-06-15
PRIOR PILICATION NUMBER: 09/072,433
PRIOR PILICATION NUMBER: 09/072,433
PRIOR PILING DATE: 198-05-04
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin version 3.0
SEQ ID NO 45
LENGTH: 2038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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                                                               APPLICANT: RAWASSAI, FILES. 5.

TITLE OF INVENTION: Detection of Carcinoma Metastases by TITLE OF INVENTION: Detection. Set SEQUENCES: 42

CORRESPONDENCE ADDRESS: ADDRESSE: Hoffman-La Roche Inc. STREET: 340 Kingsland Street
CITY: Nutley STREET: 0.3.A.

ZIP: Now Jersey
CONTRY: U.S.A.

ZIP: OCUTEN: IS ADDRESSED FORM: MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SUFFWARE: Patentin Release #1.01, version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.5%; Score 18; DB 4; Length 2038; Best Local Similarity 100.0%; Pred. No. 42; Matches 18; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.01, ver CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/454,720A FILING DATE: May 31, 1995
CLASSIPTICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/357,565
FILING DATE: December 16, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas 187
REGISTATION NUMBER: 35321
REFERENCE/DOCKET NUMBER: 9178
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.5%; Score 18; Best Local Similarity 100.0%; Pred. No. Matches 18; Conservative 0; Mismatc
                                                   Kawasaki, Ernest S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 35
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sobol, Robert E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            576 AGAAATTTTTTTTTT 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Thauera aromatica
US-09-323-872A-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qγ
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42;
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                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application PC/TUS9309636
GENERAL INFORMATION:
APPLICANT: Birkenbach, Mark
APPLICANT: Kieff, Elliot
TITLE OF INVENTION: Epstein Barr Virus Induced Genes NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox STRET: 1100 New York Avenue N.W., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTY. U.S.A.

ZIP: 2005-3934

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/09636
FILING DATE: herewith
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18; DB 5; Pred. No. 42; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                       Query Match 0.5%; Sc
Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.5%; Sc
Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACIERISTICS:
LENGTH: 1643 base pairs
TYPE: nucleic acid
SIRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         540 GTTGATGAGGAGTGGGAG 523
                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: 34..1116
US-08-352-678-3
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34..1116
                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 20
PCT-US93-09636-3/c
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PCT-US93-09636-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 21
US-08-454-720A-35
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                                                                                                                                                           FEATURE
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APPLICANT: TAJIMA, HISAO
APPLICANT: KITAGAWA, KOICHIRO
APPLICANT: KITAGAWA, KOICHIRO
APPLICANT: OHNOWINI
TITLE OF INVENTION: A No. 5506205el Polypeptide of Protein p140 and DNAS
TITLE OF INVENTION: encoding it
NUMBER OF SEQUENCES: 16
CORRESPONDENCES: 16
CORRESPONDENCES: SUGHRUE, MION, ZINN, MACPEAK & SEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                 Query Match 0.5%; Score 18; DB 1; Length 2669; Best Local Similarity 100.0%; Pred. No. 43; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: 0.C.
COUNTRY: U.S.A.
2101: 2003-3202
COMPUTER: DE PROPY disk
COUNTRY: U.S.A.
2101: 2003-3202
COMPUTER: DE PROPY disk
COMPUTER: DE PROPY disk
COMPUTER: PLOPPY disk
COMPUTER: DE PROPY disk
COMPUTER: DE PROPY disk
COMPUTER: PLOPPY disk
COMPUTER: PLOPPY disk
COMPUTER: PAPELCATION DATA:
APPLICATION NUMBER: US/08/348,143
FILING DATE: 24-NOV-1993
FILING DATE: 24-NOV-1993
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 
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TISSUE TYPE: skeletal muscle myoblast
CELL LINE: L6
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Patent No. 5506205
GENERAL INFORMATION:
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TELEX: 6491103
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4027 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                 1376 TCTTTTGTTGATGAGGAG 1393
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                                                                                                                                                                                                                                                                                                                                                                                                                      74 ATTTGGTTGTGCTTCAGT 91
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STRANDEDNESS: single
; TOPOLOGY: linear; MOLECULE TYPE: CDNA; FEATURE: NAME/KEY: CDS; LOCATION: 1..2669 US-08-118-101A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-348-143-3
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Sequence 3, Application US/08118101A

Patent No. 5620892

GENERAL INFORMATION:
APPLICANT: Kurtz, Stephen E.
APPLICANT: Kurtz, Stephen E.
APPLICANT: McCullough, John R.
TILLE OF INVENTION: EXPRESSING THE GENE ENCODING POTASSIUM TRANSPORTER MINK
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Button Rodney
STREET: P.O. Box 4000
CITY: Princeton
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 08543-4000
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATION NUMBER: US/OB/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PTING PATENTON NUMBER: US/OB/118,101A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                 US-09-620-412C-328/c
; Sequence 328, Application US/09620412C
; Sequence 328, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
TOTHE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: COMPOSITIONS OF CHLANYDIAL INFECTION
TITLE OF INVENTION: DIAGNOSTS OF CHLANYDIAL INFECTION
CURRENT PAPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SEQ ID NOS: 363
LENGTHARE EASTSEQ for Windows Version 3.0/4.0
LENGTH: 2148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.5%; Score 18; DB 4; Length 2148; Best Local Similarity 100.0%; Pred. No. 43; Matches 18; Conservative 0; Mismatches 0; Indels
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ATORNEY/AGENT INFORMATION:
NAME: Gaul, Timothy J.
REGISTRATION NUMBER: 33,111
REFERENCE/DOCKET NUMBER: DC27
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Chlymadia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (609) 252-450
TELEFAX: (609) 252-4526
INFORMATION FOR SEQ ID NO. 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                    1368 TICGIGITICITITGITG 1385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1700 ATGCAGTACTCTAAGAAA 1683
                                                                         1212 TTCGTGTTTCTTTTGTTG 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3657 AIGCAGIACICIAAGAAA 3674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-620-412C-328
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US-08-118-101A-3
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Sequence 4, Application US/08571785

Patent No. 5804411

GENERAL INFORMATION:
APPLICANT: TAJIMA, HISAO
APPLICANT: TAJIMA, KITAGAMA, KOICHIRO
APPLICANT: OHNO, HIROYUKI
APPLICANT: OHNO, TOSHIO
TITLE OF INVENTION: A No. 5804411el Polypeptide of Protein pl40
TITLE OF INVENTION: and DNAs encoding it
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MICN, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                     CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 2007-3202
ZIP: 20073-3202
ZIP: 20077-3202
ZIP: Plopy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: IB PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/571,785
FILING DATE: 13-DEC-1995
FILING DATE: 23-NOV-1994
APPLICATION NUMBER: UP 315806/1993
FILING DATE: 24-NOV-1994
APPLICATION NUMBER: UP 315806/1993
FILING DATE: 22-NOV-1994
APPLICATION NUMBER: UP 315806/1993
FILEPRAY: (202)293-7860
TELEFRAX: (202)293-7860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: D.C.
COUNTRY: U.S.A.
ZIP: 2003-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/571,785
E: SUGHRUE, MION, ZINN, MACPEAK & SEAS 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18; DB 1;
Pred. No. 44;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               skeletal muscle myoblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.5%; Soc
Best Local Similarity 100.0%; P:
Matches 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: CDNA to MRNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3523 ATTTGGTTGTGCTTCAGT 3540
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            STREET: Zivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: rat
; TISSUE TYPE: S
; CELL LINE: L6
US-08-571-785-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-571-785-4
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Sequence 4, Application US/08348143
Patent No. 5506205
GENERAL INFORMATION:
APPLICANT: TAJIMA, HISAO
APPLICANT: OHNO, HISAO
APPLICANT: OHNO, HISAUKI
APPLICANT: OHNO, TOSHIO
TITLE OF INVENTION: A No. 5506205el Polypeptide of Protein pl40 and DNAS
TITLE OF INVENTION: encoding it
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Patent No. 2804411
GENERAL INFORMATION:
APPLICANT: TAJIMA, HISAO
APPLICANT: KITAGAWA, KOICHIRO
APPLICANT: OFFNO, TOSHIO
TITLE OF INVENTION: A No. 5804411e1 Polypeptide of Protein p140
TITLE OF INVENTION: and DNAs encoding it
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 262.3243
IDENTIFICATION METHOD: by similarity to some other pattern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.5%; Score 18; DB 1; Length 4027;
100.0%; Pred. No. 44;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTER EACH FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/348,143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION: 530
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 315806/1993
FILING DATE: 24-NOV-1993
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7860
"""FFAX: (202)293-7860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         skeletal muscle myoblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 3523 ATTTGGTTGTGCTTCAGT 3540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202)293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 ATTTGGTTGTGCTTCAGT 91
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE TYPE: SP
CELL LINE: L6
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: line
MOLECULE TYPE: c
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-348-143-4
                                                                                                                                                                                                                                                                                                                                                                                         CITY: V
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Patent No. 6303320

GENERAL INFORMATION:
APPLICANT: TAJUAA, HISAO
APPLICANT: TAJUAA, HISAO
APPLICANT: TAJUAA, TOSHIO
TILLE OF INVENTION: And DNAS encoding it
APPLICANE: USENON: and DNAS encoding it
TILLE OF INVENTION: AND DNAS encoding it
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MICN, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: Z0037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM 
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/192,435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.5%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 44; Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
ORIGINAL SOURCE:
ORGANISM: rat
TISSUE TYPE: skeletal muscle myoblast
US-09-192-435-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMBER: JP 315806/1993
24-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/571,785
APPLICATION NUMBER: 08/348,143
FILING DATE: 33-NOV-1994
APPLICATION NUMBER: 07 315806/199
FILING DATE: 24-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEEX: (491103
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4027 base pairs
                                                             TELEX: 6491103
INFORMATION FOR SEQ ID NO: 3;
SEQUENCE CHARACTERRISTICS:
LENGTH: 4027 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3523 ATTTGGTTGTGCTTCAGT 3540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA to mRNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 ATTIGGITGTGCTTCAGT 91
                                        (202)293-7860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 30
US-09-192-435-4
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Sequence 3, Application US/09192435

SETRET: CANNAMINA, HIGAO

APPLICANT: TAJIMA, HIGAO

TITLE OF INVENTION: A No. 6303320el Polypeptide of Protein p140

TITLE OF INVENTION: A No. 6303320el Polypeptide of Protein p140

TITLE OF INVENTION: A No. 6303320el Polypeptide of Protein p140

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS

STREET: 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ): NAME/KEY: CDS

): LOCATION: 262..3243

): IDENTIFICATION METHOD: by similarity to some other pattern

US-08-571-785-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.5%; Score 18; DB 1; Length 4027; Best Local Similarity 100.0%; Pred. No. 44; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY. U.S.A.
2IP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTOTE: BROWN PC compatible
CORPTARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/192,435
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS: 2100 Pennsylvania Avenue, N.W. Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE TYPE: skeletal muscle myoblast CELL LINE: L6 FEATURE:
                                  PRIOR APPLICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/348,143
FILING DATE: 23-NOV-1994
APPLICATION NUMBER: 1P 315806/1993
FILING DATE: 24-NOV-1993
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELETA: 6491103
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4027 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/571,785
FILING DATE: 13-DEC-1995
APPLICATION NUMBER: 08/348,143
FILING DATE: 23-NOV-1994
APPLICATION NUMBER: JP 315806/1993
FILING DATE: 24-NOV-1993
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3523 ATTTGGTTGTGCTTCAGT 3540
13-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: lines
MOLECULE TYPE: cl
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: V
STATE:
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APPLICANT: TAJIMA, HISAO
APPLICANT: TAJIMA, HISAO
APPLICANT: RITAGAMA, KOICHIRO
APPLICANT: KITAGAMA, KOICHIRO
APPLICANT: UENO, TOSHIO
TILLE OF INVENTION: A No. 6432913el Polypeptide of Protein p140
TITLE OF INVENTION: And DNAs encoding it
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
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; LOCATION: 262..3243
; IDENTIFICATION METHOD: by similarity to some other pattern
US-09-558-340-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.5%; Score 18; DB 4; Length 4027;
100.0%; Pred. No. 44;
tive 0; Mismatches 0; Indels
        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D.C.
COUNTEX: U.S.A.
COUNTEX: U.S.A.
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/558,340
FTING DATE: 26-APR-2000
          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE TYPE: skeletal muscle myoblast CELL LINE: L6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 26-APR-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 09/192,435
FILING DATE: 08-JAN.1998
APPLICATION NUMBER: 08/571,785
FILING DATE: 13-DEC-1995
APPLICATION NUMBER: 08/348,143
FILING DATE: 23-NOV-1994
APPLICATION NUMBER: JP 315806/1993
FILING DATE: 24-NOV-1993
                                                                                                                                                  RESULT 32
US-00-558-340-4
; Sequence 4, Application US/09558340
; Patent No. 6432913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATE: 24-NOV-1222
FILLING DATE: 24-NOV-1222
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TRIEFRAX: (202)293-7860
                                                                                     3523 Arrigerrerecricaer 3540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 6491103
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 4027 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3523 ATTIGGTTGTGCTTCAGT 3540
                                                74 ATTTGGTTGTGCTTCAGT 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 ATTIGGTIGIGCTICAGT 91
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Best Local Similarity 100.
Matches 18; Conservative
          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 2100 Pen
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MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
        Matches 18;
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                                                                                                                                                                                                               Gaps
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APPLICANT: KITAGAWA, KOICHIRO
APPLICANT: KITAGAWA, KOICHIRO
APPLICANT: OHNO, HIROYUKI
APPLICANT: OHNO, HIROYUKI
ITLE OF INVENTION: A No. 6432913el Polypeptide of Protein p140
ITILE OF INVENTION: and DNAs encoding it
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
                                                                                                                                                                                                             ô
                                                             : NAME/KEY: CDS
: LOCATION: 262..3243
: LIBENTIFICATION METHOD: by similarity to some other pattern US-09-192-435-4
                                                                                                                                                                    Length 4027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4027;
                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS STREET: 2100 Pennsylvania Avenue, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
44;
                                                                                                                                                                  Score 18; DB 4;
Pred. No. 44;
0; Mismatches
      skeletal muscle myoblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/192,435
FILING DATE: 08-JAN-1998
APPLICATION NUMBER: 08/51,785
FILING DATE: 13-DEC-1993
APPLICATION NUMBER: 08/348,143
FILING DATE: 23-NOV-1994
APPLICATION NUMBER: JP 315806/1993
FILING DATE: 24-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                skeletal muscle myoblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/558,340 FILING DATE: 26-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09558340 Patent No. 6432913 GENERAL INFORMATION;
                                                                                                                                                               Query Match 0.5%; Sci
Best Local Similarity 100.0%; P:
Matches 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.5%; 100.0%;
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                                                                                                                                                                                                                                                                           3523 ATTIGGTTGTGCTTCAGT 3540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA to mRNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (202)293-7060
(202)293-7860
                                                                                                                                                                                                                                                   74 ATTTGGTTGTGCTTCAGT 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 20037-3202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: rat
TISSUE TYPE: s
CELL LINE: L6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
TISSUE TYPE:
CELL LINE: I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                                                                                                                                     RESULT 31
US-09-558-340-3
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Gaps

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RESULT 35
US-09-058-3894-5/C
US-09-058-3894-5/C
Sequence 5, Application US/09058389A
Fatent No. 6130065
Fatent No. 6130065
Fatent No. 6130065
FAPLICANT: Belt, Judith A.
APPLICANT: Patel, Divyen
TITLE OF INVENTION: (NBMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
TITLE OF INVENTION: (NBMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
TITLE OF INVENTION: USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS: 32
ADDRESSEE: David A. Jackson, Esq.
STREET: Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                              DB 4; Length 5097; 44;
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: U.S/09/058,389A
FILING DATE: April 9, 1998
CLASSIFICATION STORM
APPLICATION NUMBER: 1998
REFERENCE/DOCKET NUMBER: 1340-1-013N
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
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                                                                                  Query Match 0.5%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 44; Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.5%; Score 18; DB
100.0%; Pred. No. 44;
lve 0; Mismatches
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US-09-611-781-5/c
; Sequence 5, Application US/09611781
; Patent No. 6423829
; RENERAL INFORMATION;
; APPLICANT: Belt, Judith A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) MOLECULE TYPE: DNA (genomic); HYPOTHETICAL: NO US-09-058-389A-5
                                                                                                                                                                                                                                                                                               2560 AGGAAAGITITITICACT 2577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 201-343-1684 INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2068 GGAAGCIGIAGAICAGCI 2085
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                                                                                                                                                                                                                                                   873 AGGAAAGITITITCCACT 890
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LENGTH: 6354 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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US-09-315-793-11
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Patent No. 6221597
GENERAL INFORMATION:
APPLICAMT: ROBERTS, Christopher J.
TITLE OF INVENTION: ESSENTIAL GENES OF YEAST AS TARGETS FOR ANTIFUNCAL
TITLE OF INVENTION: AGENIS, HERBICIDES, INSECTICIDES AND ANTI-PROLIFERATION
TITLE OF INVENTION: DRUGS
FILE REFERENCE: 9301-048
CURRENT APPLICATION NUMBER: US/09/315,793
CURRENT FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 5097
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                                                                                                    Sequence 1. Application US/08915868
| Patent No. 591433
| GENERAL INFORMATION:
| APPLICANT: Mundy, Gregory R. APPLICANT: Gallwitz, Wolf |
| TITLE OF INVENTION: SCREBING ASSAY FOR THE IDENTIFICATION |
| TITLE OF INVENTION: OF AGENTS WHICH INHIBIT CANCER |
| TITLE OF INVENTION: METASTASIS TO BONE |
| TITLE OF INVENTION: METASTASIS TO BONE |
| TITLE OF INVENTION: METASTASIS TO BONE |
| TITLE OF INVENTION: MATASTASIS TO BONE |
| TITLE OF INVENTION: METASTASIS TO BONE |
| TITLE OF INVENTION: METAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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Pred. No. 44;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 60/025,215
FILING DATE:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: OSTS:002P21
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION:
TELECOMMUNICATION INFORMATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4180 AGAAATTTTTTTTTTT 4197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.5
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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US-09-315-793-11
                              RESULT 33
US-08-915-868-1
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US-US-91-91-91-940A1

US-US-91-91-91-940A1

Patent No. 626170

GENERAL INPORMATION:

APPLICANT: Droathan F. Smith
APPLICANT: Droathan F. Smith
APPLICANT: Bruce Crise

APPLICANT: Bruce Crise
APPLICANT: Bruce Crise
APPLICANT: Bruce Crise
APPLICANT: Bruce Crise
APPLICANT: Bruce Crise
APPLICANT: Bruce Crise
APPLICANT: Bruce Crise
APPLICANT: Bruce Crise
APPLICANT: Bruce Crise
APPLICANT: APPLICANT:
CRISE OF SEQUENCES: 29
CORRESPONDENCE ADRESS:
ADDRESSES: Charties H. Harris
STREET: USA MRMC - MRMC-DA
CITY: FORT DETRICK, FREDERICK
STREET: USA MRML - MRMC-DA
COUNTRY: USA
MEDIUM TYPE: FLOPPY disk
COMPUTER RADBALE FORM:
MEDIUM TYPE: Apple Macintosh
COMPUTER RADBALE FORM:
MEDIUM TYPE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,840A
FILING DATE: December 16, 1997
CLASSIFICATION: 424
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                                                                                                                                                                               COMPUTER: LAD. T. COMPUTER: LAD. COMPUTER: LAD. CURRATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,219
FILING DATE: COMMUTENTLY Herewith CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/029,679
FILING DATE: 30-OCT 1996
FILING DATE: 10-CET 1996
FILING DATE: 10-CET 1996
FILING DATE: 10-CEP 
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100.0%; Pred. No.
                                                                                                                                             MEDIÚM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pr
Matches 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1384 TGATGAGGAGTGGGAGAA 1401
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                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                       Texas
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US-08-927-219-130
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Patent No. 6187533
GENERAL INFORMATION:

PAPLICANT: Bell, Graeme I.
APPLICANT: Bell, Garame I.
APPLICANT: Bell, Damela J.
APPLICANT: Maisaki, Pamela J.
APPLICANT: Marzel, Stephen
APPLICANT: Menzel, Stephen
TITLE OF INVENTION: MUTATIONS IN THE DIABETES SUSCEPTIBILITY
TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-1BETA
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
                                                                                                           NUCLEOSIDE TRANSPORT
APPLICANT: Crawford, Charles R. .
APPLICANT: Patel, Divyen
TITLE OF INVENTION: A NITROBENZYLMERCAPTOPURINERIBOSIDE
TITLE OF INVENTION: A NITROBENZYLMERCAPTOPURINERIBOSIDE
TITLE OF INVENTION: NEMBRA - INVENTION: SEQUENCE: A SEQUENCE: 22
TITLE OF INVENTION: USE
NUMBER OF SEQUENCE: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: Floor
CITY: Hackensack Ave, Continental Plaza, 4th
STREET: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPOUR READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPOURE: ISM COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.5%; Score 18; DB
100.0%; Pred. No. 44;
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-013N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/058,389
FILING DATE: APTIL 9, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-487-5806
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6354 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2068 GGAAGCTGTAGATCAGCT 2085
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Best Local Similarity 100.(
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DN
HYPOTHETICAL: NO
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Gaps

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ARPLICANT: Park, Cheonseok n.m.i
TITLE OF INVENTION: METHOD OF PRODUCING ANTIHYPERCHOLESTEROLEMIC AGENTS; FILE REFERENCE: 960.296,95718
CURRENT APPLICATION NUMBER: US/09/215,694B
CURRENT FILING DATE: 1999-12-18
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTOR: NO. 6365723el Sequences of E. coli 0157 NUMBER OF SEQUENCES: 265 CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Quarles & Brady STREET: 1 South Pinckney Street CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US

ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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APPLICATION NUMBER: 60/110,955

FILING DATE: 04-DEC-1998

ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386

TELECRENCE/DOCKET NUMBER: 960296.95017

TELEPRATION INFORMATION:
TELEPRAX: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/99453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: CURROWD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

0.5%; Score 18; DB
Best Local Similarity 100.0%; Pred. No. 48;
Matches 18; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 41
US-09-453-702B-116/C
Sequence 116, Application US/09453702B
Patent No. 6365723
GENERAL INFORMATION:
APPLICANT: Blattner, Frederick 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perna, Nicole T
                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.5%; Sc
Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perna,
Plunkett, Guy
Walch, Rod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Aspergillus terreus
US-09-215-694-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2048 GITCTCGAACAGAAGCAA 2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (608) 251-
INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: WI
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APPLICANT: GONG, Fangcheng et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
TOWN THE REPRENENCE: CLOONINGS
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 5
SOFTMARE: PASKSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 28001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Linear

FEATURE: OTHER INFORMATION: N at all occurences is = unknown.;
FEATURE: OTHER INFORMATION: K at all
US-08-991-840A-1
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100.0%; Pred. No. 46;
.ive 0; Mismatches 0; Indels
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                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: Provisional Application 60/047162,
FILING DATE: May 20, 1997

APPLICATION NUMBER: Provisional Application 60/053,652

FILING DATE: July 24, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Charles H. HARTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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Hutchinson, Charles R.
Kennedy, Jonathan n.m.i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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Pred. No.
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                                                                                                                                                                                                            NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REPERENCE/DOCKET NUMBER: 003/C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEPAX: (301) 619-5034
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-819-993-3/c
; Sequence 3, Application US/09819993
; Patent No. 6436692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature

/ LOCATION: (1)...(28001)

CTHER INFORMATION: n = A,T,C or G

US-09-819-993-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DD 19180 TTTCATTAGCTTTCCCTG 19163
                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 11492 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2636 GIGCIGACAAAAICAICA 2653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy 3409 TITCATTAGCTTTCCCTG 3426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 GTGCTGACAAAATCATCA 380
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Matches 18; Conserv
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APPLICANT: Wisconsi
APPLICANT: Hutchins
APPLICANT: Kennedy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 40
US-09-215-694-19/c
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GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NOCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: NOCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: DEPIDERALIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007
CURRENT PELLING NOMBER: US 60/064,964
PRIOR PELLING DATE: 1999-11-08
PRIOR PELLING DATE: 1997-11-08
PRIOR FILING DATE: 1997-06-14
NUMBER OF SEQ ID NOS: 5674

ILENGTH: 777

LENGTH: 777
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| Sequence 264, Application US/08961527 |
| Sequence 264 Application US/08961527 |
| Sequence 264 Application US/08961527 |
| Patent No. 6420135 |
| GENERAL INFORMATION: STREPTOCOCCUS pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391 |
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESSE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 777;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
COMPUTER: HP Vectra 486/33
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.5%; Score 17; DB 4; Le
illarity 100.0%; Pred. No. 1.3e+02;
Conservative 0; Mismatches 0;
                                         TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: DNA for encoding CFAl protein
US-08-460-739-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 44
US-09-134-001C-1886/c
| Sequence 1886, Application US/09134001C
| Parent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA; CRaphylococcus epidermidis US-09-134-001C-1886
                                                                                                                                                                                                                                                                                                                                                                                      3212 GCATCAAAAACTTTTGA 3228
                                                                                                                                                                                                                                                                                                                                                                                                                  174 GCATCAAAAACTTTTGA 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                439 CIGGITTCACCITITIC 423
                    LENGTH: 512 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Fatent No. 5698416
GENERAL INFORMATION:
MAPLICANT: Wolf, Marcia K.
APPLICANT: Cassels, Frederick J.
APPLICANT: Cassels, Frederick J.
APPLICANT: Bell, Brian A.
ITILE OF INVENTION: Improved Methods for Production of
TITLE OF INVENTION: Antigens Under Control of Temparture-Regulated Promotors
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Glenna Hendricks
STRREFT: 9669 A Main Street
CITY: Fairfax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                      Sequence 200 Application US/09188930A

Patent No. 6150502

GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
TILLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A

CURRENT FILING DATE: 1998-11-09

NUMBER OF SEQ ID NOS: 348

SEQ ID NOS: 348

SEQ ID NO 206

SEQ ID NO 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.5%; Score 17; DB 3; Length 480; 100.0%; Pred. No. 1.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,739
FILING DATE: 20-APR-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna M.
REGISTRATION NUMBER: 32,535
REGISTRATION NUMBER: woif2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 425-4250
INFORMATION FOR SEQ ID NO: 2:
               2270 AGAATATTTATTCCAAAT 2287
                                         56 AGAATATTTATTCCAAAT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 TGCTTCAGTTTCAGTCA 278
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CRGANISM: Mouse
US-09-188-930-206
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                                                                                                                                     RESULT 42
US-09-188-930-206
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-460-739-2
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Gaps

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APPLICANT: Yamada, Tadataka
APPLICANT: Yamada, Tadataka
APPLICANT: Gantz, Ira
TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
                                                                                                                                                                                                                                                                                                                              Length 896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 996;
                                                                                                                                                                                                                                                                                                                                                                     Indels
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SEC ID NO 36
LENGTH: 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
2IF: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER I BUR PC Compatible
COMPOTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/671,525B
FILING DATE: Unne 27, 1996
CLASSIFICATION NUMBER: 3683
ATTORNEY/AGENT INFORMATION:
NAME: REFERENCE/DOCKET NUMBER: 3683
REFERENCE/DOCKET NUMBER: 2115-000853DVB
TELEPHONE: (810)641-1600
TELEPHONE: (810)641-1600
TELEFAX: (810)641-0270
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                          DB 3; Leus
1.3e+02;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
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                                                                                                                                                                                                                                                                                                                          Query Match 0.5%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 1.: Matches 17; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08671525B Patent No. 5703220 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                        194 TGCTTCAGTTTCAGTCA 210
                                                                                                                                                                                                                                                                                                                                                                                                             83 TGCTTCAGTTTCAGTCA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 996 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: homo sapiens
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                                                                                                                                                                                                                                                             ORGANISM: mouse US-09-188-930-36
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US-08-671-525B-7
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US-08-671-525B-7
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Batent No. 6440663

GENERAL INFORMATION:
APPLICANT: Scanian, Matthew
APPLICANT: Scanian, Matthew
APPLICANT: Stockert, Elisabeth
APPLICANT: Old, Lloyd
APPLICANT: Old, Lloyd
APPLICANT: Old, Lloyd
APPLICANT: Dager, Elke
APPLICANT: Dager, Elke
APPLICANT: Dager, Elke
APPLICANT: Usor, Therefor
TITLE OF INVENTION: Renal Cancer Associated Antigens and
TITLE OF INVENTION: Ress Therefor
FILE REFERENCE: L0461/7051
CURRENT APPLICATION NUMBER: US/09/166,350A
EARLIER APPLICATION NUMBER: US 09/166,350
EARLIER PILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 35
SOCTHARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 833
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.5%; Score 17; DB 4; Length 795; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.5%; Score 17; DB 4; Length 833; 100.0%; Pred. No. 1.3e+02; ive 0; Mismatches 0; Indels
  APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36, Application US/09188930A
Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
                                                                                                FILLY DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BEOOKES, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 264:
SEQUENCE CHARACTERISTICS:
LENGTH: 795 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2865 ACTITCCAAAGACTGGT 2881
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Matches 17; Conservative
                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CORGANISM: Homo sapiens
US-09-166-350-10
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US-08-961-527-264
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US-09-166-350-10/c
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US-09-188-930-36
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ORGANISM: homo sapiens
FEATURE:
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Job time: 687 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NATI-SENSE: NO ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION:
US-08-842-045-7
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                              Gaps
                                                                                                                                                                                                   Sequence 7, Application US/08672109B
Patent No. 5710265
Patent No. 5710265
PAPLICANT: Yamada, Tadataka
APPLICANT: Gantz, Ira
ITTLE OF INVENTION: Genes Encoding Melanocortin Receptors
NUMBER OF SEQUENCES: 23
CORRESPONDENCES: 23
CORRESPONDENCES: 33
CORRESPONDENCES: 63
STREET: P.O. BOX 828
CITY: Bloomfield Hills
STATE: MI
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-842-045-7
Sequence 7, Application US/08842045
Patent No. 5817787
GENERAL INFORMATION:
APPLICANT: Yamada, Tadataka
APPLICANT: Gantz, Ira
TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.5%; Score 17; DB 1; Length 996; 100.0%; Pred. No. 1.3e+02; tive 0; Mismatches 0; Indels
                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CUDNIXX: US
CUDNIXX: US
CUDNIXX: US
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,109B
FILING DATE: June 27, 1996
CLASSIFICATION: 536
ATTORNEY/AGBNT INPORMATION:
NAME: Smith, DeAnn F
REFERENCE/DOCKET NUMBER: 2115-000853DVC
TELEPHONE: (810)641-600
TELEPHONE: (810)641-600
TELEPKS: (810)641-600
TELEPKS: (810)641-600
TELEPKS: (810)641-6270
SEQUENCE CHARACTERISTICS:
LENGTH: 996 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
E: DNA (genomic)
                                                              2850 TITCAATIGCAGIGGAC 2866
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                                                                                        422 TTTCAATTGCAGTGGAC 438
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ORIGINAL SOURCE:
ORGANISM: homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linea
MOLECULE TYPE: DN
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION:
US-08-672-109B-7
                                                                                                                                                                  RESULT 49
US-08-672-109B-7
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3731
1 GAMATATTCTTTACTTACTT.....AGTTTCATCTTCTAAA 3731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/DCOMB.PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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13: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
              GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                    310279 segs, 166577418 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published_Applications_NA:*
                                                                                                            nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                   OLIGO_NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                            Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                   Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 1, Appli	Sequence 4, Appli	Sequence 6, Appli	'n	194	Sequence 82, Appl	Sequence 772. App	2240,		7	946		Sequence 2690, Ap	Sequence 9, Appli	18	Sequence 1347, Ap	Sequence 4817, Ap	Sequence 11283, A	Sequence 8123, Ap
SUMMARIES	US-09-782-874-1	US-09-782-874-4	US-09-782-874-6	US-09-782-874-5	US-09-998-598-194	US-09-962-436-82	US-09-998-598-772	US-09-998-598-2240	US-09-840-787-54	US-09-782-874-7	US-09-563-817-946	US-09-864-761-11608	US-09-764-877-2690	US-09-782-874-9	US-09-923-876-1838	US-09-960-352-1347	US-09-867-701-4817	US-09-864-761-11283	US-09-783-590-8123
DB	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
% Query Match Length DB	3731	25	25	25	398	407	409	413	1750	34	267	461	4656	35	256	358	385	474	200
% Query Match	100.0	0.7	0.7	9.0	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5
Score	3731	25	25	24	20	20	20	20	20	19	19	19	19	18	18	18	18	18	18
Result No.		0	m U	O 4	Ŋ	φ υ	0	ထ ပ	σ	10	c 11	c 12	13	c 14	c 12	c 16	17	c 18	c 19

Sequence 176, App Sequence 619, App Sequence 619, App Sequence 619, App Sequence 619, App Sequence 162, App Sequence 162, App Sequence 175, Appli Sequence 7, Appli Sequence 759, App Sequence 1096, App Sequence 11956, App Sequence 2105, A	ING MATIC ACTIVITY OF AN (RGRP)
US-09-925-299-176 US-09-815-242-7347 US-09-817-576-629 US-09-817-576-629 US-09-817-576-629 US-09-817-576-629 US-10-007-693-80 US-10-007-693-80 US-09-817-445-1 US-09-817-445-1 US-09-817-445-1 US-09-817-445-1 US-09-817-46-1 US-09-817-3657 US-09-818-574-9084 US-09-818-578-9084 US-09-818-58-901 US-09-818-58-901 US-09-818-58-901 US-09-818-58-901 US-09-818-58-901	NIS AUTNG THE ENZY NA POLYMERASE ericas ericas .0, Version #1, 874 .874
1016 1497 1497 10948 10948 100 2148 3768 3768 100 49749 100 49749 100 258 100 258 100 258 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 100 378 378 100 378 378 378 378 378 378 378 378 378 378	1 10.2.4.1 10.2.2.0.0230102306741 11.2.0.0520102306741 12.0.0.0520102306741 12.0.0.0520102306741 12.0.0.0520102306741 12.0.0.052010201. 12.0.0.0.0000202020202020202020202020202
118 8 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	-874-1  No. US20010023667A1  APPLICANT: Wassenegg APPLICANT: Wassenegg APPLICANT: Wassenegg APPLICANT: Wassenegg Riedal, L Schiebel, L SCHIER ADDRE ADDRESSE: FISH STREET: L251 Av CITY: New York COUNTY: New York COUNTY: New York STATE: New York COUNTER: READABLE FO MEDIUM TYPE: FISH COUNTER: READATION NUM REFERENCE/DOCKER TELECOMMUNICATION IN
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              781
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                                                                                                                   Length 3731;
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100.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                 LOCATION: 194.3535
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-782-874-1
   INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3731 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
TELEPHONE: 212-596-9000
                                                                   ORGANISM: Tomato
                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 3731; Conservative
                                                                                NAME/KEY:
                                                                          FEATURE
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MOLECULES ENCODING
HAVING THE ENZYMATIC ACTIVITY OF AN
RNA POLYMERASE (RGRP)
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NCE ADDRESS:
SEE: FISH & NEAVE
1.1251 Avenue of the Americas
New York
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wassenegger, Michael
Riedel, Leonhard
Schiebel, Winfried
Sanger, Heinz
VENTION: WUCLEIC ACID M
POLYPEFILDES H
RNA-DIRECTED RI
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Gaps

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HAVING THE ENZYMATIC ACTIVITY OF AN RNA POLYMERASE (RdRP)
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COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPATION SYSTEM: PC-DOS/MS-DOS

SOFWWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DMARA:

FILING DATE: 08-Feb-2001

CLASSIFICATION: CURNOWN>
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ches 0;
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STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.7%; Score 25; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 25; Conservative 0; Mismatches
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APPLICATION NUMBER: US 08/811,583
FILING DATE: 05-WAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                REFERENCE/DOCKET NUMBER: MPG-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9000
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

BESCRIPTION: /desc = "primer"

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-782-874-6
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
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Riedel, Leonhard
Schlebel, Whifried
Sanger, Heinz
TITLE OF INVENTION: NUCLEIC ACID
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                                                    NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
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RNA-DIRECTED
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REGISTRATION NUMBER: 27,794
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                     ATTORNEY/AGENT INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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STRANDEDNESS: single
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US-09-782-874-5/c
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COMPUTAL: ....

ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
COMFUTER: IBM PC compatible
COMFATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PATALIT Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/782,874
FILING DATE: OB-Feb-2001
CLASSIFICATION NUMBER: US/09/782,874
FILING DATE: OS-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
TELEPROMYNICATION INFORMATION:
TELEPRAN: 212-596-9000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
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CITY: New York
STATE: New York
CONTRY: USA
ZIE: 10020
COMPUTER READABLE FORM:
COMPUTER: FIDPPY disk
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
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Schiebel, Winfried
Sanger, Heinz
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
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APPLICATION NUMBER: US/09/782,874
FILING DATE: 08.Feb-2001
CLASSIFICATION: <u >cu <u <u >cu <u <u >cu <u <u >cu <u >cu <u >cu <u <u >cu <u >cu <u <u >cu <u <u >cu <u >cu <u <u <u >cu <u <u >cu <u <u >cu <u <u >cu <u <u <u >cu <u <u >cu <u <u <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u <u >cu <u <u <u >cu <u <u <u <u >cu <u <u <u <u >cu <u <u <u <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u <u >cu <u <u <u >cu <u <u <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u <u >cu <u <u <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u <u >cu <u <u <u <u >cu <u <u <u <u >cu                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
DESCRIPTION: /desc - "primer";
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09782874
Patent No. US20010023067A1
GENERAL INFORMATION
APPLICANT: Wassenegger, Michael
Riedel, Leonhard
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.0
Matches 25; Conservative
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US-09-782-874-6/c
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Gaps
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                                                                                                                                               RESULT 7

US-09-98-588-772/c

US-09-998-598-772/c

SQUENCE 772, Application US/09998598

Patent No. US20020150922A1

GENERAL INFORMATION:

APPLICANT: Stolk, John A.

APPLICANT: Xu, Jangchun A.

APPLICANT: And STANGCHUN A.

APPLICANT: Madalein Joy

TITLE OF INVENTION: OMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: OMPOSITIONS OF COLON CANCER

FILE REFERENCE: 210121.561

CURRENT APPLICATION NUMBER: US/09/998,598

CURRENT FILING DATE: 2001-11-16

NUMBER OF SEQ ID NOS: 2606

SOFTWARE: COLIKA INVENTION DISCLOSUTE DATAbase

SEQ ID NO 772

SEQ ID NO 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2240, Application US/0998598
Fatent No. US20020150922A1
GENERAL INFORMATION:
APPLICANT: Stolk, John A.
APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Chenault, Ruth A.
TITLE OF INVENTION: CMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILER REFERENCE: 210121.561
CURRENT APPLICATION NUMBER: US/09/998,598
CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: COLIXA INVENTION DISCLOSURE DATAbase
SOFTWARE: COLIXA INVENTION DISCLOSURE DATAbase
SEQ ID NO 2240
LENGTH: 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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2.8;
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2.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.5%; Score 20; DB 100.0%; Pred. No. 2.8 iive 0; Mismatches
      Mismatches
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US-09-840-787-54
Sequence 54, Application US/09840787
Patent No. US20020058264A1
      ;
                                              1916 TTGAGAAGAGCATGTCGAA 1935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1916 TTGAGAAGGGCATGTCGAA 1935
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                                                                     384 TIGAGAAAGAGCAIGICGAA 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.5°
Best Local Similarity 100.0
Matches 20; Conservative
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Best Local Similarity 100.0
Matches 20; Conservative
    20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-998-598-772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-998-598-2240
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US-09-998-598-2240/c
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      Matches
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Sequence 82, Application US/09962436
Patent No. US20020081301A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Sets
FILE REPERBNCE: 68929-75
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/60/235,082
PRIOR APPLICATION NUMBER: US/60/234,924
PRIOR PILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 568
NUMBER OF SEQ ID NOS: 568
SOFTWARE: Patentin version 3.0
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Patent No. US20020150922A1

GENERAL INFORMATION:
APPLICANT: Stolk, John A.
APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Chenault, Ruth A.
APPLICANT: Chenault, Ruth A.
APPLICANT: Chenault, Ruth A.
APPLICANT: Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 21012.561

CURRENT APPLICATION NUMBER: US/09/998,598

CURRENT FILING DATE: 2001-11-16

NUMBER OF SEQ ID NOS: 2606

SOFTWARE: Corixa Invention Disclosure Database

SEQ ID NO 194

LENGTH: 398
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                                                                                   Query Match 0.6%; Score 24; DB 10; Length 25; Best Local Similarity 100.0%; Pred. No. 0.015; Matches 24; Conservative 0; Mismatches 0; Indels
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Pred. No.
DESCRIPTION: /desc = "primer" SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                         1879 TGTGGGTGTTGATCCGGATTCATC 1902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) NAME/KEY: misc_feature

) LOCATION: 381

) OTHER INFORMATION: n = A,T,C or G

US-09-998-598-194
                                                                                                                                                                                                  24 TGTGGGTGTTGATCCGGATTCATC 1
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-962-436-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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US-09-962-436-82/C
                                                                                                                                                                                                                                                                                                      US-09-998-598-194
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LENGTH: 407
                                       US-09-782-874-5
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Sequence 0.40.2017 at ve/C.

Sequence 0.40.20020095031A1

Sequence 0.40.20020095031A1

GENERAL INFORMATION:

APPLICANT: Bambrowicz, Brian

APPLICANT: Sands, Arthur T.

TITLE OF INVENTION: No. US20020095031A1e1 Human Polynucleotides and the TITLE OF INVENTION: No. US20020095031A1e1 Human Polynucleotides and the FILE REPRENSICE: LESS. 001.06.41

FILE REPRENSICE: LESS. 001.06.41

PRIOR PLILING DATE: 1999-05-06.41

PRIOR PLILING DATE: 1999-05-06.4

NUMBER OF SEQ ID NOS: 1008

SOFTWARE: PASSEQ for Windows Version 4.0

SEQ ID NO 946
                                                                                                                                                  COMPUTER REALMALE FORM;

WEDIUM TYPE: FOLDPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATE COMPATION FOLDS/MS-DOS
COTHWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,874
FILING DATE: 08-Feb-2001
CLASSIFICATION CURNOWN>
PRIOR APPLICATION NUMBER: US/08/811,583
FILING DATE: 05-MAR-1997
ATTORNORYAGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.5%; Score 19; DB 10; Length 34; 100.0%; Pred. No. 7.3; 1ve 0; Mismatches 0; Indels
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                          1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
DESCRIPTION: /desc = "primer";
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-782-874-7
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; LCCATION: (1)...(267)
; OTHER INFORMATION: n = A,T,C or G
US-09-563-817-946
    ADDRESSEE: FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 34 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS
                                                                                                              ZIP: 10020
COMPUTER READABLE FORM:
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Best Local Similarity
Matches 19; Conservi
                                                                                          COUNTRY:
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Schiebel, Winfried
Sanger, Heinz
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
POLYPEPTIDES HAVING THE ENZYMATIC ACTIVITY OF AN
RNA-DIRECTED RNA POLYMERASE (RGRP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                     Shah, Purvister Shah, Purvister Shah, Purvister Shance Yua Yungy Janice Yua Gueglar, Rarl J. Corley, Nail C. TITLE OF INVENTION: HUMAN REGULATORY MOLECULES NUMBER OF SEQUENCES: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRSTSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/09/840,787
FILING DATE: 23-Apr.-2001
CLASSIFICATION: <unknown>
                                                                                                                                                                                                                                                                          ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION DATA:

ATORNEY/AGENT INFORMATION:

NAME: Blilings, Lucy J.

REGISTRATION NUMBER: 36,749

TELECOMOUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFRAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 54 : US-09-840-787-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/09782874
Patent No. US20010023067A1
GENERAL INFORMATION:
APPLICANT: Wassenegger, Michael
                      Lal, Preeti
Hillman, Jennifer L.
Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGIH: 1750 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA ZIP: 94304
COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1355 TTGAGAAGAGCATGTCGAA 1374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: <UNKNOWN>
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY: HMCINOT01
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                                                                                                                                                                                                                                                                                                                       CITY: Palo Alto
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GENERAL INFORMATION:
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US-09-782-874-7
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Schlebel, Winfried
Sanger, Heinz
TITLE OF INVENTION: NUCLECE ACID MOLECULES ENCODING
POLYPEPTIDES HAVING THE ENZYMATIC ACTIVITY OF AN
RNA-DIRECTED RNA POLYMERASE (RGRP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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GENERAL INCRMATION: William of al.

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC005

CURRENT APPLICATION NUMBER: US/09/764,877

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.5%; Score 19; DB 10; Length 4656;
.00.0%; Pred. No. 12;
                                Length 461;
                                                                                          Indels
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWRARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,874
FILING DATE: 08-Feb-2001
CLASSIFICATION: <UNKNOWN>
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                                   Query Match 0.5%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 9.5 Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. No. 12;
tive 0; Mismatches
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FILING DATE: 05-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                         Sequence 2690, Application US/09764877 Patent No. US20020147140A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wassenegger, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3567 TATATATGTAATAGGGTG 3585
                                                                                                                                               629 TCATATGAAAATATATGGC 647
                                                                                                                                                                                                   56 TCATATGAAATATATGGC 38
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CONGANISM: Homo sapiens
US-09-764-877-2690
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                                                                                                                                                                                                                                                                                     RESULT 13
US-09-764-877-2690
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LENGTH: 4656
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SEQUENCE 11009, ASPLICATION US/09864761

SEQUENCE 11009, ASPLICATION US/09864761

SEQUENCE 11009, ASPLICATION US

SEQUENCE 11009, ASPLICATION US

SEQUENCE 11009, ASPLICATION US

APPLICANT: RANK, DAVIG K.

TITLE OF INVERTION: GENE SEXMED-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVERTION: GENE SEXMED-SEXMED ANALYSIS BY MICROARRAY CORRENT PELLOAD NUMBER: 2007-202-312

PRIOR FILED DAVIG NUMBER: 2007-202-326

PRIOR APPLICATION NUMBER: 2000-202

PRIOR APPLICATION NUMBER: 2000-203

PRIOR APPLICATION NUMBER: 2000-203

PRIOR PLIES DAVIE: 2000-2
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                                   Gaps
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EXPRESSED IN FETAL LIVER, SIGNAL = 0.96
EXPRESSED IN BONE MARNOW, SIGNAL = 0.73
EXPRESSED IN PLACENTA, SIGNAL = 0.96
EXPRESSED IN BRAIN, SIGNAL = 0.79
EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
                                   Indels
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SOFTWARE: Annomax Sequence Listing Engine vers, 1.1
SEQ ID NO 11608
LENGTH: 461
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     ed. No. 9;
Mismatches
     Pred. No.
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO ACCO6204.1
OTHER INFORMATION: EXPRESSED IN LUNG, S.
OTHER INFORMATION: EXPRESSED IN FETAL L.
OTHER INFORMATION: EXPRESSED IN PLACENT
OTHER INFORMATION: EXPRESSED IN PLACENT
OTHER INFORMATION: EXPRESSED IN BRAIN,
OTHER INFORMATION: EXPRESSED IN BRAIN,
US-09-864-761-11608
Best Local Similarity 100.0%; P
Matches 19; Conservative 0;
                                                                                    TCTTCTTATTTGAAGGCTT 428
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Sequence 11283, Application US/09864761

Sequence 11283, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Rankenger, Wensheng

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT PELLING DATE: 2000-05-20

PRIOR FILING DATE: 2000-05-26

PRIOR PELLING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 69/632,366

PRIOR PELLING DATE: 2000-06-36

PRIOR PELLING DATE: 2000-06-36

PRIOR FILING DATE: 2000-06-36

PRIOR FILING DATE: 2000-06-37

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Fatent No. US2020123237A1
Fatent No. US2020123237A1
FAPLICANT: APPLICANT: Adlate, Paul A.
APPLICANT: Adlate, Paul A.
APPLICANT: BAIlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF COVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE FASTSEQ for Windows Version 4.0
SEQ ID NO 4817
LENGTH: 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 385; 32;
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                                                                                             TYPE: DNA
CAGANISM: Bos taurus
ORGANISM: Bos taurus
OCHER INFORMATION: Clone ID: 06-LIB34-055-Q1-E1-B5
US-09-960-352-1347
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32;
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Pred. No.
           2001-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.5%;
                                                                                                                                                                                                                                                                                                                  263 TITTTTTTTTTATCT 246
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         CURRENT FILING DATE: 2001-(NUMBER OF SEQ ID NOS: 15112 SEQ ID NO 1347 LENGTH: 358
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Best Local Similarity 100.(
Matches 18; Conservative
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CORGANISM: Homo sapien
US-09-867-701-4817
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US-09-864-761-11283/c
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US-09-867-701-4817
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Fatent No. US20020013958A1

GENERAL INFORMATION:

APPLICANT: Lalgudi, Raghunath V.

APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNOCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING

FILE REFERENCE: PL-0012-1 CON

CURRENT APPLICATION NUMBER: US/09/923,876

CURRENT FILING DATE: 1090-04-21

FRIOR FILING DATE: 1999-04-21

FRIOR PELING DATE: 1999-04-21

FRIOR PELING DATE: 1999-05-05

NUMBER OF SEQ ID NOS: 6332

SEQ ID NO 1838

LENGTH: 256
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Patent No. US2002013713941
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FOR TOPE MOLECULES ASSOCIATED WITH LACTATION AND FILE REFERENCE: 16511.006/37-21(10299)
CURRENT APPLICATION NUMBER: US/09/960,352
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; OTHER INFORMATION: Incyte ID No. US20020013958A1 700159613H2
US-09-923-876-1838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 256;
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                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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25;
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100.0%; Pred. No. 25;
ive 0; Mismatches
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REFERENCE/DOCKET NUMBER: MPG-1
TELECOMMUNICATION INFORMATION:
TELEPHONS: 1212-596-9000
TELEFAX: 212-596-9000
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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100.0%; Pred. No.
tive 0; Mismatci
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SEQUENCE DESCRIPTION: /desc = "primer";
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-782-874-9
                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                      3615 GACTACCTTTTGTCTTTA 3632
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Best Local Similarity 100.09
Matches 18; Conservative
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Best Local Similarity 100.0
Matches 18; Conservative
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US-09-923-876-1838/c
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COTHER INFORMATION: D equals a,t,g, or C NAME/KEY: misc feature LOCATION: (134)
COTHER INFORMATION: D equals a,t,g, or C NAME/KEY: misc feature LOCATION: (135)
COTHER INFORMATION: D equals a,t,g, or C NAME/KEY: misc feature LOCATION: (138)
COTHER INFORMATION: D equals a,t,g, or C NAME/KEY: misc feature LOCATION: (186)
COCATION: (186)
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
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LOCATION: (325)
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NAME/KEY: misc feature
LOCATION: (366)
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LOCATION: (405)
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NAME/KEY: misc feature
LOCATION: (369)
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                                                                                                                                                                              LOCATION: (13)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (79)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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LOCATION: (391)
                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                    NAME/KEY: misc feature
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LOCATION: (411)
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| Sequence 8123, Application US/09783590
| Patent No. US20020110850A1
| GENERAL INFORMATION:
| APPLICANT: Dillon, Patrick J.
| APPLICANT: Haseltine, William A.
| APPLICANT: Haseltine, William A.
| APPLICANT: Ruben, Steven M.
| FILE REFERENCE: PO-16.2cl
| CURRENT APPLICATION NUMBER: US/09/783,590
| CURRENT FILING DATE: 1995-04-12
| PRIOR FILING DATE: 1995-04-12
| PRIOR FILING DATE: 1994-11-21
| PRIOR FILING DATE: 1994-11-21
| NUMBER OF SEQ ID NOS: 12485
| SOFTWARE: Patentin Ver. 2.0
| TYPE: DNA
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARKOW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.86
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.86
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.4
US-09-864-761-11283
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/USO1/00667

PRIOR APPLICATION NUMBER: PCT/USO1/00664

PRIOR APPLICATION NUMBER: PCT/USO1/00669

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

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PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/USO1/00670

PRIOR APPLICATION NUMBER: PCT/USO1/00670

PRIOR APPLICATION NUMBER: PCT/USO1/00670

PRIOR PILING DATE: 2000-09-21

PRIOR FILING DATE: 2000-06-30

PRIOR PILING DATE: 2000-06-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR FILING PRIOR PRIOR PR
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US-09-783-590-8123/c
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APPLICANT: Obligate, Kari L.
APPLICANT: 2yskind, Judith W.
APPLICANT: Mall, Daniel
APPLICANT: Transley, Abn D.
APPLICANT: Transley, Robert T.
APPLICANT: Vamamoto, Robert T.
APPLICANT: Vamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: PROXARYOTES
TITLE OF INVENTION: 10000 11A
CURRENT APPLICATION NUMBER: 60,719,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60,200,107
PRIOR APPLICATION NUMBER: 60,200,727
PRIOR APPLICATION NUMBER: 60,200,727
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.5%; Score 18; DB 10; Best Local Similarity 100.0%; Pred. No. 35; Matches 18; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 6/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 66/257,931
PRIOR APPLICATION NUMBER: 66/269,308
PRIOR APPLICATION NUMBER: 66/269,308
PRIOR PLING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7347
                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (895)
COTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (928)
COTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (970)
COTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (992)
COTHER INFORMATION: n equals a,t,g, or c
LOCATION: (902)
LOCATION: (1001)
LOCATION: (1001)
COTHER INFORMATION: n equals a,t,g, or c
USCATION: (1001)
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Helicobacter pylori
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; LOCATION: (1)...(1467)
US-09-815-242-7347
                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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US-09-815-242-7347
    SEQ ID NO 176
LENGTH: 1016
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Patent No. US20020055527A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
ITILE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.5%; Score 18; DB 10; Length 500; 100.0%; Pred. No. 33; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                             LOCATION: (455)
OTHER INFORMATION: n equals a,t,g, or c
NAME/ERT: misc feature
LOCATION: (461)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
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NAME/KET: misc feature
LOCATION: (487)
OTHER INFORMATION: n equals a,t,g, or c
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OTHER INFORMATION: n equals a,t,g, or of the control of the contr
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature LOCATION: (480)
                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (467)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LOCATION: (468)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
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LOCATION: (479)
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                                                                    LOCATION: (433)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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LOCATION: (495)
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Matches 18; Conserve
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US-09-925-299-176/c
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Sequence 328, Application US/09841132

Patent No. US2002066848A1

Sether No. US2002066848A1

SPAPLICANT: Bhatia. Ajay

APPLICANT: Bratia. Ajay

APPLICANT: Probst, Peter

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DAGNOSIS OF CHLAMYDIAL INFECTION

FILE REFERENCE: 21012.469C8

CURRENT FILING DATE: 2001-04-23

NUMBER OF SEQ ID NOS: 599

SOFTWARE: PastSEQ for Windows Version 3.0/4.0

SEQ ID NO 328

LENTH: 2148
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US-10-007-693-80/c
US-10-007-693-80/c
US-20020146776A1
Sequence 80, Application US/10007693
Patent No. US20020146776A1
SERVERAL INFORMATION:
APPLICANT: Bhatia, Alay
TITLE OF INVENTION: OMPOUNDS AND METHODS FOR TREATMENT;
TITLE OF INVENTION: OMPOUNDS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.515c2
CURRENT APPLICATION NUMBER: US/10/007,693
CURRENT FILING DATE: 2001-12-05
WUMBER OF SEQ ID NOS: 157
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0.5%; Score 18; DB 10; Length 2148;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                        Length 1944;
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                                                                                                                                                        DB 10;
38;
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0.5%; Score 18; DB
Best Local Similarity 100.0%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Chlymadia trachomatis
US-09-841-132-328
                                               TYPE: DNA
CRGANISM: Arabidopsis thaliana
US-09-887-576-619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2603 ATGCAGTACTCTAAGAAA 2586
                                                                                                                                                                                                                                                            1189 GTATGATGGGTATCTCAA 1206
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                                                                                                                                                                                                                                                                                        RESULT 24
US-09-841-132-328/c
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LENGTH: 3048
SEQ ID NO 619
LENGTH: 1944
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                                                                             Gaps
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APPLICANT: Brown, D.
APPLICANT: Chang, H.
APPLICANT: Chang, H.
APPLICANT: APPLICANT: APPLICANT: Han, B.
APPLICANT: Mang, X.
APPLICANT: Cooper, Bret
APPLICANT: Cooper, Bret
CURRENT APPLICATION NUMBER: US/09/887,576
CURRENT APPLICATION NUMBER: US 60/213,848
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 875
SOFTWARE: FESTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Chang, H.
APPLICANT: Chang, H.
APPLICANT: Ann, B.
APPLICANT: Han, B.
APPLICANT: Wang, A.
APPLICANT: Wang, A.
APPLICANT: Word: Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
FILE REPERENCE: 1360.001051
CURRENT APPLICATION NUMBER: US 60/213,848
PRIOR PILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
SPRIOR FILING DATE: 2000-06-23
SOFTWARE: FastSEQ for Windows Version 4.0
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                      Query Match

0.5%; Score 18; DB 10; Length 1467;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 18; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                           Sequence 629, Application US/09887576
Patent No. US20020144047A1
GENERAL INFORMATION:
APPLICANT: Budworth, P.
APPLICANT: Brown, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 619, Application US/09887576; Patent No. US20020144047A1; GENERAL INFORMATION: APPLICANT: Budworth, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-887-576-629
                                                                                                                            3628 CTTTAAAACTGCATGAAG 3645
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                                                                                                                                                                                                                                                            RESULT 22
US-09-887-576-629/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-887-576-619/c
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PRIOR PILING DATE: 1997-10-28
PRIOR PAPLICATION NUMBER: 60/063734
PRIOR PILING DATE: 1997-10-29
PRIOR PAPLICATION NUMBER: 60/063870
PRIOR PILING DATE: 1997-10-29
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-11-34
PRIOR PILING DATE: 1997-12-12
PRIOR PILING DATE: 1997-12-12
PRIOR PILING DATE: 1997-12-12
PRIOR PILING DATE: 1997-12-13
PRIOR PILING DATE: 1997-12-13
PRIOR PILING DATE: 1998-03-10
PRIOR PILING DATE: 1998-03-3-10
PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1998-04-02
PRIOR PILING DATE: 1998-04-02
PRIOR PILING DATE: 1998-04-02
PRIOR PILING DATE: 1998-04-03
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APPLICANT: Watenabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILER REPERENCE: P3430Nc1.
CURRENT APPLICATION NUMBER: US/10/052,586
CURRENT PILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063250
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-24
                                                                                                                                                                                                                             APPLICANT: Howes, Steven H.
APPLICANT: Resnick, Richard J.
APPLICANT: Resnick, Richard J.
APPLICANT: Gulukota, Kamalakar
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
TILE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6403
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICANTON NUMBER: 60/195,582
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 598
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 162
LENGTH: 3760
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0.5%; Score 18; DB 10;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 18; Conservative 0; Mismatches 0;
                                           Sequence 162, Application US/09822849A
Patent No. US20020045170A1
GENERAL INFORMATION:
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Howes, Steven H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 453, Application US/10052586 Patent No. US20020127584a1 GENERAL INFORMATION:
APPLICANT: Baker Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/063486
FILING DATE: 1997-10-21
APPLICATION NUMBER: 60/063540
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APPLICATION NUMBER: 60/063541
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Godowski, Paul J.
Gurney, Austin L.
Pan, James
Smith, Victoria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Homo sapiens
US-09-822-849A-162
                       US-09-822-849A-162/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-052-586-453/c
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APPLICANT:
RESULT 26
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PRIOR APPLICATION NUMBER: 0.008414
PRIOR APPLICATION NUMBER: 0.008463
PRIOR APPLICATION NUMBER: 0.008464
PRIOR APPLICATION NUMBER: 0.008464
PRIOR PLILING DATE: 1998 0.515
PRIOR APPLICATION NUMBER: 0.008539
PRIOR PLILING DATE: 1998 0.515
PRIOR PLILING DATE: 1998 0.512
PRIOR PLILING DATE: 1998 0.512
PRIOR PLILING DATE: 1998 0.512
PRIOR PLILING DATE: 1998 0.528
PRIOR PLILING DATE: 1998 0.609
PRIOR PRILING DATE: 1998 0.609
PRIOR PRILING DATE: 19
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Gaps
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Gallwitz, Wolf
Gallwitz, Wolf
TITLE OF INVENTION: SCREENING ASSAY FOR THE IDENTIFICATION
OF AGENTS WHICH INHIBIT CANCER
METASTASIS TO BONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 12; Length 3781; 40;
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,445
FILING DATE: 11-Jun-2001
CLASSIFICATION NUMBER: 08/915,868
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/915,868
FILING DATE: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
NAME: Highlander, Steven L.
RECISTRATION NUMBER: 37,642
RETERENCE/DOCKET NUMBER: 0512674
TELEFAX: 512/4748-3000
TELEFAX: 512/474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.5%; Score 18; DB 100.0%; Pred. No. 40; ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
PRIOR APPLICATION NUMBER: 60/088863
PRIOR FILING DATE: 1998-06-11
PRIOR FILING DATE: 1998-06-11
PRIOR FILING DATE: 1998-06-11
PRIOR PAPPLICATION NUMBER: 60/08900
PRIOR PAPPLICATION NUMBER: 60/089105
PRIOR PAPLICATION NUMBER: 60/089105
PRIOR PELING DATE: 1998-06-12
PRIOR PELING DATE: 1998-06-16
PRIOR PELING DATE: 1998-06-16
PRIOR FILING DATE: 1998-06-16
PRIOR FILING DATE: 1998-06-16
PRIOR FILING DATE: 1998-06-16
PRIOR PILING DATE: 1998-06-17
PRIOR PAPLICATION NUMBER: 60/089518
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR PELING DATE: 1998-06-17
PRIOR PELING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR PELING DATE: 1998-06-17
PRIOR PELING DATE: 1998-06-17
PRIOR PELING DATE: 1998-06-17
PRIOR PELING DATE: 1998-06-17
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STATE: TEXAS
COUNTRY: USA
ZIP: 77210
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09879445; Patent No. US20020061509A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 4348 base par
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1159 GGGCCTTGAGGAAGGAGG 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3267 GGGCCTTGAGGAAGGAGG 3284
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Best Local Similarity 100.0
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 28
US-09-879-445-1
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KESDUI. 3754

1 Sequence 3754, Application US/09923876

2 Sequence 3754, Application US/09923876

3 Sequence 3754, Application US/09923876

5 Patent No. US20202013958A1

5 CENERAL INFORMATION:

APPLICANT: Lalguidi, Raghunath V.

APPLICANT: Sherman, Bradlay K.

TILLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING

FILE REFERENCE: PL-0012-1 CON

CURRENT FILLING DATE: 2001-08-06

PRIOR APPLICATION NUMBER: 09/298,329

PRIOR FILLING DATE: 1999-04-21

PRIOR PLICATION NUMBER: 60/085,331

PRIOR FILLING DATE: 1998-06-05

NUMBER OF SEQ ID NOS: 6332

SOFTWARE: PERL PROGram

SEQ ID NO 3754

LENTH: 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 170834;
                                  Sequence 7, Application US/09835232;
Patent No. US2002009848941;
GENERAL INFORMATION:
APPLICANT: Leader, Philip
TITLE OF INVENTION: Benjamin
TITLE OF INVENTION: ROBAIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
TITLE OF INVENTION: ROBAIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
TITLE OF INVENTION: AND USES THEREOF;
FILE REFERENCE: 00383/052002
CURRENT APPLICATION NUMBER: US/09/835,232
CURRENT APPLICATION NUMBER: US 60/196,811
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 170834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020013958A1 700453751H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.5%; Score 17; DB 10; Length 150;
100.0%; Pred. No. 99;
tive 0; Mismatches 0; Indels
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red. No. 59;
Mismatches 0;
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) COCATION: 115, 118, 121, 129, 138, 147

) CHER INFORMATION: a, t, c, g, or other

US-09-923-876-3754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; NAME/KEY: misc_feature
LOCATION: (1)...(170834)
; OTHER INFORMATION: n= A,T,C, or G
US-09-835-232-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 36324 GTTTGCAGTGTTGGGAAG 36307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    523 GTTTGCAGTGTTGGGAAG 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2464 TCCATGCTTGCATCCTG 2480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.C
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                          Sequence 3657, Application US/09764877

Patent No. US20020147140A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005

CURRENT APPLICATION NUMBER: US/09/764,877

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper

NUMBER OF SEQ ID NOS: 4031

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3657

LENGTH: 32192
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red. No. 53;
Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.5%; Score 18; DB 10; Length 32192;
100.0%; Pred. No. 51;
tive 0; Mismatches 0; Indels 0
                                                                            Length 4348;
                                                                                                                            0; Indels
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| Sequence 4, Application US/09927091
| Patent No. US20020119541A1
| GENERAL INFORMATION:
| APPLICANT: KILLARY, ANN
| APPLICANT: LOTT, STEVE
| APPLICANT: LOTT, STEVE
| APPLICANT: CHANDLER, DAWN
| TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
| TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
| CURRENT FILING DATE: 2010-08-09
| CURRENT FILING DATE: 2010-08-09
| PRIOR FILING DATE: 2000-08-23
| PRIOR FILING DATE: 2000-08-23
| PRIOR APPLICATION NUMBER: 60/225,033
| PRIOR APPLICATION NUMBER: 60/225,033
| PRIOR PILING DATE: 2000-08-10
| NUMBER OF SEQ ID NOS: 9
| SOFTWARE: PATENTIN VET: 2.1
                                                                       DB 10;
41;
                                                                       Query Match 0.5%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 41; Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18;
Pred. No.
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-879-445-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.5%; SC.
ilarity 100.0%; P.
Conservative 0;
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                                                                                                                                                                                                        4180 AGAATTTTTTTTTTT 4197
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                                                                                                                                                                         576 AGAAATTTTTTTTTT 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 TTAAGTCATTCTTAGAGA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: Homo sapiens
US-09-764-877-3657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 18; Conserva
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US-09-927-091-4
                                                                                                                                                                                                                                                                                                  RESULT 29
US-09-764-877-3657
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Gaps

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Gaps

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Matches

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APPLICANT: Lalgudi, Raghunath, V.
APPLICANT: Ito, Laura, Y.
APPLICANT: Ito, Laura, Y.
ITILE OF INVENTION: BOLINUCLECTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
ITILE REPERENCE: PL-0009 US.
CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR ELLING DATE: 40F11 21, 1998
NUMBER OF SEQ ID NOS: 6207
SOFTWARE:
SEQ ID NO 1096
LENGTH: 274
TYPP.
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GENERAL INFORMATION:
APPLICANT: Pan, Sharron G.
APPLICANT: Rank, David K.
APPLICANT: Harzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION WINBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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NAME/KEY: misc_feature
CTHER INFORMATION: Incyte ID No. US20010051335A1 700343770H1
US-09-294-093B-1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 274;
                                                                                                                                                                                                                                                                                                                                                                                   Length 269;
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.5%; Score 17; DB 10; L. Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 17; Conservative 0; Mismatches 0;
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            CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 09/754,853
PRIOR FILING DATE: 2001-01-05
PRIOR FILING DATE: 2001-01-13
PRIOR PLICATION NUMBER: US 09/760,427
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-05-15
NUMBER: OF SEQ ID NOS: 4593
SEQ ID NO 41
LENGTH: 269
FILE REFERENCE: 38-10(52679)A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 TTTTTTCTTTTATCT 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        582 TITITITITITITY 598
                                                                                                                                                                                                                                                                                          TYPE: DNA
CORGANISM: Glycine max
US-09-969-373-41
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Best Local Similarity
Matches 17; Conserv
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ORGANISM: Zea mays
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US-09-294-093B-1096
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                                                      Sequence 9084 Application US/09878574

Sequence 9084 Application US/09878574

Patent No. US2002011054881

GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.

APPLICANT: La Rosa, Thomas J.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: NUMBER: US/09/878,574

CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT FILING DATE: 1990-06-14

NUMBER OF SEQ ID NOS: 15775

LENGTH: LENGTH: 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7593, Application US/09878574

Sequence 7593, Application US/09878574

Patent No. US20020110548A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

CURRENT FILING DATE: 38-21 (15401)B

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 09/333,535

PRIOR APPLICATION NUMBER: 09/333,535

PRIOR APPLICATION NUMBER: 09/333,535

PRIOR FILING DATE: 1999-06-14

NUMBER OF SEQ ID NOS: 15775

SEQ ID NOS: 15775
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US-09-969-373-41/C
US-09-969-373-41/C
Sequence 41, Application US/09969373
Fatent No. US20020133852A1
GENERAL INFORMATION:
APPLICANT: Effertz. Roger J.
APPLICANT: Hauge, Brian M.
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.5%; Score 17; DB 10; Length 25
100.0%; Pred. No. 1e+02;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
CRGANIEN: Glycine max
CTER INFORMATION: Clone ID: 701100084H2
US-09-878-574-7593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
SCRANLEN Glycine max
OTHER INFORMATION: Clone ID: 701102066H1
US-09-878-574-9084
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Best Local Similarity 100.
Matches 17; Conservative
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                                              US-09-878-574-9084
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OTHER INFORMATION: Genbank Accession No. US20020119462A1 AI045253
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US-09-880-107-706
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                                                                           TITLE OF INVESTIGATION: Gene Expression Profiles in Liver Cancer FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-66-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 706
LENGTH: 329
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mark
APPLICANT: Denter, Mark
APPLICANT: Gastle, Arthur
APPLICANT: MOUBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR PELING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-12
PRIOR FILING DATE: 2001-05-13
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-13
PRIOR PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-07-03
PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR
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1.1e+02;
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; LOCATION: (1)..(353)
; OTHER INFORMATION: n = a or c or g or
US-09-917-800A-623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.5%; Some Best Local Similarity 100.0%; P. Matches 17; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           578 AAATTTTTTTTTT 594
                                                       Gene Logic, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 39
US-09-917-800A-623/c
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N: EXPRESSED IN FETAL LITER, SIGNAL = 0.95
N: EXPRESSED IN PETAL LITER, SIGNAL = 1
N: EXPRESSED IN HELLOO, SIGNAL = 1.7
N: EXPRESSED IN HELLO, SIGNAL = 2.5
N: EXPRESSED IN LUNG, SIGNAL = 1.2
N: EXPRESSED IN LUNG, SIGNAL = 1.2
N: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
N: MY HIT: U52951, EVALUE 1.00e-108
N: EXT HUMAN HIT: BF025728.1, EVALUE 1.00e-108
N: SWISSPROT HIT: 015910, EVALUE 6.00e-13
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PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 02/05/32,366
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PIL
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; Sequence 706, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
APPLICANT: Scherf, Useph G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3712 AGTITCAICTITCTICT 3728
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Best Local Similarity 100.
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ORGANISM: Homo sapiens
FEATURE;
OTHER INFORMATION: MAP T
OTHER INFORMATION: EXPRE
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OTHER INFORMATION: CTHER INFOR
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Gaps

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# PATENT NO. USJOURGAVEOUSAL

# PATENT NO. USJOURGAVEOUSAL

# APPLICANT: Fenn, Sharron G.

# APPLICANT: Rank, David K.

# APPLICANT: Rank, David K.

# APPLICANT: Hanzel, David K.

# APPLICANT: Hanzel, David K.

# APPLICANT: Chen, Wensheng

# TITLE OF INVENTION: GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO.

# TITLE OF INVENTION: GENOME EXPRESSION ANALYSIS BY MICROARRAY

# TITLE OF INVENTION: GENOME ACOUNT OF A PARTICATION NUMBER: US 60/180,312

# PRIOR APPLICATION NUMBER: US 60/207,456

# PRIOR FILING DATE: 2000-08-03

# PRIOR FILING DATE: 2000-08-03

# PRIOR APPLICATION NUMBER: US 60/232,366

# PRIOR APPLICATION NUMBER: US 60/236,359

# PRIOR APPLICATION NUMBER: US 60/236,359

# PRIOR FILING DATE: 2000-09-02

# PRIOR FILING DATE: 2000-09-02

# PRIOR FILING DATE: 2000-09-02

# PRIOR FILING DATE: 2000-09-03

# PRIOR APPLICATION NUMBER: PCT/US01/00666

# PRIOR APPLICATION NUMBER: PCT/US01/00666
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0.5%; Score 17; DB 10; Length 368; 100.0%; Pred. No. 1.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                    Sequence 7289, Application US/09974300

Batent No. US20020146721A1

GENERAL INFORMATION:

APPLICANT: Berka. Randy M.

TITLE OF INVENTION: Methods For Monitoring Multiple Gene

TITLE OF INVENTION: Methods For Monitoring Multiple Gene

TITLE OF INVENTION: Muthers in Sports

TITLE OF INVENTION: Muther: US/09/974,300

CURRENT APPLICATION NUMBER: US/09/974,300

CURRENT FILING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: 60/289

PRIOR APPLICATION NUMBER: 60/2995

PRIOR APPLICATION NUMBER: 60/279,526

PRIOR PLING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 8481

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.5%; Score 17; DB 10; I Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 30520, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LCCATION: (1)...(387)
COTHER INFORMATION: n = A,T,C or G
US-09-974-300-7289
                                                                       116 TTTATTTGCATAACTT 132
                                                                                            578 AAATTTTTTTTTTT 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 AAATTTTTTTTTT 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Bacillus clausii
   Query Match 0.55
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 42
US-09-864-761-30520/c
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US-09-974-300-7289/c
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                    Length 353;
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ORGANIZM: Homo sapiens
FORGANIZM: HOMO sapiens
OTHER INFORMATION: MAP TO AF130350.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
                                                       0; Indels
                    0.5%; Score 17; DB 10; I 100.0%; Pred. No. 1.1e+02;
                                                     0; Mismatches
                                                                                        578 AAATTTTTTTTTT 594
                                                                                                              64 AAATTTTTTTTTT 48
                                   Local Similarity 100.
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                      Query Match
                                                     Matches
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Sequence 1095, Application US/09867550

Fatent No. US2020208206A1

Fatent No. US20202082206A1

APPLICANT: Leach, Martin D.

APPLICANT: Conley, Pamela

APPLICANT: Topper. James

APPLICANT: Topper. James

TITLE OF INVENTION: Thereby
FILE OF INVENTION: Thereby

TITLE OF INVENTION: Thereby

FILE REFREDENCE: 21402-013 (Cura-313)

CURRENT APPLICATION NUMBER: US/09/867,550

FILE OF ELING DATE: 2001-09-20

PRIOR FILING DATE: 2000-05-30

NUMBER OF SEQ ID NOS: 2125

SEQ ID NO 1095

ELENT: APPLICATION NUMBER: US/080427

PRIOR FILING DATE: AND NOS: 2125

SEQ ID NO 1095

ELENT: APPLICATION NUMBER: US/080427

PRIOR FILING DATE: AND NOS: 2125

SEQ ID NO 1095

ELENT: APPLICATION NUMBER: US/080427

PRIOR FILING DATE: APPLICATION NUMBER: US/0804427

PRIOR FILING DATE: APPLICATION NU
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Sequence 401, Application US/09983965
Sequence 401, Application US/09983965
Sequence 401, Application US/09983965
Sequence 401, Application US/09983965
Setent INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEE AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: NUCLEE AND FAT DEPOSITION
FILLE REPERBANCE: 37-21(10297)C
CURRENT APPLICATION NUMBER: US/09/983,965
CURRENT FILING DATE: 2001-10-26
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
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                                                                                                                                       Length 391;
                                                                                                                                                                                                                          0; Indels
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                                                                                                                         Query Match
0.5%; Score 17; DB 10; 1
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                            754 CITITAAGGAAACICCIG 770
                                                                                                                                                                                                                                                                                                                                                                      118 CTTTAAGGAAACTCCTG 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 5912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (336)..(359)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 45
US-09-867-550-1095
                                           US-09-563-817-878
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LENGTH: 406
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Sequence 878, Application US/09563817
Sequence 878, Application US/09563817
GENERAL INFORMATION:
APPLICANT: Dambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILLE REPERENCE: LEX-0021-USA
CURRENT APPLICATION NUMBER: US/09/563,817
CURRENT APPLICATION NUMBER: US 60/132,343
PRIOR APPLICATION NUMBER: US 60/132,343
PRIOR APPLICATION NUMBER: US 60/132,343
PRIOR FILING DATE: 1999-05-04
NUMBER OF SEQ ID NOS: 1008
SOFTWARE: FRSESEQ for Windows Version 4.0
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OTHER INFORMATION: EXPRESSED IN PLACENRA, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
OTHER INFORMATION: NT HIT: AL163248.2, EVALUE 0.00e+00
OTHER INFORMATION: ST. HUMAN HIT: AA001786.1, EVALUE 3.00e-84
US-09-864-761-30520
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0.5%; Score 17; DB 10; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: FCT/USO1/00664
PRIOR APPLICATION NUMBER: FCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR PLICATION NUMBER: PCT/USO1/00668
PRIOR PLICATION NUMBER: PCT/USO1/00668
PRIOR PLICATION NUMBER: PCT/USO1/00668
PRIOR PRIOR DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00663
PRIOR PRIOR DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00662
PRIOR PRIOR DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00661
PRIOR PLICATION NUMBER: US 60/234,687
PRIOR PLICATION NUMBER: US 99/608,408
PRIOR FILING DATE: 2000-09-21
PRIOR PLICATION NUMBER: US 99/774,203
PRIOR PLICATION NUMBER: US 90/774,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: MAP TO AF130350.1
OTHER INFORMATION: EXPRESSED IN HELA,
OTHER INFORMATION: EXPRESSED IN PLACE
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LOCATION: (1)...(391)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 TITATITIGCATAACIT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-563-817-878/c
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LENGIH: 391
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Sequence 14966, Application US/09864761
Pattent No. US20020048763A1
GENERAL INFORMATION:
GENERAL INFORMATION: Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Hancel, David K.
APPLICANT: Hancel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXPRESSED IN BT474, SIGNAL = 2.9
EXPRESSED IN FETAL LIVER, SIGNAL = 0.95
EXPRESSED IN PLACEMEA, SIGNAL = 1
EXPRESSED IN HBL100, SIGNAL = 1.7
EXPRESSED IN HBL100, SIGNAL = 1.5
EXPRESSED IN LUNG, SIGNAL = 1.5
EXPRESSED IN LUNG, SIGNAL = 1.2
EXPRESSED IN BONE MARROW, SIGNAL = 1.2
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SEQTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 14986
LENGHH: 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THILE OF INTENTION GENE EXPRESSION ANALYSIS THE REPRENCE: ABOOM COS 23 CURRENT APPLICATION NUMBER: US/09/664,761 CURRENT FILING DATE: 2000-05-23 PRIOR PELLOATION NUMBER: US/09/664,761 PRIOR PLING DATE: 2000-02-04 66/180,312 PRIOR PLING DATE: 2000-05-26 PRIOR PLING DATE: 2000-05-26 PRIOR PLING DATE: 2000-05-26 PRIOR PLING DATE: 2000-05-26 PRIOR PLING DATE: 2000-10-04 PRIOR PLING DATE: 2000-10-04 PRIOR PLING DATE: 2000-10-04 PRIOR PLING DATE: 2000-10-04 PRIOR PLING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/US01/00663 PRIOR PLING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/US01/00661 PRIOR PLING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/US01/00661 PRIOR PLING DATE: 2001-01-30 PRIOR PLING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/US01/00661 PRIOR PLING DATE: 2001-01-30 PRIOR PRIOR PLING DATE: 2001-01-30 PRIOR PRIOR PRIOR PRIOR PRIO
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OTHER INFORMATION: MAP TO AC006323.3
OTHER INFORMATION: EXPRESSED IN FETAL I.
OTHER INFORMATION: EXPRESSED IN FETAL I.
OTHER INFORMATION: EXPRESSED IN PLACENY:
OTHER INFORMATION: EXPRESSED IN HELLO.
OTHER INFORMATION: EXPRESSED IN HELA. S.
OTHER INFORMATION: EXPRESSED IN LUNG. S.
OTHER INFORMATION: EXPRESSED IN BONE MAR US-09-864-761-14986
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PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                                                        1954 AAAGTTAGATGTCCTTG 1970
                                                                                                       388 AAAGTTAGATGTCCTTG 404
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ORGANISM: Homo sapiens
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Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
CURRENT APPLICANTON NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
LENGTH: 419
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Patent No. US20020142981A1

Sequence 2.07.60. Application US/09880107

Patent No. US20020142981A1

September 1. NorMay 1. N
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US-09-880-107-2705
                                                                                                                                 Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 419;
; OTHER INFORMATION: Wherein any n is one of a or t or c or g us-09-867-550-1095
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                                                                                                                    Query Match 0.5%; Score 17; DB 10; Length 41 Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.5%; Score 17; DB 10; Length 41 100.0%; Pred. No. 1.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: CLone ID: 46-LIB3057-002-Q1-K1-D6
US-09-960-352-10698
                                                                                                                                                                                                                                                                                        1508 GATAAAAATTTGAATT 1524
                                                                                                                                                                                                                                                                                                                                   580 ATTITITITITITIAT 596
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Best Local Similarity 100.
Matches 17; Conservative
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Best Local Similarity
Matches 17; Conserva
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Sequence 2934, Application US/09983965.

Sequence 2934, Application US/09983965.

Patent No. US20020137160A1

GENERAL INFORMATION:

APPLICANT: Waster, Wesley C.

APPLICANT: Byatt, John C.

APPLICANT: Byatt, John C.

APPLICANT: Mathialagan, Nagappan

APPLICANT: Mathialagan, Nagappan

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

TITLE OF INVENTION: NUMBER: US/09/983,965

CURRENT APPLICATION NUMBER: US 09/465,231

PRIOR APPLICATION NUMBER: US 60/113,678

PRIOR PILING DATE: 1998-12-15

PRIOR PILING DATE: 1998-12-17

NUMBER OF SEQ ID NOS: 5912
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                                                                                                                                                                                                      Length 436;
                                                                                                                                                                                                                                                                 0; Indels
                      OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6 CTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.6 CTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.8 US-09-864-761-2826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: CLone ID: 19-LIB3058-019-Q1-K1-E11 US-09-983-965-2934
                                                                                                                                                                                                      Query Match 0.5%; Score 17; DB 10; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6, 2002, 03:42:03
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Job time: 850 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 50
US-09-983-965-2934/c
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Sequence 2855, Application US/09664761

PRETER NO. USSO0000048763A1

GENERAL INFORMATION:

APPLICANT: Beni, Sharton o.

APPLICANT: WINNER: COUNTY OR DEPRIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF PRIVENTING DATE: 2001-05-90 (64.761)

CURRENT FILING DATE: 2001-05-90 (64.761)

PRIOR FILING DATE: 2000-05-90 (64.761)

PRIOR FILING DATE: 2000-05-90 (64.761)

PRIOR FILING DATE: 2000-05-90 (66.762)

PRIOR FILING DATE: 2000-05-90 (66.762)

PRIOR FILING DATE: 2000-05-90 (66.762)

PRIOR FILING DATE: 2000-10-10 (66.762)

PRIOR FILING DATE: 2000-10-10 (66.762)

PRIOR FILING DATE: 2000-10-10 (66.762)

PRIOR PRIOR PLING DATE: 2000-10-10 (66.762)

PRIOR PLING DATE: 2000-10-10 (66.762)

PRIOR PLING DATE: 2000-10-10 (66.762)

PRIOR PLING DATE: 2000-10-10 (66.762)

PRIOR PLING DATE: 2001-01-10 (66.762)

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core 17; DB 10; Length 430;
red. No. 1.1e+02;
Mismatches 0: 7-7
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OTHER INFORMATION: EXPRESSED IN BEONE MARROW, SIGNAL = 3.6

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.3

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9
                                  Score 17;
Pred. No.
                                  Ouery Match 0.5%; Soc
Best Local Similarity 100.0%; Pi
Matches 17; Conservative 0;
                                                                                                                                                      3712 AGTTTCATCTTTCT 3728
                                                                                                                                                                                            405 AGTTTCATCTTTCT 389
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                    RESULT 49
US-09-864-761-2826
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